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OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 58.6907 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVMTQSLPLVTLGPAS.....CWQGHFFPTFGQTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	112	4	Aae06949 Humanised
2	590	100.0	112	4	Aau09921 Humanised
3	590	100.0	112	5	Abg75530 Humanised
4	590	100.0	112	5	Aao14973 Humanised
5	590	100.0	112	5	Adf98233 Humanised
6	590	100.0	112	8	Adq89234 Humanised
7	590	100.0	112	9	Aeb09507 Humanised
8	584	99.0	114	4	Aae07035 Humanised
9	584	99.0	114	8	Adq89328 Humanised
10	584	99.0	114	9	Aeb09601 Humanised
11	577	97.8	112	4	Aae06950 Humanised
12	577	97.8	112	4	Aau09922 Humanised
13	577	97.8	112	5	Abg75531 Humanised
14	577	97.8	112	5	Adf98234 Humanised
15	577	97.8	112	8	Adq89235 Humanised
16	577	97.8	112	9	Aeb09508 Humanised
17	572	96.9	112	4	Aae07036 Humanised
18	572	96.9	112	4	Aau09925 Humanised
19	572	96.9	112	5	Abg75534 Humanised
20	572	96.9	112	5	Adf98237 Humanised
21	572	96.9	112	8	Adq89329 Humanised
22	572	96.9	112	9	Aeb09602 Humanised
23	572	96.9	112	4	Aae06951 Humanised
24	572	96.6	112	4	Aau09923 Humanised

25	570	96.6	112	5	Abg75532 Humanised
26	570	96.6	112	5	Adf98235 Humanised
27	570	96.6	112	8	Adq89236 Humanised
28	570	96.6	112	9	Aeb09509 Humanised
29	569	96.4	112	8	Adq31290 Humanised
30	566	95.9	112	8	Adq31289 Humanised
31	565	95.8	112	4	Aae06952 Humanised
32	565	95.8	112	4	Aau09924 Humanised
33	565	95.8	112	5	Abg75533 Humanised
34	565	95.8	112	5	Aao14976 Humanised
35	565	95.8	112	5	Adf98236 Humanised
36	565	95.8	112	8	Adq89237 Humanised
37	565	95.8	112	9	Aeb09510 Humanised
38	559	94.7	113	6	Abp58270 Humanised
39	559	94.7	219	6	Abp58272 Humanised
40	559	94.7	239	6	Abp58274 Humanised
41	557.5	94.5	111	5	Aao14977 Humanised
42	554.5	94.0	111	5	Aao14975 Humanised
43	549	93.1	110	5	Aao14974 Humanised
44	542	91.9	132	5	Abg76931 Humanised
45	542	91.9	132	8	Adr88415 Humanised

#### ALIGNMENTS

RESULT 1					
AAE06949					
ID	AAE06949	standard; protein; 112 AA.			
XX	XX				
AC	AAE06949;				
DT	11-SEP-2003	(revised)			
DT	16-OCT-2001	(first entry)			
XX	XX				
DE	Humanised murine ID9 antibody kappa light chain variable region, ID9RKA.				
XX	XX				
KW	Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;				
KW	neuroprotective; immunosuppressive; human immunodeficiency virus;				
KW	HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;				
KW	inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;				
KW	multiple sclerosis; atherosclerosis; restenosis; asthma;				
KW	anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;				
KW	fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;				
KW	inflammatory glomerulopathy; vascular intervention; ID9 antibody;				
KW	neointimal hyperplasia; VK; kappa light chain variable region; ID9RKA.				
XX	XX				
OS	Mus sp.				
OS	Homo sapiens.				
OS	Chimeric.				
XX	XX				
PH	Key	Location/Qualifiers			
FT	Region	23..39			
FT	Region	/label= CDR1			
FT	Region	/note= "Complementarity determining region 1"			
FT	Region	55..61			
FT	Region	/label= CDR2			
FT	Region	/note= "Complementarity determining region 2"			
FT	Region	94..102			
FT	Region	/label= CDR3			
FT	Region	/note= "Complementarity determining region 3"			
XX	XX				
WO	WO200157226-A1.				
PD	09-AUG-2001.				
XX	XX				
PF	02-FEB-2001; 2001WO-US003537.				
XX	XX				
PR	03-FEB-2000; 2000US-00497625.				
XX	XX				
PA	(MILL-) MILLENNIUM PHARM INC.				
XX	XX				
PI	Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;				

XX WPI; 2001-48888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated

XX disorder in a patient, comprises a binding specificity for CCR2, and a

XX non-human antigen binding region and human immunoglobulin.

XX Claim 61; Fig 11; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding

XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),

XX comprising an antigen binding region of non-human origin and at least a

XX portion of an immunoglobulin of human origin. The humanised antibodies

XX are useful for inhibiting the interaction of a cell expressing CCR2. They

XX are useful for inhibiting or treating HIV infection. The proteins of the

XX CCR2-mediated disorders such as inflammatory disorder, autoimmune

XX disorders such as rheumatoid arthritis and multiple sclerosis,

XX atherogenesis and atherosclerosis, and for inhibiting restenosis. They

XX are useful in therapy or diagnosis, and in the manufacture of a

XX medicament for treating CCR-2 mediated disease. They are also useful for

XX treating allergy, anaphylaxis, malignancy, chronic and acute

XX inflammation, histamine and IgE-mediated allergic reaction, shock,

XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory

XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis

XX associated with vascular intervention, including angioplasty and/or stent

XX placement in a mammal. Humanised antibodies are also useful for

XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting

XX neointimal hyperplasia of a vessel in a mammal, preferably associated

XX with vascular intervention. The present sequence is humanised murine 1D9

XX antibody kappa light chain variable (VK) region, 1D9KA. (Updated on 11-

XX SEP-2003 to standardise OS field)

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 4; Length 112;

Best Local Similarity 100.0%; Pred. No. 2.4e-46;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60

Db 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCQGHPTFPYFGQGTLEIK 112

Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCQGHPTFPYFGQGTLEIK 112

RESULT 2

AAU09921

ID AAU09921 standard; protein; 112 AA.

AC AAU09921;

XX 18-JUN-2002 (first entry)

XX Humanised 1D9 light chain variable region, 1D9KA protein sequence.

XX Human; mouse; 1D9 light chain variable region; vasotropic;

XX antiinflammatory; collagen disease; immunosuppressive; antiaesthetic;

XX insulin-dependent diabetes mellitus; inflammatory bowel disease;

XX ulcerative colitis; HF-21/28; graft rejection; allergic disease;

XX antipneumatic; 1D9KA; antiarthritic; nephrotropic; antithyroid;

XX restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;

XX vascular injury; autoimmune disease; immunoglobulin;

XX complementarity determining region; CDR; CD18; CCR2; atherosclerosis;

XX mutant; mutein.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

OS Chimeric.

XX

PH Key Location/Qualifiers

FT Region 24..39

FT /note= "Complementarity determining region 1 (CDR1),

FT grafted from mouse mAb 1D9 light chain sequence

FT (AAU09918)"

FT Region 55..61

FT /note= "Complementarity determining region 2 (CDR2),

FT grafted from mouse mAb 1D9 light chain sequence

FT (AAU09918)"

FT Region 94..102

FT /note= "Complementarity determining region 3 (CDR3),

FT grafted from mouse mAb 1D9 light chain sequence

FT (AAU09918)"

FT Misc-difference 112

FT /note= "Addition of Lys residue normally present in mouse

FT mAb 1D9 sequence and absent in human antibody HF-21/28

FT sequence (AAU09920)"

PN WO200170266-A2.

PD 27-SEP-2001.

XX 15-MAR-2001; 2001WO-US008266.

XX 17-MAR-2000; 2000US-00528267.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CV, Rao PE;

XX WPI; 2001-607511/69.

XX Inhibiting stenosis or restenosis of a blood vessel following vascular

XX injury or angioplasty in a subject by administering agent which inhibits

XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.

XX Claim 32; Fig 17; 108pp; English.

XX The present invention relates to a new method of inhibiting stenosis or

XX restenosis of a blood vessel following vascular injury in a subject. The

XX new method comprises administering to the subject agents which inhibit

XX the adhesion and/or recruitment of neutrophils and mononuclear cells to a

XX site of vascular injury by binding CD18 or CCR2. The method of the

XX invention inhibits stenosis or restenosis of a blood vessel following

XX vascular injury arising from a vascular intervention procedure such as

XX vascular by-pass or transplantation surgery. The method is also useful

XX for treating a subject having an inflammatory disease or condition

XX mediated by neutrophil and mononuclear cell activity e.g. asthma and

XX graft versus host disease. Chronic inflammatory diseases of the lung,

XX collagen diseases, and insulin-dependent diabetes mellitus can also be

XX treated. The method is further useful for treating inflammatory bowel

XX diseases, such as ulcerative colitis. Additional diseases or conditions

XX include inflammatory or allergic diseases and conditions, including

XX systemic anaphylaxis of hypersensitivity responses, drug allergies,

XX psoriasis and inflammatory dermatoses, autoimmune diseases such as

XX arthritis, graft rejection and other diseases including atherosclerosis.

XX The present sequence represents the variable region of one of several

XX humanised 1D9 light chains (AAU09921-AAU09925). These light chains were

XX used in the invention for the production of anti-CCR2 antibody or antigen

XX -binding fragment

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 4; Length 112;

Best Local Similarity 100.0%; Pred. No. 2.4e-46;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60

Db 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCQGHPTFPYFGQGTLEIK 112

61 SGVDPFRSGSGTDFTLKISRVEADVGVYCWQGTTHFPYTFGGQTRLEIK 112

# RESULT 3

ABG75530

ID ABG75530 standard; protein; 112 AA.

AC ABG75530;

DT 16-APR-2003 (first entry)

DE Humanised mouse mAb 1D9 light chain variable region, 1D9RKAVK.

XX Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
 KW antigen binding fragment; cellular adhesion molecule; adhesion;  
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
 KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
 KW endovascular stenting; prosthetic valve; transplantation;  
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
 KW chronic bronchitis; asthma; graft-versus-host disease;  
 KW chronic inflammatory disease; hypersensitivity pneumonitis;  
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HP-21/28;  
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
 KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RKAVK;  
 KW light chain variable region; VK; complementarity determining region; CDR;  
 KW mutant; mutein.

XX Mus sp.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Region 24..39 /note= "Mouse complementarity determining region 1 (CDR1)"

FT Region 55..61 /note= "Mouse complementarity determining region 2 (CDR2)"

FT Region 94..102 /note= "Mouse complementarity determining region 3 (CDR3)"

FT Misc-difference 112 /note= "Lys derived from the mouse 1D9 mAb sequence"

XX US2002106369-A1.

XX 08-AUG-2002.

XX 15-MAR-2001; 2001US-00809739.

XX 17-MAR-2000; 2000US-00528267.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CJ, Rao PE;

XX WPI; 2002-697861/75.

XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
 PT administering first and second agents that inhibit adhesion and/or  
 PT recruitment of neutrophils and mononuclear cells, respectively to site of  
 PT vascular injury.  
 XX Claim 32; Fig 17; 59pp; English.  
 XX The invention discloses a method for inhibiting stenosis or restenosis of  
 CC a blood vessel following vascular injury in a subject. The method  
 CC involves administering to the subject a first therapeutic agent, which  
 CC comprises an antibody or its antigen binding fragment which binds a  
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment

CC of neutrophils to a site of vascular injury and a second therapeutic  
 CC agent, which comprises an antagonist of CCR2 function, that inhibits  
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
 CC injury. The vascular injury arises from a vascular intervention procedure  
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
 CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
 CC stenting, insertion of a prosthetic valve and transplantation of organs,  
 CC tissues or cells. The method is also useful for treating inflammatory  
 CC diseases or conditions mediated by early neutrophil activity and later  
 CC mononuclear cell activity. Preferably, the method is useful for treating  
 CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
 CC asthma and graft-versus-host disease, chronic inflammatory disease of  
 CC lung, hypersensitivity pneumonitis, pancreatitis and insulin dependent diabetes  
 CC other idiopathic conditions, collagen diseases, sarcoidosis and  
 CC mellitus. The method is also useful for treating inflammatory bowel  
 CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
 CC chain variable region (VK), 1D9RKAVK, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human HP-21/28  
 CC mAb VK regions with a mouse derived Lys at position 112

XX Sequence 112 AA;

Query Match 100.0%; Score 590; DB 5; Length 112;

Best Local Similarity 100.0%; Pred. No. 2.4e-46;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVWMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60

Db 1 DVWMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLD 60

QY 61 SGVDPFRSGSGTDFTLKISRVEADVGVYCWQGTTHFPYTFGGQTRLEIK 112

Db 61 SGVDPFRSGSGTDFTLKISRVEADVGVYCWQGTTHFPYTFGGQTRLEIK 112

## RESULT 4

AAO14973

ID AAO14973 standard; protein; 112 AA.

XX AAO14973;

XX 05-SEP-2002 (first entry)

XX Humanised murine light chain variable region (1D9RKA VK).

XX Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
 KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
 KW bowel transplant; heart transplant; graft versus host disease;  
 KW chronic graft rejection; antibody light chain variable region; 1D9RKA VK.  
 OS Mus musculus.  
 OS Synthetic.  
 XX US2002042370-A1.  
 XX 11-APR-2002.  
 XX 13-APR-2001; 2001US-00835087.  
 XX 14-APR-2000; 2000US-00549448.  
 XX (MILL-) MILLENNIUM PHARM INC.

PI Hancock WW;  
 XX WPI; 2002-351265/38.  
 XX Inhibiting graft rejection, graft versus host disease or chronic  
 PT rejection of a transplanted graft, involves administering a CCR2  
 PT antagonist.  
 XX  
 XX Claim 26; Fig 1; 16pp; English.  
 XX The invention comprises a method of inhibiting graft rejection, graft  
 CC versus host disease or chronic rejection of a transplanted graft. The  
 CC method involves administering an antagonist of CC chemokine receptor 2  
 CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
 CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
 CC complementarity determining regions from various non-human origins). CCR2  
 CC is known to be involved in the rejection of transplanted grafts. The  
 CC method of the invention is useful for inhibiting graft rejection -  
 CC particularly allografts such as kidney, liver, lung, heart-lung,  
 CC pancreas, bowel and heart. The method of the invention is also useful for  
 CC inhibiting graft versus host disease and for inhibiting chronic rejection  
 CC of a transplanted graft. The present amino acid sequence represents a  
 CC humanised murine antibody light chain variable region (ID9Rka V<sub>K</sub>)  
 XX  
 XX Sequence 112 AA;  
 SQ  
 Query Match 100.0%; Score 590; DB 5; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-46;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DVVMTQSLPLPVTILGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVS<sub>K</sub>LD 60  
 Db 1 DVVMTQSLPLPVTILGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVS<sub>K</sub>LD 60  
 Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVYCWQGTTHFPYTFGGQTRLEIK 112  
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVYCWQGTTHFPYTFGGQTRLEIK 112  
 RESULT 5  
 ID ADF98233 standard; protein; 112 AA.  
 XX  
 XX ADF98233;  
 DT 26-FEB-2004 (first entry)  
 DE Humanised ID9 light chain variable region, ID9Rka V kappa, SEQ ID 3.  
 KW Immunosuppressive; CCR2 function inhibitor; graft rejection;  
 KW graft versus host disease; CC chemokine receptor 2; CCR2;  
 KW anti-CCR2 antibody.  
 XX Synthetic.  
 OS Mus musculus.  
 OS Homo sapiens.  
 XX WO200178653-A2.  
 XX  
 XX 25-OCT-2001.  
 XX  
 XX 13-APR-2001; 2001WO-US012139.  
 XX 14-APR-2000; 2000US-00549448.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Hancock WW;  
 PI  
 XX WPI; 2002-017543/02.  
 XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
 PT involves use of CC chemokine receptor 2 inhibitor.

XX Claim 26; Fig 1; 44pp; English.  
 XX The present invention relates to a method for inhibiting graft rejection  
 CC or graft versus host diseases. The method comprises administration of a  
 CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
 CC recipient of a transplanted graft. The CCR2 function antagonist is an  
 CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
 CC ADF98240-ADP98249). The method is useful for inhibiting rejection,  
 CC particularly chronic rejection of a graft, particularly an allograft of  
 CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
 CC inhibiting graft versus host disease for a bone marrow graft.  
 XX  
 XX Sequence 112 AA;  
 SQ  
 Query Match 100.0%; Score 590; DB 5; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-46;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DVVMTQSLPLPVTILGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVS<sub>K</sub>LD 60  
 Db 1 DVVMTQSLPLPVTILGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVS<sub>K</sub>LD 60  
 Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVYCWQGTTHFPYTFGGQTRLEIK 112  
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVYCWQGTTHFPYTFGGQTRLEIK 112  
 RESULT 6  
 ID ADF98234 standard; protein; 112 AA.  
 XX  
 XX ADF98234;  
 DT 21-OCT-2004 (first entry)  
 DE Humanised immunoglobulin protein #1.  
 XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
 KW inflammatory disease; autoimmune disorder; graft rejection;  
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 KW anti-HIV; virucide; antiarteriosclerotic.  
 XX Synthetic.  
 OS  
 XX US2004151721-A1.  
 XX  
 XX 05-AUG-2004.  
 XX  
 XX 10-DEC-2003; 2003US-00733563.  
 XX 19-OCT-2001; 2001US-0350166P.  
 XX 26-JUN-2002; 2002US-0392364P.  
 XX 17-OCT-2002; 2002US-00272899.  
 XX (OKEE/) O'KEEFE T.  
 PA (PONA/) PONATH P.  
 XX  
 XX O'keefe T, Ponath P;  
 XX  
 XX WPI; 2004-580175/56.  
 XX  
 XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
 PT useful for diagnosing and/or treating inflammatory or autoimmune  
 PT diseases, and HIV infection.  
 XX  
 XX Claim 5; SEQ ID NO 12; 128pp; English.  
 XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised



CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a humanized  
 CC immunoglobulin protein of the invention.

XX  
 SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 8; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-46;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILYLVSKLD 60

DB 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILYLVSKLD 60

QY 61 SGVDPFRPSGSGTDFTLKISRVEADVGYYCWQTHPPYTFGGQTRLEIK 112

DB 61 SGVDPFRPSGSGTDFTLKISRVEADVGYYCWQTHPPYTFGGQTRLEIK 112

RESULT 7  
 AEB09507  
 ID AEB09507 standard; protein; 112 AA.

XX AC AEB09507;

XX DT 08-SEP-2005 (first entry)

XX DE Humanized 1D9 kappa light chain variable region SEQ ID NO 12.

XX KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW light chain variable region.

XX OS Homo sapiens.

XX OS Mus musculus.

XX OS Synthetic.

XX FN WO2005060368-A2.

XX PD 07-JUL-2005.

XX PP 10-DEC-2003; 2003WO-US039599.

XX PR 10-DEC-2003; 2003WO-US039599.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Okeefe T, Ponath P;

XX DR WPI; 2005-488561/49.

XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.

XX PS Claim 1; SEQ ID NO 12; 192pp; English.

XX The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for  
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized

CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
 CC construct comprising nucleic acid molecule encoding (I); and host cell  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocytic-mediated disorders such as atherosclerosis. (I) is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of a humanized 1D9  
 CC kappa light chain variable region used in the creation of a humanized  
 CC anti-CCR2-antibody.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 9; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-46;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILYLVSKLD 60

DB 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILYLVSKLD 60

QY 61 SGVDPFRPSGSGTDFTLKISRVEADVGYYCWQTHPPYTFGGQTRLEIK 112

DB 61 SGVDPFRPSGSGTDFTLKISRVEADVGYYCWQTHPPYTFGGQTRLEIK 112

RESULT 8

ID AAE07035

XX AC AAE07035 standard; protein; 114 AA.

XX AC AAE07035;

XX DT 11-SEP-2003 (revised)

XX DT 16-OCT-2001 (first entry)

XX DE Humanised murine antibody light chain 1D9RKA protein.

XX KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherosclerosis; atherosclerosis; stenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; antibody 1D9 light chain; 1D9RKA.

XX OS Mus sp.

XX OS Homo sapiens.

XX OS Chimeric.

XX FN WO200157226-A1.

XX PD 09-AUG-2001.

XX PF 02-FEB-2001; 2001WO-US003537.

XX PR 03-FEB-2000; 2000US-00497625.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;

XX DR WPI; 2001-488888/53.

XX DR N-PSDB; AAD13180.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
PT disorder in a patient, comprises a binding specificity for CCR2, and a  
PT non-human antigen binding region and human immunoglobulin.  
XX Disclosure; Fig 24; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding  
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
CC comprising an antigen binding region of non-human origin and at least a  
CC portion of an immunoglobulin of human origin. The humanised antibodies  
CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
CC are useful for inhibiting or treating HIV infection. The proteins of the  
CC invention are useful for inhibiting leukocyte trafficking, for treating  
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
CC disorders such as rheumatoid arthritis and multiple sclerosis,  
CC atherosclerosis and arteriosclerosis, and for inhibiting restenosis. They  
CC are useful in therapy or diagnosis, and in the manufacture of a  
CC medicament for treating CCR-2 mediated disease. They are also useful for  
CC treating allergy, anaphylaxis, malignancy, chronic and acute  
CC inflammation, histamine and IgE-mediated allergic reaction, shock,  
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
CC associated with vascular intervention, including angioplasty and/or stent  
CC placement in a mammal. Humanised antibodies are also useful for  
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
CC with vascular intervention. The present sequence is humanised murine  
CC antibody light chain region, 1D9RKA. (Updated on 11-SEP-2003 to  
CC standardise OS field)

XX Sequence 114 AA;  
SQ

Query Match 99.0%; Score 584; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-46;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFILNWFQQRPGQSPRLIYLVSKLDS 61  
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFILNWFQQRPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTTHPPYFGQGTLEIK 112  
Db 62 GVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTTHPPYFGQGTLEIK 112

RESULT 9  
ADQ89328  
ID ADQ89328 standard; protein; 114 AA.  
XX AC ADQ89328;  
XX DT 21-OCT-2004 (first entry)  
XX DE Humanised immunoglobulin protein #10.  
XX KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
XX inflammatory disease; autoimmune disorder; graft rejection;  
XX HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
XX anti-HIV; virucide; antiarteriosclerotic.  
XX OS Synthetic.  
XX FN US2004151721-A1.  
XX PD 05-AUG-2004.  
XX PF 10-DEC-2003; 2003US-00733563.  
XX PR 19-OCT-2001; 2001US-0350166P.  
XX PR 26-JUN-2002; 2002US-0392364P.  
XX PR 17-OCT-2002; 2002US-00272899.  
XX

PA (OKEE/) O'KEEFE T.  
PA (PONA/) PONATH P.  
XX O'Keefe T, Ponath P;  
XX WPI; 2004-580175/56.  
XX N-PSDB; ADQ89320.  
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX Disclosure; SEQ ID NO 106; 128pp; English.  
XX The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and arteriosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.

XX Sequence 114 AA;  
SQ

Query Match 99.0%; Score 584; DB 8; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-46;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFILNWFQQRPGQSPRLIYLVSKLDS 61  
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFILNWFQQRPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTTHPPYFGQGTLEIK 112  
Db 62 GVPDRFSGSGGTFTLKISRVEAEDVGVYVCWQGTTHPPYFGQGTLEIK 112

RESULT 10  
AEB09601  
ID AEB09601 standard; protein; 114 AA.  
XX AC AEB09601;  
XX DT 08-SEP-2005 (first entry)  
XX DE Humanized light chain 1D9RKA.  
XX KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
XX antibody engineering; therapeutic; diagnosis; inflammation;  
XX autoimmune disease; immune disorder; graft rejection; HIV infection;  
XX infection; arteriosclerosis; cardiovascular disease; metabolic disorder;  
XX light chain variable region.  
XX OS Synthetic.  
XX FN WO2005060368-A2.  
XX PD 07-JUL-2005.  
XX PF 10-DEC-2003; 2003WO-US039599.  
XX PR 10-DEC-2003; 2003WO-US039599.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX O'Keefe T, Ponath P;  
XX WPI; 2005-488561/49.  
XX N-PSDB; AEB09593.  
XX

XX New humanized immunoglobulin or its antigen binding portion having  
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
PT diseases.  
XX Disclosure; SEQ ID NO 106; 192pp; English.  
XX The invention describes a humanized immunoglobulin (I) or its antigen  
CC binding portion having binding specificity for CC-chemokine receptor 2  
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
CC sequence, given in specification or its portion, and the light chain  
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
CC in specification. Also described are: a humanized immunoglobulin heavy  
CC chain, or its antigen binding fragment, having binding specificity for  
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
CC immunoglobulin light chain, or its antigen binding fragment, having  
CC binding specificity for CCR2 and comprising the amino acid sequence of  
CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
CC sequence, given in specification. The following are disclosed: isolated  
CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
CC construct comprising nucleic acid molecule encoding (I); and host cell  
CC comprising the nucleic acid molecule. (I) is useful as a therapeutic  
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
CC reducing inflammatory response, for use in the treatment of diseases  
CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
CC infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
CC fluid), and for modulating binding function and/or leukocyte trafficking  
CC modulated by CCR2. This is the amino acid sequence of humanized light  
CC chain 1D9RKA.  
XX Sequence 114 AA;

Query Match 99.0%; Score 584; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-46;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VVMTQSLPLVTLGQPASISCKSSQSLSDSGKTFLNWFQORPQSPRLIYLVSKLDS 61  
DB 2 VVMTQSLPLVTLGQPASISCKSSQSLSDSGKTFLNWFQORPQSPRLIYLVSKLDS 61  
QY 62 GVPDRFSGSGGTFTLKISRVEAEDVGVVYCWQGTTHPPYTFGQGTLEIK 112  
DB 62 GVPDRFSGSGGTFTLKISRVEAEDVGVVYCWQGTTHPPYTFGQGTLEIK 112

RESULT 11  
AAE06950  
ID AAE06950 standard; protein; 112 AA.

XX AAE06950;  
XX 11-SEP-2003 (revised)  
XX 16-OCT-2001 (first entry)  
XX Humanised murine 1D9 antibody kappa light chain variable region, 1D9RKB.  
XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW multiple sclerosis; atherosclerosis; atherosclerosis; stenosis; asthma;  
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody;  
KW neointimal hyperplasia; VK; kappa light chain variable region; 1D9RKB.  
XX Mus sp.

OS Homo sapiens.  
OS Chimeric.  
XX Key  
XX Region  
XX Location/Qualifiers  
XX 23..39  
XX /label= CDR1  
XX /note= "Complementarity determining region 1"  
XX 55..61  
XX /label= CDR2  
XX /note= "Complementarity determining region 2"  
XX 94..102  
XX /label= CDR3  
XX /note= "Complementarity determining region 3"  
XX WO200157226-A1.  
XX 09-AUG-2001.  
XX 02-FEB-2001; 2001WO-US003537.  
XX 03-FEB-2000; 2000US-00497625.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
XX WPI; 2001-48888/53.  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
XX disorder in a patient, comprises a binding specificity for CCR2, and a  
XX non-human antigen binding region and human immunoglobulin.  
XX Claim 61; Fig 11; 183pp; English.  
XX The patent discloses a humanised antibody or its antigen-binding  
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
XX comprising an antigen binding region of non-human origin and at least a  
XX portion of an immunoglobulin of human origin. The humanised antibodies  
XX are useful for inhibiting the interaction of a cell expressing CCR2. They  
XX are useful for inhibiting or treating HIV infection. The proteins of the  
XX invention are useful for inhibiting leukocyte trafficking, for treating  
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune  
XX disorders such as rheumatoid arthritis and multiple sclerosis,  
XX atherosclerosis and atherosclerosis, and for inhibiting restenosis. They  
XX are useful in therapy or diagnosis, and in the manufacture of a  
XX medicament for treating CCR-2 mediated disease. They are also useful for  
XX treating allergy, anaphylaxis, malignancy, chronic and acute  
XX inflammation, histamine and Igs-mediated allergic reaction, shock,  
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
XX associated with vascular intervention, including angioplasty and/or stent  
XX placement in a mammal. Humanised antibodies are also useful for  
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
XX neointimal hyperplasia of a vessel in a mammal, preferably associated  
XX with vascular intervention. The present sequence is humanised murine 1D9  
XX antibody kappa light chain variable (VK) region, 1D9RKB. (Updated on 11-  
XX SEP-2003 to standardise OS field)  
XX Sequence 112 AA;  
Query Match 97.8%; Score 577; DB 4; Length 112;  
Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DVMTQSLPLVTLGQPASISCKSSQSLSDSGKTFLNWFQORPQSPRLIYLVSKLD 60  
DB 1 DVMTQSLPLVTLGQPASISCKSSQSLSDSGKTFLNWFQORPQSPRLIYLVSKLD 60  
QY 61 SGVDPDRFSGSGGTFTLKISRVEAEDVGVVYCWQGTTHPPYTFGQGTLEIK 112  
DB 61 SGVDPDRFSGSGGTFTLKISRVEAEDVGVVYCWQGTTHPPYTFGQGTLEIK 112

RESULT 12  
AAU09922  
ID AAU09922 standard; protein; 112 AA.  
XX AC  
XX AAU09922;  
XX 18-JUN-2002 (first entry)  
XX  
DE Humanised ID9 light chain variable region, ID9RKB protein sequence.  
XX  
XX Human; mouse; ID9 light chain variable region; vasotropic;  
KW antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;  
KW insulin-dependent diabetes mellitus; inflammatory bowel disease;  
KW ulcerative colitis; HF-21/28; graft rejection; allergic disease;  
KW antipsoriatic; ID9RKB; antirheumatic; nephrotropic; antichyroid;  
KW restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;  
KW vascular injury; autoimmune disease; immunoglobulin;  
KW complementarity determining region; CDR; CD18; CCR2; atherosclerosis;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT Region 24. .39  
FT /note= "Complementarity determining region 1 (CDR1),  
FT grafted from mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Misc-difference 41  
FT /note= "Substitution of Phe residue normally present in  
FT human HF-21/28 sequence (AAU09920) by Leu residue  
FT normally present in mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Misc-difference 42  
FT /note= "Substitution of Gln residue normally present in  
FT human HF-21/28 sequence (AAU09920) by Leu residue  
FT normally present in mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Region 55. .61  
FT /note= "Complementarity determining region 2 (CDR2),  
FT grafted from mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Region 94. .102  
FT /note= "Complementarity determining region 3 (CDR3),  
FT grafted from mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Misc-difference 112  
FT /note= "Addition of Lys residue normally present in mouse  
FT mAb ID9 sequence and absent in human antibody HF-21/28  
FT sequence (AAU09920)"  
FT  
FT  
PN WO200170266-A2.  
XX  
PD 27-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-US008266.  
XX  
XX 17-MAR-2000; 2000US-00528267.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Horvath CJ, Rao PE;  
XX  
XX WPI; 2001-607511/69.  
XX  
XX Inhibiting stenosis or restenosis of a blood vessel following vascular  
PT injury or angioplasty in a subject by administering agent which inhibits  
PT recruitment or adhesion of neutrophils, mononuclear cells to injury site.  
XX  
XX Claim 32; Fig 17; 108pp; English.  
XX

CC The present invention relates to a new method of inhibiting stenosis or  
CC restenosis of a blood vessel following vascular injury in a subject. The  
CC new method comprises administering to the subject agents which inhibit  
CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a  
CC site of vascular injury by binding CD18 or CCR2. The method of the  
CC invention inhibits stenosis or restenosis of a blood vessel following  
CC vascular injury arising from a vascular intervention procedure such as  
CC vascular by-pass or transplantation surgery. The method is also useful  
CC for treating a subject having an inflammatory disease or condition  
CC mediated by neutrophil and mononuclear cell activity e.g. asthma and  
CC graft versus host disease. Chronic inflammatory diseases of the lung,  
CC collagen diseases, and insulin-dependent diabetes mellitus can also be  
CC treated. The method is further useful for treating inflammatory bowel  
CC diseases, such as ulcerative colitis. Additional diseases or conditions  
CC include inflammatory or allergic diseases and conditions, including  
CC systemic anaphylaxis of hypersensitivity responses, drug allergies,  
CC psoriasis and inflammatory dermatoses, autoimmune diseases such as  
CC arthritis, graft rejection and other diseases including atherosclerosis.  
CC The present sequence represents the variable region of one of several  
CC humanised ID9 light chains (AAU09921-AAU09925). These light chains were  
CC used in the invention for the production of anti-CCR2 antibody or antigen  
CC -binding fragment  
XX  
XX Sequence 112 AA;  
SQ  
Query Match 97.8%; Score 577; DB 4; Length 112;  
Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DVVMTQPSLSIPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPGSPRLIYLVSKLD 60  
DB 1 DVVMTQPSLSIPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRLIYLVSKLD 60  
QY 61 SGVPDRFSGSGSDFTLKISRVEAEDVGVVYCWQGTTHFPYTCQGTGLEIK 112  
DB 61 SGVPDRFSGSGSDFTLKISRVEAEDVGVVYCWQGTTHFPYTCQGTGLEIK 112  
RESULT 13  
ABG75531  
ID ABG75531 standard; protein; 112 AA.  
XX  
XX AC ABG75531;  
XX  
XX DT 16-APR-2003 (first entry)  
XX  
XX DE Humanised mouse mAb ID9 light chain variable region, ID9RKBVK.  
XX  
XX KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
KW antigen binding fragment; cellular adhesion molecule; adhesion;  
KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
KW endovascular stenting; prosthetic valve; transplantation;  
KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
KW chronic bronchitis; asthma; graft-versus-host disease;  
KW chronic inflammatory disease; hypersensitivity pneumonitis;  
KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;  
KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
KW graft rejection; atherosclerosis; myositis; therapy; ID9; ID9RKBVK;  
KW light chain variable region; VK; complementarity determining region; CDR;  
KW mutant; mutein.  
XX  
XX Mus sp.  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX FH Key Location/Qualifiers  
XX Region 24. .39  
XX /note= "Mouse complementarity determining region 1  
XX (CDR1)"  
XX

FT Misc-difference 41. .42  
 FT /note= "Leu's derived from the mouse 1D9 mAb sequence"  
 FT Region 55. .61  
 FT /note= "Mouse complementarity determining region 2  
 FT (CDR2)"  
 FT Region 94. .102  
 FT /note= "Mouse complementarity determining region 3  
 FT (CDR3)"  
 FT Misc-difference 112  
 FT /note= "Lys derived from the mouse 1D9 mAb sequence"  
 FT  
 PN US2002106369-A1.  
 XX  
 XX 08-AUG-2002.  
 XX  
 PF 15-MAR-2001; 2001US-00809739.  
 XX  
 PR 17-MAR-2000; 2000US-00528267.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Horvath CJ, Rao PE;  
 XX  
 DR WPI; 2002-697861/75.  
 XX  
 XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
 PT administering first and second agents that inhibit adhesion and/or  
 PT recruitment of neutrophils and mononuclear cells, respectively to site of  
 PT vascular injury.  
 XX  
 PS Claim 32; Fig 17; 59pp; English.  
 XX  
 CC The invention discloses a method for inhibiting stenosis or restenosis of  
 CC a blood vessel following vascular injury in a subject. The method  
 CC involves administering to the subject a first therapeutic agent, which  
 CC comprises an antibody or its antigen binding fragment which binds a  
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
 CC of neutrophils to a site of vascular injury and a second therapeutic  
 CC agent, which comprises an antagonist of CCR2 function, that inhibits  
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
 CC injury. The vascular injury arises from a vascular intervention procedure  
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
 CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
 CC stenting, insertion of a prosthetic valve and transplantation of organs,  
 CC tissues or cells. The method is also useful for treating inflammatory  
 CC diseases or conditions mediated by early neutrophil activity and later  
 CC mononuclear cell activity. Preferably, the method is useful for treating  
 CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
 CC asthma and graft-versus-host disease, chronic inflammatory disease of  
 CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
 CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
 CC mellitus. The method is also useful for treating inflammatory bowel  
 CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
 CC chain variable region (VK), 1D9K3VK, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human HP-21/28  
 CC positions 41 and 42  
 XX  
 SQ Sequence 112 AA;  
 Query Match 97.8%; Score 577; DB 5; Length 112;  
 Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRRILYLVSKLD 60  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 RESULT 14  
 ADF98234  
 ID ADF98234 standard; protein; 112 AA.  
 XX  
 AC ADF98234;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Humanised 1D9 light chain variable region, 1D9RKB V kappa, SEQ ID 4.  
 XX  
 KW Immunosuppressive; CCR2 function inhibitor; graft rejection;  
 KW graft verses host disease; CC chemokine receptor 2; CCR2;  
 KW anti-CCR2 antibody.  
 XX  
 OS Synthetic.  
 OS Mus musculus.  
 OS Homo sapiens.  
 XX  
 PN WO200178653-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 13-APR-2001; 2001WO-US012139.  
 XX  
 PR 14-APR-2000; 2000US-00549448.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Hancock MW;  
 XX  
 DR WPI; 2002-017543/02.  
 XX  
 FT Inhibition of rejection of graft e.g. heart or graft verses host disease  
 FT involves use of CC chemokine receptor 2 inhibitor.  
 XX  
 PS Claim 26; Fig 1; 44pp; English.  
 XX  
 CC The present invention relates to a method for inhibiting graft rejection  
 CC or graft verses host diseases. The method comprises administration of a  
 CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
 CC recipient of a transplanted graft. The CCR2 function antagonist is an  
 CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
 CC ADP98240-ADP98249). The method is useful for inhibiting rejection,  
 CC particularly chronic rejection of a graft, particularly an allograft of  
 CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
 CC inhibiting graft verses host disease for a bone marrow graft.  
 XX  
 SQ Sequence 112 AA;  
 Query Match 97.8%; Score 577; DB 5; Length 112;  
 Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRRILYLVSKLD 60  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 RESULT 15  
 ADQ89235

ID ADQ89235 standard; protein; 112 AA.  
XX AC ADQ89235;  
XX DT 21-OCT-2004 (first entry)  
XX DE Humanised immunoglobulin protein #2.  
XX KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX OS Synthetic.  
XX FN US2004151721-A1.  
XX PD 05-AUG-2004.  
XX PF 10-DEC-2003; 2003US-00733563.  
XX PR 19-OCT-2001; 2001US-0350166P.  
XX PR 26-JUN-2002; 2002US-0392364P.  
XX PR 17-OCT-2002; 2002US-00272899.  
XX PA (OKEE/) O'KEEFE T.  
XX PA (PONA/) PONATH P.  
XX FI O'Keefe T, Ponath P;  
XX DR WPI; 2004-580175/56.  
XX PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX PS Example 2; SEQ ID NO 13; 128pp; English.  
XX CC The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.  
XX SQ Sequence 112 AA;  
Query Match 97.8%; Score 577; DB 8; Length 112;  
Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 DVNMTQSPFLSPVTLGQPASISCKSSQSLSDSGKTFILNWFQRPQSPRLIYLVSKLD 60  
Db 1 DVNMTQSPFLSPVTLGQPASISCKSSQSLSDSGKTFILNWFQRPQSPRLIYLVSKLD 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDGIVYYCWOGTHPPYTFGQGTLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGIVYYCWOGTHPPYTFGQGTLEIK 112

Search completed: January 28, 2006, 09:38:12  
Job time : 58.6907 secs









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|||||
Db      81  SGVPDRFSGSGGDTFLTKISRVEADVGVYCMQGTHTWSPTFGQGTKEIK 132
|||||

RESULT 11
S22658
Ig kappa chain precursor V region (0-81VL) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 31-Dec-2004
C/Accession: S22658
R/Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A/Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-a
A/Reference number: S22657; MUID:92285150; PMID:1598223
A/Accession: S22658
A/Molecule type: mRNA
A/Residues: 1-140 <HIR>
A/Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI00001769CF; EMBL:X59135
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match      85.7%; Score 505.5; DB 2; Length 140;
Best Local Similarity 87.6%; Pred. No. 2.2e-40;
Matches 99; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy      1  DVNMTQSLSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
Db      21  DVNMTQSLSPVLTIGQPASISCKSSQSLVHSDGNTYLNWFQQRPGQSPRLIYRVNRD 80

Qy      61  SGVPDRFSGSGGDTFLTKISRVEADVGVYCMQGTHTF-PYTFGQGTRLIK 112
Db      81  SGVPDRFSGSGGDTFLTKISRVEADVGLVYCMQHTWSPTFGQGTRLIK 133

RESULT 12
S40324
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C/Accession: S40324
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40324
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-133 <KLE>
A/Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI0000176CAA; EMBL:X72434
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;33-112/Domain: immunoglobulin homology <IMM>

Query Match      85.6%; Score 505; DB 2; Length 133;
Best Local Similarity 84.8%; Pred. No. 2.3e-40;
Matches 95; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy      1  DVNMTQSLSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
Db      18  DVLTQSLSPVLTIGQPASISCKSDQSLVSDGKTYLNWYQQRPGQSPRLIYKVNRD 77

Qy      61  SGVPDRFSGSGGDTFLTKISRVEADVGVYCMQGTHTFPTFGQGTRELK 112
Db      78  SGVPDRFSGSGGDTFLTKISRVEADVGVYCMQGTHTWPGTFGQGTKEIK 129

RESULT 13
S31577
Ig kappa chain - mouse (house mouse)
C/Species: Mus musculus (house mouse)
```

```
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31577
R/Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
submitted to the EMBL Data Library, January 1993
A/Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antic
A/Reference number: S31577
A/Accession: S31577
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-131 <REC>
A/Cross-references: UNIPARC:UPI000011469C; EMBL:Z19575; NID:953983; PIDN:CAA79627.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match      85.3%; Score 503; DB 2; Length 131;
Best Local Similarity 84.8%; Pred. No. 3.5e-40;
Matches 95; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy      1  DVNMTQSLSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
Db      20  DVNMTQAPLTLSVTIGQPASISCKSSHLSIDGKTYLNMLLQRPQSPKRLIYLVSKLD 79

Qy      61  SGVPDRFSGSGGDTFLTKISRVEADVGVYCMQGTHTFPTFGQGTRELK 112
Db      80  SGVPDRFSGSGGDTFLTKISRVEADLGVIYCMQHTFPYTFGGTKLEMK 131

RESULT 14
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C/Accession: PL0273
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PL0231; MUID:90111618; PMID:2104919
A/Accession: PL0273
A/Molecule type: mRNA
A/Residues: 1-112 <SHL>
A/Cross-references: UNIPROT:Q8K0F8; UNIPARC:UPI0000115487
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology <IMM>
F;24-39/Region: complementarity-determining 1
F;40-54/Region: framework 2
F;55-61/Region: complementarity-determining 2
F;62-93/Region: framework 3
F;94-102/Region: complementarity-determining 3
F;103-112/Region: framework 4

Query Match      84.9%; Score 501; DB 2; Length 112;
Best Local Similarity 84.8%; Pred. No. 4.5e-40;
Matches 95; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy      1  DVNMTQSLSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSKLD 60
Db      1  DVNMTQTLTSLVTIGQPASISCKSSQSLVRYNGKTYLNMLLQRPQSPKRLIYLVSKLD 60

Qy      61  SGVPDRFSGSGGDTFLTKISRVEADVGVYCMQGTHTFPTFGQGTRELK 112
Db      61  SGVPDRFSGSGGDTFLTKISRVEADLGVIYCMQGTHTFPWTGGTKLEIK 112

RESULT 15
S42611
HUNK protein precursor - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S42611
R/Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.
```

J. Neuroimmunol. 36, 29-39, 1992  
A>Title: DNA sequence analysis and comparison of the variable heavy and light chain regi  
A;Reference number: S42610; MUID:92138794; PMID:1370957  
A;Accession: S42611  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-133 <SPA>  
A;Cross-references: UNIPARC:UPI000011378B; EMBL:X54137; NID:9433889; PIDN:CAA38072.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match	84.9%	Score	501;	DB	2;	Length	133;
Best Local Similarity	85.6%	Pred. No.	5.4e-40;				
Matches	95;	Conservative	7;	Mismatches	9;	Indels	0;
						Gaps	0;

Qy	1	DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLYLVS	60
Db	21	DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLLYLVS	80
Qy	61	SGVPRFSGSGSGTDFTLKISRVEAEDVGVVYCWQGHFPPYTFGQGRLEI	111
Db	81	SGVPRFSGSGSGTDFTLKISRVEAEDVGVVYCWQGHFPPYTFGQGRLEI	131

Search completed: January 28, 2006, 09:45:38  
Job time : 12.4354 secs

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Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	514	87.1	133	1	KV2F HUMAN	P06310 homo sapien	
2	511	86.6	239	2	08TCD0 HUMAN	P06300 homo sapien	
3	496.5	84.2	114	2	Q9UL80 HUMAN	Q9UL80 homo sapien	
4	491	83.2	239	2	Q58E08 MOUSE	Q58E08 mus musculus	
5	459	77.8	239	2	Q6P491 HUMAN	Q6P491 homo sapien	
6	450	76.3	113	1	KV2D HUMAN	P01617 homo sapien	
7	449	76.1	113	1	KV2B HUMAN	P01615 homo sapien	
8	447	75.8	239	2	08NEK0 HUMAN	P08NE0 homo sapien	
9	445	75.4	248	2	Q65ZQ7 9MURI	Q65ZQ7 homo sp. B3(	
10	444.5	75.3	115	1	KV2A HUMAN	P01614 homo sapien	
11	438	74.2	117	1	KV2E HUMAN	P06309 homo sapien	
12	430.5	73.0	115	2	Q5F210 MOUSE	Q5F210 mus musculus	
13	430	72.9	113	1	KV2G MOUSE	P01631 mus musculus	
14	428	72.5	112	2	Q53VP8 MOUSE	Q53VP8 mus musculus	
15	418	70.8	219	2	Q65ZC0 MOUSE	Q65ZC0 mus musculus	
16	417.5	70.8	240	2	Q6PHI6 HUMAN	Q6PHI6 homo sapien	
17	411	69.7	234	2	Q5XKG4 MOUSE	Q5XKG4 mus musculus	
18	405.5	68.7	112	1	KV2C HUMAN	P01616 homo sapien	
19	402	68.1	113	1	KV2E MOUSE	P03976 mus musculus	
20	397	67.3	113	1	KV2C MOUSE	P01628 mus musculus	
21	396	67.1	112	1	KV2D MOUSE	P01629 mus musculus	
22	396	67.1	113	1	KV2F MOUSE	P01630 mus musculus	
23	390	66.1	112	1	KV2A MOUSE	P01626 mus musculus	
24	390	66.1	112	2	Q6LBM8 MOUSE	Q6LBM8 mus musculus	
25	386.5	65.5	134	1	KV4C HUMAN	P06314 homo sapien	
26	385.5	65.3	108	1	KV1 CANFA	P01618 canis famil	
27	380.5	64.5	114	1	KV4I HUMAN	P01625 homo sapien	
28	378.5	64.2	111	1	KV3L MOUSE	P01664 mus musculus	
29	378.5	64.2	111	1	KV3M MOUSE	P01665 mus musculus	
30	377.5	64.0	111	1	KV3O MOUSE	P01667 mus musculus	
31	372.5	63.1	111	1	KV3Q MOUSE	P01669 mus musculus	

Best Local Similarity 87.5%; Pred. No. 5,3e-45;  
Matches 98; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVVMTQPSLSPLVTLGPASISCKSSQSLDSDGKTFNLWFQQRPGSQPRLLIYLVSKLD 60  
Db 21 DVVMTQPSLSPLVTLGPASISCKSSQSLVYSDGNTYLNWFQQRPGSQPRLLIYKVSNRD 80

Qy 61 SGVDPDRFSGSGGDTFTLKISRVEADVGYYVCMQGHPTFPYFGQGTLEIK 112  
Db 81 SGVDPDRFSGSGGDTFTLKISRVEADVGYYVCMQGHPTFPYFGQGTLEIK 132

RESULT 2

Q8TCD0\_HUMAN  
ID Q8TCD0 HUMAN PRELIMINARY; PRT; 239 AA.  
AC Q8TCD0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarathne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RA Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1598223;  
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;  
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus  
nephritis-associated idiotype.";  
RL Nucleic Acids Res. 20:2601-0(1992).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1551402;  
RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,  
RA Thiebe R., Zocher I., Zachau H.G.;  
RT "The human immunoglobulin kappa locus. Characterization of the  
duplicated A regions.";  
RL Eur. J. Immunol. 22:1023-1029(1992).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8258341;  
RA Klein R., Jaenichen R., Zachau H.G.;

"Expressed human immunoglobulin kappa genes and their hypermutation.";  
Eur. J. Immunol. 23:3248-3262(1993).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
distributed over a large portion of the V kappa locus and do not show  
somatic mutation.";  
RL Eur. J. Immunol. 23:391-397(1993).  
DR EMBL; BC022362; AAH22362.1; -, mRNA.  
DR PIR; S22658; S22658.  
DR PIR; S34095; S34095.  
DR PIR; S40324; S40324.  
DR PIR; S40374; S40374.  
DR PIR; S42267; S42267.  
DR PIR; S42268; S42268.  
DR HSSP; P01834; 117Z.  
DR SMR; Q8TCD0; 21-237.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 239 AA; 26235 MW; FAGEDC3A3B03871D CRC64;

Query Match 86.6%; Score 511; DB 2; Length 239;  
Best Local Similarity 86.6%; Pred. No. 2.1e-44;  
Matches 97; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVVMTQPSLSPLVTLGPASISCKSSQSLDSDGKTFNLWFQQRPGSQPRLLIYLVSKLD 60  
Db 21 DVVMTQPSLSPLVTLGPASISCKSSQSLVYSDGNTYLNWFQQRPGSQPRLLIYKVSNRD 80

Qy 61 SGVDPDRFSGSGGDTFTLKISRVEADVGYYVCMQGHPTFPYFGQGTLEIK 112  
Db 81 SGVDPDRFSGSGGDTFTLKISRVEADVGYYVCMQGHPTFPYFGQGTLEIK 132

RESULT 3

Q9UL80\_HUMAN  
ID Q9UL80 HUMAN PRELIMINARY; PRT; 114 AA.  
AC Q9UL80;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
(Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1322670;  
RA Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,  
RA Gaskin F., Fu S.M.;  
RT "A rheumatoid factor from a normal individual encoded by VH2 and V  
kappa II gene segments.";  
RL Arthritis Rheum. 35:900-904(1992).

```
[3]
RA NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RT Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
[4]
RA NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint.";
RL Eur. J. Immunol. 22:1561-1565(1992).
DR EMBL; AF035034; AAD56270.1; -; mRNA.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; P01625; 1LVE.
DR SMR; Q9UL80; 1-114.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 84.2%; Score 496.5; DB 2; Length 114;
Best Local Similarity 85.8%; Pred. No. 2.9e-43;
Matches 97; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Qy 1 DVVMTQSLPSLVTLGQPASISCKSSQSLSDSGKTFNLWFQQRQSPRLIYLVSKLD 60
Db 1 DVVMTQSLPSLVTLGQPASISCKSSQSPVSDGNTYLNWFQQRQSPRLIYKVSNRD 60

Qy 61 SGVDPFRSGSGTGDTFTLKISRVAEDVGVYCMQGTHTF-PYTFQGTGLEIK 112
Db 61 SGVDPFRSGSGTGDTFTLKISRVAEDVGVYCMQGTHTFWPTFQGTKLEIK 113

RESULT 4
ID Q58E08_MOUSE PRELIMINARY; PRT; 239 AA.
AC Q58E08;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2EHC II;
RX TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Mnt1 model.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RA NUCLEOTIDE SEQUENCE.
RC STRAIN=C2EHC II;
RX TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Mnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091750; AAH91750.1; -; mRNA.
DR SMR; Q58E08; 21-239.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS02290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 239 AA; 26302 MW; 98FC4BA8EB404215 CRC64;

Query Match 83.2%; Score 491; DB 2; Length 239;
Best Local Similarity 83.9%; Pred. No. 2.4e-42;
Matches 94; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DVVMTQSLPSLVTLGQPASISCKSSQSLSDSGKTFNLWFQQRQSPRLIYLVSKLD 60
Db 21 DVVMTQPLTSLVIGQPASISCKSSQSLHNSKTYLNWLLQRPQSPKLLIYLVSKLE 80

Qy 61 SGVDPFRSGSGTGDTFTLKISRVAEDVGVYCMQGTHTF-PYTFQGTGLEIK 112
Db 81 SGVDPFRSGSGTGDTFTLKISRVAEDVGVYCMQGTHTFPRTPFGGTGLEIK 132

RESULT 5
Q6P491_HUMAN PRELIMINARY; PRT; 239 AA.
ID Q6P491_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skin;  
RA Strauberg R.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC063599; AAH63599.1; -, mRNA.  
DR HSSP; P01837; 1KCU.  
DR SMR; G6P491; 21-237.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.C1.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig.V.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS0290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;  
  
Query Match 77.8%; Score 459; DB 2; Length 239;  
Best Local Similarity 77.7%; Pred. No. 4.9e-39;  
Matches 87; Conservative 11; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 DVVMTQPSLPLVTLGPASISCKSSQSLSDSGKTFNLWFQRPQSPRLIYLVSCLD 60  
Db 21 DIVMTQPSLPLVTLGPASISCKSSQSLSDSGKTFNLWFQRPQSPRLIYLVSCLD 80  
  
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCYWQTHFPYTFGQTRLEIK 112  
Db 81 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCYWQTHFPYTFGQTRLEIK 132  
  
RESULT 6  
KV2B HUMAN  
ID KV2B HUMAN STANDARD; PRT; 113 AA.  
AC P01617;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-II region TEW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE (BENCE-JONES PROTEIN TEW).  
RX MEDLINE=74148480; PubMed=4596149;  
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
RT "Amino acid sequence of a kappa Bence Jones protein from a case of  
RT primary amyloidosis.";  
RL Biochemistry 12:3763-3780 (1973).  
RN [2]  
RP PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
RX MEDLINE=73166638; PubMed=4700495;  
RA Terry W.D., Page D.B., Kimura S., Isobe T., Osseman E.F.,  
RA Glenner G.G.;  
RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
RT patient with plasma cell dyscrasia and amyloidosis.";  
RL J. Clin. Invest. 52:1276-1281 (1973).

CC -!- MISCELLANEOUS: The major amyloid protein appears to be identical  
CC with the Bence Jones protein isolated from the same patient.  
CC -!- MISCELLANEOUS: This protein was isolated from the urine of a  
CC patient with plasma cell dyscrasia and amyloidosis.  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
CC marker.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC PIR; A90370; K2HUTW.  
DR HSSP; Q99W37; 1I91.  
DR SMR; P01617; 1-113.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig.V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Amyloid; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin domain; Immunoglobulin V region.  
FT REGION 1 23 Framework-1.  
FT REGION 24 39 Complementarity-determining-1.  
FT REGION 40 54 Framework-2.  
FT REGION 55 61 Complementarity-determining-2.  
FT REGION 62 93 Framework-3.  
FT REGION 94 102 Complementarity-determining-3.  
FT REGION 103 112 Framework-4.  
FT DISULFID 23 93 By similarity.  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;  
  
Query Match 76.3%; Score 450; DB 1; Length 113;  
Best Local Similarity 77.7%; Pred. No. 1.8e-38;  
Matches 87; Conservative 8; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 DVVMTQPSLPLVTLGPASISCKSSQSLSDSGKTFNLWFQRPQSPRLIYLVSCLD 60  
Db 1 DIVMTQPSLPLVTLGPASISCKSSQSLSDSGKTFNLWFQRPQSPRLIYLVSCLD 60  
  
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCYWQTHFPYTFGQTRLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCYWQTHFPYTFGQTRLEIK 112  
  
RESULT 7  
KV2B HUMAN  
ID KV2B HUMAN STANDARD; PRT; 113 AA.  
AC P01615;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-II region FR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=76253627; PubMed=821524;  
RA Riesen W.F., Jaton J.-C.;  
RT "Variable region sequence of the light chain from a Waldenstroms Igm  
RT with specificity for phosphorylcholine.";  
RL Biochemistry 15:3829-3833 (1976).  
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's  
CC macroglobulin that binds phosphorylcholine.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration



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DR PIR: A01886; K2HUPF.  
 DR HSSP; Q99M37; 1191.  
 DR SMR; P01615; 1-109.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 Immunoglobulin V region.  
 FT REGION 1 23  
 FT REGION 24 39  
 FT REGION 40 54  
 FT REGION 55 61  
 FT REGION 62 93  
 FT REGION 94 102  
 FT REGION 103 112  
 FT DISULFID 23 93  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 76.1%; Score 449; DB 1; Length 113;  
 Best Local Similarity 75.0%; Pred. No. 2.3e-38;  
 Matches 84; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVVMTQSPFLSVLTIGQPASISCKSSQSLSDSGKTFNLNFWQRPQSPRRILYLVSKLD 60  
 |||||  
 1 DVVMTQSPFLSVLTIGQPASISCKSSQSLSVBGTLYLWYKQSPPELLIYLVSSYRD 60  
 |||||

QY 61 SGVPRFRSGSGSGTDTFTLKISRVAEADVGVYVCWGTHPPYTFGQGTREIK 112  
 |||||

Db 61 SGVPRFRSGSGSGTDTFTLKISRVAEADVGVYVCWGTHPPYTFGQGTREIK 112  
 |||||

# RESULT 8

QBNK0 HUMAN PRELIMINARY; PRT; 239 AA.  
 AC QBNK0;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE IGKV1-5 protein.  
 GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.B., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate;  
 RA Director MGC Project;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1601042;  
 RA Huber C., Klobbeck H.G., Zachau H.G.;  
 RT "Ongoing V kappa-J kappa recombination after formation of a productive  
 V kappa-J kappa coding joint.";  
 RL Eur. J. Immunol. 22:1561-1565 (1992).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8436174;  
 RA Wagner S.D., Luzzatto L.;  
 RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are  
 distributed over a large portion of the v kappa locus and do not show  
 somatic mutation.";  
 RL Eur. J. Immunol. 23:391-397 (1993).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8258341;  
 RA Klein R., Jaenichen R., Zachau H.G.;  
 RT "Expressed human immunoglobulin kappa genes and their hypermutation.";  
 RL Eur. J. Immunol. 23:3248-3262 (1993).  
 DR EMBL; BC030814; AAH30814.1; -; mRNA.  
 DR PIR; S23638; S23638.  
 DR PIR; S34091; S34091.  
 DR PIR; S40342; S40342.  
 DR PIR; S40357; S40357.  
 DR HSSP; P01834; 117Z.  
 DR SMR; QBNK0; 21-237.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG CL.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 75.8%; Score 447; DB 2; Length 239;  
 Best Local Similarity 75.9%; Pred. No. 8.5e-38;  
 Matches 85; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVVMTQSPFLSVLTIGQPASISCKSSQSLSDSGKTFNLNFWQRPQSPRRILYLVSKLD 60  
 |||||  
 21 DVVMTQSPFLSVLTIGQPASISCKSSQSLSDSGKTFNLNFWQRPQSPRRILYLVSKLD 80  
 |||||

QY 61 SGVPRFRSGSGSGTDTFTLKISRVAEADVGVYVCWGTHPPYTFGQGTREIK 112  
 |||||

Db 81 SGVPRFRSGSGSGTDTFTLKISRVAEADVGVYVCWGTHPPYTFGQGTREIK 132  
 |||||

# RESULT 9

Q65ZQ7 9MURI PRELIMINARY; PRT; 248 AA.  
 ID Q65ZQ7 9MURI PRELIMINARY; PRT; 248 AA.  
 AC Q65ZQ7;  
 DT 25-OCT-2004 (TRENBLrel. 28, Created)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
 DE B3(FV)-PE40 (Fragment).  
 GN Name=B3(FV)-PE40;  
 OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92020904; PubMed=1924323;  
 RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;  
 RT "B3(FV)-PE38KDEL, a single-chain immunotoxin that causes complete  
 regression of a human carcinoma in mice."  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).  
 DR EMBL; S57990; AAB19971.2; -; mRNA.  
 DR SMR; O65207; 4-247.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGv; 2.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 FT NON TER 248 248  
 SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;  
 Query Match 75.4%; Score 445; DB 2; Length 248;  
 Best Local Similarity 74.1%; Pred. No. 1.4e-37;  
 Matches 83; Conservative 15; Mismatches 14; Indels 0; Gaps 0;  
 Qy 1 DVVMTQSLPLVLTGQPASISCKSSQSLLSDGKTFNLWFWQRPQGPSPRLIYLVSCLD 60  
 Db 136 DVLMTQSLPLVSLIGDQASISCRSSQIVHNSNGNTYLEWYKQGPSPKLLIYKVSNR 195  
 Qy 61 SGVDPDRFSGSGGTDTFLTKISRVEADGVVYCMQGTFFPYTFGGTGLEIK 112  
 Db 196 SGVDPDRFSGSGGTDTFLTKISRVEADGVVYCFQGSHPVPTFGSGTKLEIK 247  
 RESULT 10  
 KV2A HUMAN  
 ID KV2A HUMAN STANDARD; PRT; 115 AA.  
 AC P01614;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-II region Cum.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=68242259; PubMed=5586923;  
 RA Hillechmann N.;  
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-  
 type).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [2]  
 RP SEQUENCE REVISION TO 50; 52; 96 AND 97.  
 RX MEDLINE=70063440; PubMed=4188189;  
 RA Hillechmann N.;  
 RT "Molecular basis of antibody formation.";  
 RL Naturwissenschaften 56:195-205(1969).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; B91639; K2HUCM.  
 DR HSSP; P01751; INOB.  
 DR SMR; P01614; 2-115.

DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DISULFID 24 95 By similarity.  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;  
 Query Match 75.3%; Score 444.5; DB 1; Length 115;  
 Best Local Similarity 76.1%; Pred. No. 6.8e-38;  
 Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 Qy 1 DVVMTQSLPLVLTGQPASISCKSSQSLLSDGKTFNLWFWQRPQGPSPRLIYLVSCL 59  
 Db 2 DVMITQSLPLVTPGEPASISCRSSQSLLSDGNTYLNWYLRAGQSPQLIYTLTYR 61  
 Qy 60 DSGVDPDRFSGSGGTDTFLTKISRVEADGVVYCMQGTFFPYTFGGTGLEIK 112  
 Db 62 ASGVDPDRFSGSGGTDTFLTKISRVEADGVVYCMQRLIYTFGGTGLEIR 114  
 RESULT 11  
 KV2E HUMAN  
 ID KV2E HUMAN STANDARD; PRT; 117 AA.  
 AC P06309;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-II region GM607 precursor (Fragment).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=84191506; PubMed=6325927;  
 RA Klobeck H.G., Solomon A., Zachau H.G.;  
 RT "Contribution of human V kappa II germ-line genes to light-chain  
 RT diversity.";  
 RL Nature 309:73-76(1984).  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; Z00009; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
 DR PIR; A01889; K2HUGM.  
 DR HSSP; Q99M37; 1191.  
 DR SMR; P06309; 5-117.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL <1 4  
 FT CHAIN 5 117 Ig kappa chain V-II region GM607.  
 FT REGION 5 27 Framework-1.  
 FT REGION 28 43 Complementarity-determining-1.  
 FT REGION 44 58 Framework-2.  
 FT REGION 59 65 Complementarity-determining-2.  
 FT REGION 66 97 Framework-3.  
 FT REGION 98 106 Complementarity-determining-3.

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FT REGION 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match
Best Local Similarity 74.2%; Score 438; DB 1; Length 117;
Matches 85; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVVMTQSLPLSVTLGQPASISCKSSQSLSDGKTFLNWFQRPQSPRRLLIYLVSKLD 60
DB 5 DIVMTQSLPLSVTPGEPASISCKSSQSLHNGNYLWDYIQLKQPSQLLIYLGSNRA 64

QY 61 SGVDPFRFSGSGTGDTFTLKISRVEADGVVYCWQGTTHPPYTFGGQTRLEIK 112
DB 65 SGVDPFRFSGSGTGDTFTLKISRVEADGVVYCWQGLQTFPQTFGGQTKVEIK 116

RESULT 12
QSF210 MOUSE
ID QSF210_MOUSE PRELIMINARY; PRT; 115 AA.
AC QSF210.
DT 10-MAY-2005 (TREMELrel. 30, Created)
DE 10-MAY-2005 (TREMELrel. 30, Last sequence update)
DE Kappa light chain variable region (Fragment).
GN Name=IGL1 anti-TS1 VL;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Erlandsson A.; Holm P.; Ullén A.; Stigbrand T.; Sundström B.E.;
RT "Studies of the interactions between the anticytokerin 8 monoclonal
antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1."
RL J. Mol. Recognit. 16:157-163(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Erlandsson A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ884575; CAI56337.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;

Query Match
Best Local Similarity 73.0%; Score 430.5; DB 2; Length 115;
Matches 84; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 DVVMTQSLPLSVTLGQPASISCKSSQSLSDGKTFLNWFQRPQSPRRLLIYLVSKLD 60
DB 1 DVVMTQSLPLSVTLGQDQASISCKSSQSLVHSGNYLWYIQLKQPSQLLIYKVSNR 60

QY 61 SGVDPFRFSGSGTGDTFTLKISRVEADGVVYCWQGTTHP-PYTFGGQTRLEIK 112
DB 61 SGVDPFRFSGSGTGDTFTLKISRVEADLVGYFCSQTHVPPTFGGQTKLEMK 113

RESULT 13
KV2G MOUSE
ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC F01631;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J.; Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC 1- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
protein that binds digoxin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01914; KVM326.
DR HSP; 099M37; 1191.
DR Ensembl; ENSMUSG00000055315; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23
FT REGION 24 39 Complementarity-determining-1.
FT REGION 40 54 Complementarity-determining-2.
FT REGION 55 61 Complementarity-determining-2.
FT REGION 62 93 Complementarity-determining-3.
FT REGION 94 102 Complementarity-determining-3.
FT REGION 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match
Best Local Similarity 72.9%; Score 430; DB 1; Length 113;
Matches 83; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVVMTQSLPLSVTLGQPASISCKSSQSLSDGKTFLNWFQRPQSPRRLLIYLVSKLD 60
DB 1 DVVMTQSLPLSVTLGQDQASISCKSSQSLVHSGNYLWYIQLKQPSQLLIYKVSNR 60

QY 61 SGVDPFRFSGSGTGDTFTLKISRVEADGVVYCWQGTTHPPYTFGGQTRLEIK 112
DB 61 SGVDPFRFSGSGTGDTFTLKISRVEADLVGYFCSQTHVPPTFGGQTKLEIK 112

RESULT 14
Q53VP8 MOUSE
ID Q53VP8_MOUSE PRELIMINARY; PRT; 112 AA.
AC Q53VP8.
DT 13-SEP-2005 (TREMELrel. 31, Created)
DT 13-SEP-2005 (TREMELrel. 31, Last sequence update)
DE Kappa chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., There J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RL antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 108-109.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03386; CAA27113.1; -; mRNA.
FT NON TER 1
FT NON TER 112
SQ SEQUENCE 112 AA; 12266 MW; C844B7881A89C18A CRC64;

Query Match 72.5%; Score 428; DB 2; Length 112;
Best Local Similarity 72.3%; Pred. No. 3.3e-36;
Matches 81; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 DVNVTQSPLSVTLGQPASISCKSSQSLSDGKTFNLWFQRPQSPRLIYLVSKLD 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DVNVTQSPLSVTLGQPASISCKSSQSLSDGKTFNLWFQRPQSPRLIYLVSKLD 60
EMBO J. 4:3681-3688(1985).

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQTHFPYTFGGGTREIK 112
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQTHFPYTFGGGTREIK 112

RESULT 15
Q65ZC0 MOUSE PRELIMINARY; PRT; 219 AA.
ID Q65ZC0 MOUSE PRELIMINARY; PRT; 219 AA.
AC Q65ZC0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t.I.";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CAA85724.1; -; mRNA.
DR SMR; Q65ZC0; 1-219.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON TER 1
FT NON TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAP845 CRC64;

Query Match 70.8%; Score 418; DB 2; Length 219;
Best Local Similarity 71.4%; Pred. No. 7.6e-35;
Matches 80; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 DVNVTQSPLSVTLGQPASISCKSSQSLSDGKTFNLWFQRPQSPRLIYLVSKLD 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 DVNVTQSPLSVTLGQPASISCKSSQSLSDGKTFNLWFQRPQSPRLIYLVSKLD 60
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Db 1 ELVMTQSPLSVSLGDOASISCRSSQSLVHTNGTYLHWYLRKPGCLSPKLLIYVSNRF 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQTHFPYTFGGGTREIK 112
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQTHFPYTFGGGTREIK 112

Search completed: January 28, 2006, 09:44:18
Job time : 60.3634 secs
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 16.4805 Seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVWMTQSLPLVTLGQPAS.....CWOQTHFFPTFGQTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	112	2	US-09-809-739-14
2	590	100.0	112	2	US-09-840-459-12
3	590	100.0	112	2	US-09-497-625A-12
4	584	99.0	114	2	US-09-840-459-106
5	584	99.0	114	2	US-09-497-625A-106
6	577	97.8	112	2	US-09-809-739-15
7	577	97.8	112	2	US-09-840-459-13
8	577	97.8	112	2	US-09-497-625A-13
9	572	96.9	112	2	US-09-809-739-18
10	572	96.9	112	2	US-09-840-459-107
11	570	96.6	112	2	US-09-809-739-16
12	570	96.6	112	2	US-09-840-459-14
13	570	96.6	112	2	US-09-497-625A-14
14	565	95.8	112	2	US-09-809-739-17
15	565	95.8	112	2	US-09-840-459-15
16	565	95.8	112	2	US-09-497-625A-15
17	536	90.8	112	2	US-09-809-739-11
18	536	90.8	112	2	US-09-840-459-9
19	536	90.8	112	2	US-09-497-625A-9
20	536	90.8	142	2	US-09-840-459-102
21	536	90.8	142	2	US-09-497-625A-102
22	527	89.3	257	2	US-09-419-788-113
23	526	89.2	111	2	US-09-809-739-13
24	526	89.2	111	2	US-09-840-459-59
25	526	89.2	111	2	US-09-497-625A-11
26	526	89.2	111	2	US-09-497-625A-59
27	526	89.2	112	1	US-08-477-877B-89

28	526	89.2	112	1	US-08-472-281A-89	Sequence 89, Appl
29	526	89.2	112	1	US-08-477-989B-89	Sequence 89, Appl
30	526	89.2	112	2	US-09-462-140D-97	Sequence 97, Appl
31	524	88.8	113	2	US-09-698-705-7	Sequence 7, Appl
32	524	88.8	218	2	US-09-698-705-12	Sequence 12, Appl
33	521	88.3	112	2	US-09-840-459-54	Sequence 54, Appl
34	521	88.3	112	2	US-09-497-625A-54	Sequence 54, Appl
35	521	88.3	112	2	US-09-254-180C-8	Sequence 8, Appl
36	521	88.3	353	2	US-09-203-958A-4	Sequence 4, Appl
37	520	88.1	111	2	US-09-840-459-11	Sequence 11, Appl
38	520	88.1	112	2	US-09-840-459-58	Sequence 58, Appl
39	520	88.1	112	2	US-09-497-625A-58	Sequence 58, Appl
40	518	87.8	112	2	US-09-647-468-149	Sequence 149, Appl
41	518	87.8	112	2	US-09-647-468-150	Sequence 150, Appl
42	518	87.8	131	2	US-09-647-468-163	Sequence 163, Appl
43	518	87.8	131	2	US-09-647-468-164	Sequence 164, Appl
44	518	87.8	243	2	US-09-297-181-2	Sequence 2, Appl
45	516	87.5	535	2	US-08-983-035A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-09-809-739-14  
; Sequence 14, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-14

Query Match	100.0%	Score 590;	DB 2;	Length 112;
Best Local Similarity	100.0%	Pred. No. 3.1e-51;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DVWMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORQSPRLIYLVSKLD	60	
Db	1	DVWMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORQSPRLIYLVSKLD	60	
Qy	61	SGVPRFSGSGGTDFTLKISRVEAEDGIVYICWGTHPPVTFGQGTREIK	112	
Db	61	SGVPRFSGSGGTDFTLKISRVEAEDGIVYICWGTHPPVTFGQGTREIK	112	

RESULT 2  
US-09-840-459-12  
; Sequence 12, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; METHODS OF USE THEREFOR

```

; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-12

Query Match      100.0%; Score 590; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.1e-51;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLD 60

Qy 61 SGVDFRFGSGSGDTFTLKISRVEADVGVVYCMQGTFFPYTFGQGTREIK 112
Db 61 SGVDFRFGSGSGDTFTLKISRVEADVGVVYCMQGTFFPYTFGQGTREIK 112

RESULT 3
US-09-497-625A-12
; Sequence 12, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-12

Query Match      100.0%; Score 590; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.1e-51;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLD 60

Qy 61 SGVDFRFGSGSGDTFTLKISRVEADVGVVYCMQGTFFPYTFGQGTREIK 112
Qy
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; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-840-459-106

Query Match      99.0%; Score 584; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLDS 61
Db 2 VVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGSGDTFTLKISRVEADVGVVYCMQGTFFPYTFGQGTREIK 112
Db 62 GVPDRFSGSGSGDTFTLKISRVEADVGVVYCMQGTFFPYTFGQGTREIK 112

RESULT 5
US-09-497-625A-106
; Sequence 106, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-497-625A-106

Query Match      99.0%; Score 584; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLDS 61
Db 2 VVMTQSLSPVLTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGSGDTFTLKISRVEADVGVVYCMQGTFFPYTFGQGTREIK 112
Db 62 GVPDRFSGSGSGDTFTLKISRVEADVGVVYCMQGTFFPYTFGQGTREIK 112
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; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-497-625A-106

Query Match
Best Local Similarity 99.0%; Score 584; DB 2; Length 114;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILIYLVSKLDS 61
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILIYLVSKLDS 61

QY 62 GVPDRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112
Db 62 GVPDRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112

RESULT 6
US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Query Match
Best Local Similarity 97.8%; Score 577; DB 2; Length 112;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILIYLVSKL 60
Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRILIYLVSKL 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112

RESULT 7
US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
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; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-13

Query Match
Best Local Similarity 97.8%; Score 577; DB 2; Length 112;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILIYLVSKL 60
Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRILIYLVSKL 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112

RESULT 8
US-09-497-625A-13
; Sequence 13, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-13

Query Match
Best Local Similarity 97.8%; Score 577; DB 2; Length 112;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1' DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILIYLVSKL 60
Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRILIYLVSKL 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADGVVYVCWQGTTHPPTFGQGTREIK 112
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; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-14

Query Match          96.6%; Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 3e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60
DB 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60

QY 61 SGVPRFRSGSGTDTTLKISRVEADVGVYVCWQTHPPYTFGGTRLEIK 112
DB 61 SGVPRFRSGSGTDTTLKISRVEADVGVYVCWQTHPPYTFGGTRLEIK 112

RESULT 13
US-09-497-625A-14
; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

Query Match          96.6%; Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 3e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60
DB 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60

QY 61 SGVPRFRSGSGTDTTLKISRVEADVGVYVCWQTHPPYTFGGTRLEIK 112
DB 61 SGVPRFRSGSGTDTTLKISRVEADVGVYVCWQTHPPYTFGGTRLEIK 112

RESULT 14
US-09-809-739-17
; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
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; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-17

Query Match          95.8%; Score 565; DB 2; Length 112;
Best Local Similarity 96.4%; Pred. No. 9.3e-49;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60
DB 1 DVVMTQSPSLPVTILGHPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60

QY 61 SGVPRFRSGSGTDTTLKISRVEADVGVYVCWQTHPPYTFGGTRLEIK 112
DB 61 SGVPRFRSGSGTDTTLKISRVEADVGVYVCWQTHPPYTFGGTRLEIK 112
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RESULT 15
US-09-840-459-15
; Sequence 15, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-15

Query Match          95.8%; Score 565; DB 2; Length 112;
Best Local Similarity 96.4%; Pred. No. 9.3e-49;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60
DB 1 DVVMTQSPSLPVTILGHPASISCKSSQSLSDSGTKTFLNWFQRPQSPRRILYLVSKLD 60
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Qy 61 SGVPDRFSGSGTDTTLKISRVEADVGYYVCWGTHPPYTFGGTRLEIK 112  
Db 61 SGVPDRFSGSGTDTTLKISRVEADVGYYVCWGTHPPYTFGGTRLEIK 112

Search completed: January 28, 2006, 09:47:28  
Job time : 17.4805 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 47.7598 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVVMTQSPSLPVTIGQPAS.....CWSQTHFFYTFGGTRLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	112	3	US-09-835-087-3
2	590	100.0	112	3	US-09-809-739-14
3	590	100.0	112	3	US-09-840-459-12
4	590	100.0	112	4	US-10-766-773-12
5	590	100.0	112	4	US-10-766-610-12
6	590	100.0	112	4	US-10-733-563-12
7	590	100.0	112	5	US-10-662-061-14
8	584	99.0	114	3	US-09-840-459-106
9	584	99.0	114	4	US-10-766-773-106
10	584	99.0	114	4	US-10-766-610-106
11	584	99.0	114	4	US-10-733-563-106
12	577	97.8	112	3	US-09-835-087-4
13	577	97.8	112	3	US-09-809-739-15
14	577	97.8	112	3	US-09-840-459-13
15	577	97.8	112	4	US-10-766-773-13
16	577	97.8	112	4	US-10-766-610-13
17	577	97.8	112	4	US-10-733-563-13
18	577	97.8	112	5	US-10-662-061-15
19	572	96.9	112	3	US-09-835-087-7
20	572	96.9	112	3	US-09-809-739-18
21	572	96.9	112	3	US-09-840-459-107
22	572	96.9	112	4	US-10-766-610-107
23	572	96.9	112	4	US-10-733-563-107
24	572	96.9	112	5	US-10-662-061-18
25	570	96.6	112	3	US-09-835-087-5
26	570	96.6	112	3	US-09-809-739-16
27	570	96.6	112	3	US-09-840-459-14

28	570	96.6	112	4	US-10-766-773-14	Sequence 14, Appl
29	570	96.6	112	4	US-10-766-610-14	Sequence 14, Appl
30	570	96.6	112	4	US-10-733-563-14	Sequence 14, Appl
31	570	96.6	112	5	US-10-662-061-16	Sequence 16, Appl
32	565	95.8	112	3	US-09-835-087-6	Sequence 6, Appl
33	565	95.8	112	3	US-09-809-739-17	Sequence 17, Appl
34	565	95.8	112	3	US-09-840-459-15	Sequence 15, Appl
35	565	95.8	112	4	US-10-766-773-15	Sequence 15, Appl
36	565	95.8	112	4	US-10-766-610-15	Sequence 15, Appl
37	565	95.8	112	4	US-10-733-563-15	Sequence 15, Appl
38	565	95.8	112	5	US-10-662-061-17	Sequence 17, Appl
39	559	94.7	113	5	US-10-476-265-9	Sequence 9, Appl
40	559	94.7	219	5	US-10-476-265-11	Sequence 11, Appl
41	559	94.7	239	5	US-10-476-265-19	Sequence 19, Appl
42	542	91.9	132	4	US-10-010-942B-11	Sequence 11, Appl
43	542	91.9	132	4	US-10-388-389-11	Sequence 11, Appl
44	542	91.9	132	4	US-10-703-713-11	Sequence 11, Appl
45	542	91.9	132	4	US-10-704-070-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-835-087-3  
; Sequence 3, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; FILE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-3

Query Match	100.0%	Score 590;	DB 3;	Length 112;
Best Local Similarity	100.0%	Pred. No. 2.8e-47;		
Matches 112;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
Qy	1	DVVMTQSPSLPVTIGQPASISCKSSQSLSDGKTFELNWFQORPGQSPRLIYLVSKLD	60	
Db	1	DVVMTQSPSLPVTIGQPASISCKSSQSLSDGKTFELNWFQORPGQSPRLIYLVSKLD	60	
Qy	61	SGVPRPFGSGSGTDTFLKISRVEADVGVIYCWQTHFFYTFGGTRLEIK	112	
Db	61	SGVPRPFGSGSGTDTFLKISRVEADVGVIYCWQTHFFYTFGGTRLEIK	112	

RESULT 2  
US-09-809-739-14  
; Sequence 14, Application US/09809739  
; Patent No. US20020106369A1  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-14

Query Match      100.0%; Score 590; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYICWGTHFPYTFGGQTRLEIK 112
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYICWGTHFPYTFGGQTRLEIK 112

RESULT 3
US-09-840-459-12
; Sequence 12, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-12

Query Match      100.0%; Score 590; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYICWGTHFPYTFGGQTRLEIK 112
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYICWGTHFPYTFGGQTRLEIK 112

RESULT 4
US-10-766-773-12
; Sequence 12, Application US/10766773
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-610-12

Query Match      100.0%; Score 590; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLD 60
Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112

RESULT 6
US-10-733-563-12
; Sequence 12, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-12

Query Match      100.0%; Score 590; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLD 60
Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112

RESULT 7
US-10-662-061-14
; Sequence 14, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
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; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-662-061-14

Query Match      100.0%; Score 590; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLD 60
Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112

RESULT 8
US-09-840-459-106
; Sequence 106, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-840-459-106

Query Match      99.0%; Score 584; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLDS 61
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFNLNWFQORFGQSPRRILYLVSKLDS 61

QY 62 GVPDRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112
Db 62 GVPDRFSGSGGTDFTLKISRVEAEDGIVYYCWQGTFFPYTFGGQTRLEIK 112

RESULT 9
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US-10-766-773-106
; Sequence 106, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-10-766-773-106

Query Match          99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61
Db  2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61

Qy  62 GVPDRFSGSGGTFTLKISRVEAEDVGVYYCWQGTTHFPYTFGGQTRLEIK 112
Db  62 GVPDRFSGSGGTFTLKISRVEAEDVGVYYCWQGTTHFPYTFGGQTRLEIK 112

RESULT 10
US-10-766-610-106
; Sequence 106, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
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; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-10-766-610-106

Query Match          99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61
Db  2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61

Qy  62 GVPDRFSGSGGTFTLKISRVEAEDVGVYYCWQGTTHFPYTFGGQTRLEIK 112
Db  62 GVPDRFSGSGGTFTLKISRVEAEDVGVYYCWQGTTHFPYTFGGQTRLEIK 112

RESULT 11
US-10-733-563-106
; Sequence 106, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized light chain
US-10-733-563-106

Query Match          99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61
Db  2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQORPGQSPRLIYLVSKLDS 61

Qy  62 GVPDRFSGSGGTFTLKISRVEAEDVGVYYCWQGTTHFPYTFGGQTRLEIK 112
Db  62 GVPDRFSGSGGTFTLKISRVEAEDVGVYYCWQGTTHFPYTFGGQTRLEIK 112

RESULT 12
US-09-835-087-4
; Sequence 4, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
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; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-4

Query Match          97.8%; Score 577; DB 3; Length 112;
Best Local Similarity 98.2%; Pred. No. 4.5e-46;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRLIYLVSKLD 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFPYTFQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFPYTFQGTRLRIK 112

RESULT 13
US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Query Match          97.8%; Score 577; DB 3; Length 112;
Best Local Similarity 98.2%; Pred. No. 4.5e-46;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTTLGQPASISCKSSQSLDSDGKTFLNWFQORPGQSPRRLIYLVSKLD 60
Db 1 DVVMTQSPSLPVTTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRLIYLVSKLD 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFPYTFQGTRLRIK 112
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTTHFPYTFQGTRLRIK 112

RESULT 14
US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

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Db 1 DVVMTQSPVLTIGQPASISCKSSQSLDSDGKTFLNWLLQRFQSPRLLIYVSKLD 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCQGTHFPYTFGQGTREIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYYCQGTHFPYTFGQGTREIK 112

Search completed: January 28, 2006, 10:11:21  
Job time : 47.7598 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 6.72673 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-12  
Perfect score: 590  
Sequence: 1 DVWMTQSLPLVTLGQPAS.....CMQGTHTFPYFGQTRLLEIK 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_New.\*  
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2: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/2/pubpaa/PCR\_NEW\_PUB.pep.\*  
5: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	590	100.0	112	7	US-11-075-184A-3	Sequence 3, Appl1
2	577	97.8	112	7	US-11-075-184A-4	Sequence 4, Appl1
3	572	96.9	112	7	US-11-075-184A-7	Sequence 7, Appl1
4	570	96.6	112	7	US-11-075-184A-5	Sequence 5, Appl1
5	565	95.8	112	7	US-11-075-184A-6	Sequence 6, Appl1
6	542	91.9	132	6	US-10-789-273-11	Sequence 11, Appl1
7	536	90.8	112	7	US-11-075-184A-1	Sequence 1, Appl1
8	536	90.8	132	6	US-10-789-273-2	Sequence 2, Appl1
9	520	88.1	132	6	US-10-789-273-5	Sequence 5, Appl1
10	510	86.4	253	7	US-11-054-515-1964	Sequence 1964, Ap
11	507	85.9	112	6	US-10-477-950-4	Sequence 4, Appl1
12	491.5	83.3	244	7	US-11-054-515-1991	Sequence 1991, Ap
13	490.5	83.1	261	7	US-11-056-825-2	Sequence 2, Appl1
14	485.5	82.3	259	7	US-11-056-825-7	Sequence 7, Appl1
15	483	81.9	113	7	US-11-054-669-122	Sequence 122, App
16	480	81.4	139	7	US-11-128-900-25	Sequence 25, Appl1
17	480	81.4	139	7	US-11-128-900-114	Sequence 114, App
18	474	80.3	132	6	US-10-489-866-30	Sequence 30, Appl1
19	470	79.7	100	7	US-11-054-669-75	Sequence 75, Appl1
20	470	79.7	100	7	US-11-054-669-76	Sequence 76, Appl1
21	470	79.7	100	7	US-11-084-554-103	Sequence 103, App
22	470	79.7	100	7	US-11-084-554-107	Sequence 107, App
23	470	79.7	100	7	US-11-128-900-113	Sequence 113, App
24	470	79.7	100	7	US-11-004-590-82	Sequence 82, Appl1
25	470	79.7	100	7	US-11-004-590-83	Sequence 83, Appl1

26	459	77.8	112	7	US-11-012-353-57	Sequence 57, Appl1
27	457	77.5	112	7	US-11-012-353-61	Sequence 61, Appl1
28	457	77.5	131	7	US-11-012-353-63	Sequence 63, Appl1
29	456	77.3	112	7	US-11-012-353-65	Sequence 65, Appl1
30	456	77.3	131	7	US-11-012-353-67	Sequence 67, Appl1
31	451	76.4	112	7	US-11-012-353-60	Sequence 60, Appl1
32	451	76.4	113	6	US-10-834-397-15	Sequence 15, Appl1
33	447	75.8	113	6	US-10-932-334-60	Sequence 60, Appl1
34	447	75.8	113	6	US-10-932-334-65	Sequence 65, Appl1
35	447	75.8	131	7	US-11-125-837-23	Sequence 23, Appl1
36	446	75.6	113	6	US-10-932-334-59	Sequence 59, Appl1
37	445	75.4	112	7	US-11-012-353-55	Sequence 55, Appl1
38	445	75.4	112	7	US-11-012-353-56	Sequence 56, Appl1
39	445	75.4	263	7	US-11-089-266-66	Sequence 66, Appl1
40	444	75.3	144	7	US-11-055-163-16	Sequence 16, Appl1
41	443	75.1	113	6	US-10-932-334-61	Sequence 61, Appl1
42	443	75.1	149	7	US-11-089-266-2	Sequence 2, Appl1
43	443	75.1	239	7	US-11-139-499-6	Sequence 6, Appl1
44	441	74.7	113	6	US-10-489-866-20	Sequence 20, Appl1
45	441	74.7	116	7	US-11-065-943-49	Sequence 49, Appl1

ALIGNMENTS

RESULT 1  
US-11-075-184A-3  
; Sequence 3, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelhiem International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; PRIOR FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine ID9 antibody kappa light chain variable region,  
; OTHER INFORMATION: ID9RKA  
US-11-075-184A-3

Query Match	100.0%;	Score 590;	DB 7;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 1.2e-40;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DVWMTQSLPLVTLGQPASISCKSSQSLSDSGKTFPLNWFQQRFGQSPRLIYLVS	KLD 60	
Db	1	DVWMTQSLPLVTLGQPASISCKSSQSLSDSGKTFPLNWFQQRFGQSPRLIYLVS	KLD 60	
QY	61	SGVDPDRFGSGSGTDTFTLKISRVEADVGVIYCMQGTHTFPYFGQGT	RLLEIK 112	
Db	61	SGVDPDRFGSGSGTDTFTLKISRVEADVGVIYCMQGTHTFPYFGQGT	RLLEIK 112	

RESULT 2  
US-11-075-184A-4  
; Sequence 4, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelhiem International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669

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; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; OTHER INFORMATION: 1D9RKB
US-11-075-184A-4

Query Match          97.8%; Score 577; DB 7; Length 112;
Best Local Similarity 98.2%; Pred. No. 1.3e-39;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112

RESULT 3
US-11-075-184A-7
; Sequence 7, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelhiem International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; OTHER INFORMATION: 1D9RKE
US-11-075-184A-7

Query Match          96.9%; Score 572; DB 7; Length 112;
Best Local Similarity 97.3%; Pred. No. 3.3e-39;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db 1 DVWMTQSLSLPVTLGHPASISCKSSQSLLSDSGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112

RESULT 4
US-11-075-184A-5
; Sequence 5, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelhiem International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; OTHER INFORMATION: 1D9RKC
US-11-075-184A-5

Query Match          95.8%; Score 565; DB 7; Length 112;
Best Local Similarity 96.4%; Pred. No. 1.2e-38;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db 1 DVWMTQSLSLPVTLGHPASISCKSSQSLLSDSGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112

RESULT 5
US-11-075-184A-6
; Sequence 6, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelhiem International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; OTHER INFORMATION: 1D9RKC
US-11-075-184A-6

Query Match          95.8%; Score 565; DB 7; Length 112;
Best Local Similarity 96.4%; Pred. No. 1.2e-38;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFLNWFQRPQSPRRLIYLVSKLD 60
Db 1 DVWMTQSLSLPVTLGHPASISCKSSQSLLSDSGKTFLNWLLQRPQSPRRLIYLVSKLD 60

Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVVYCWQGTFFPYTFGGQTRLEIK 112

RESULT 6
US-10-789-273-11
; Sequence 11, Application US/10789273
; Publication No. US20050249725A1
```

; GENERAL INFORMATION:  
 ; APPLICANT: Basi, Gurig  
 ; APPLICANT: Saldanha, Jose  
 ; APPLICANT: Yednock, Ted  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
 ; FILE REFERENCE: ELN-002CP  
 ; CURRENT APPLICATION NUMBER: US/10/789,273  
 ; CURRENT FILING DATE: 2004-02-27  
 ; PRIOR APPLICATION NUMBER: US/10/388,389  
 ; PRIOR FILING DATE: 2003-03-12  
 ; PRIOR APPLICATION NUMBER: US 10/010,942  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: US 60/251,892  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 132  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: SIGNAL  
 ; LOCATION: (1)...(20)  
 ; OTHER INFORMATION: humanized 3D6 light chain variable region  
 US-10-789-273-11

Query Match 91.9%; Score 542; DB 6; Length 132;  
 Best Local Similarity 91.1%; Pred. No. 8.6e-37;  
 Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFNWFQRPQSPRRLLIYLVSKLD 60  
 DB 21 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTYLNWLLQKPGQSPQRLIYLVSKLD 80  
 QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCWQGTTHPFTFGQGTREIK 112  
 DB 81 SGVPRFSGSGGTDTFTLKISRVEADVGYYCWQGTTHPFTFGQGTREIK 132

RESULT 7  
 US-11-075-184A-1  
 ; Sequence 1, Application US/11075184A  
 ; Publication No. US20050260139A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boehringer Ingelheim International GmbH  
 ; APPLICANT: PAIBET, Michel  
 ; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
 ; FILE REFERENCE: 1/1669  
 ; CURRENT APPLICATION NUMBER: US/11/075,184A  
 ; CURRENT FILING DATE: 2005-03-08  
 ; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
 ; PRIOR FILING DATE: 2004-03-30  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1  
 ; LENGTH: 112  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Murine 1D9 antibody kappa light chain variable (VK) region;  
 ; OTHER INFORMATION: presumably Mus musculus  
 US-11-075-184A-1

Query Match 90.8%; Score 536; DB 7; Length 112;  
 Best Local Similarity 89.3%; Pred. No. 2.2e-36;  
 Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFNWFQRPQSPRRLLIYLVSKLD 60  
 DB 1 DVVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTYLNWLLQKPGQSPQRLIYLVSKLD 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCWQGTTHPFTFGQGTREIK 112  
 DB 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCWQGTTHPFTFGQGTREIK 112

RESULT 8  
 US-10-789-273-5  
 ; Sequence 5, Application US/10789273  
 ; Publication No. US20050249725A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Basi, Gurig  
 ; APPLICANT: Saldanha, Jose  
 ; APPLICANT: Yednock, Ted  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
 ; FILE REFERENCE: ELN-002CP  
 ; CURRENT APPLICATION NUMBER: US/10/789,273  
 ; CURRENT FILING DATE: 2004-02-27  
 ; PRIOR APPLICATION NUMBER: US/10/388,389  
 ; PRIOR FILING DATE: 2003-03-12  
 ; PRIOR APPLICATION NUMBER: US 10/010,942  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: US 60/251,892  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 132  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: SIGNAL  
 ; LOCATION: (1)...(20)  
 ; OTHER INFORMATION: humanized 3D6 light chain variable region  
 US-10-789-273-5

Query Match 90.8%; Score 536; DB 6; Length 132;  
 Best Local Similarity 91.0%; Pred. No. 2.5e-36;  
 Matches 101; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 VVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTFNWFQRPQSPRRLLIYLVSKLDS 61  
 DB 22 VVMTQSPVLSPLVTGQPASISCKSSQSLDSDGKTYLNWLLQKPGQSPQRLIYLVSKLDS 81  
 QY 62 GVPDRFSGSGGTDTFTLKISRVEADVGYYCWQGTTHPFTFGQGTREIK 112  
 DB 82 GVPDRFSGSGGTDTFTLKISRVEADVGYYCWQGTTHPFTFGQGTREIK 132

RESULT 9  
 US-10-789-273-2  
 ; Sequence 2, Application US/10789273  
 ; Publication No. US20050249725A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Basi, Gurig  
 ; APPLICANT: Saldanha, Jose  
 ; APPLICANT: Yednock, Ted  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
 ; FILE REFERENCE: ELN-002CP  
 ; CURRENT APPLICATION NUMBER: US/10/789,273  
 ; CURRENT FILING DATE: 2004-02-27  
 ; PRIOR APPLICATION NUMBER: US/10/388,389  
 ; PRIOR FILING DATE: 2003-03-12  
 ; PRIOR APPLICATION NUMBER: US 10/010,942  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: US 60/251,892  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 132  
 ; TYPE: PRT



Qy		1	DVWMTQSPSLPVTILGQPASISCKSSQSLLDSGKTFLNWFQORFGSQPRRLIYLVSULD	60
			:	
Db		133	DVWMTQSPSLPVTILGQPASISCRSSVLHSDGNTLYLNMFFQORFGSQPRRLIYKVSNRD	192
			:	
Qy		61	SGVPDRFGSGSGDTFTLKISRVEADVGVIYCWGTHPPYTFGGQTRLEIK	112
			:	
Db		193	FGVPDRFGSGSGTFTLKISRVEADVGVIYCWGTH-RIYTFGGQTRLEIK	243

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RESULT 13
US-11-056-825-2
: Sequence 2, Application US/11056825
: Publication No. US20050255109A1
: GENERAL INFORMATION:
: APPLICANT: Pelding-Habermann, Brunhilde
: APPLICANT: Janda, Kim D.
: APPLICANT: Saven, Alan
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
: FILE REFERENCE: SRCP-0042
: CURRENT APPLICATION NUMBER: US/11/056,825
: CURRENT FILING DATE: 2005-02-11
: PRIOR APPLICATION NUMBER: US 60/626,726
: PRIOR FILING DATE: 2004-11-10
: PRIOR APPLICATION NUMBER: US 60/544,807
: PRIOR FILING DATE: 2004-02-13
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 2
: LENGTH: 261
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Synthetic Construct
US-11-056-825-2

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Query Match      83.1%; Score 490.5; DB 7; Length 261;
Best Local Similarity 82.3%; Pred. No. 1.7e-32;
Matches 93; Conservative 12; Mismatches 7; Indels 1; Gaps 1;
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Qy    1 DVVMTQSPLSLPVTLGPASISCKSSQLSDSDGKTFILNWFQQRPQGSPRLIYLVSKLD 60
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   134 EIVLTQSLPSLVLTPGLPASPISCSSQNLYVDGNTVLSWFPQRPQGSPRLIYKVSNRD 193

Qy    61 SGVPDRSGSGSGETDFTLKISRVAEDVGVIYCQGTHP-PYTGGQTGLEIK 112

Db   194 SGVPDRSGSGSGETDFTLKISRVAEDI GVVIYCQGTHTWPRTTGGQGVKEIK 246
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RESULT 14
US-11-056-825-7
; Sequence 7, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SSCP-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626, 726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544, 807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-825-7

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```

Query Match      82.3%; Score 485.5; DB 7; Length 259;
Best Local Similarity 81.4%; Pred. No. 4.2e-32;
Matches 92; Conservative 12; Mismatches 8; Indels 1; Gaps 1

Qy      1  DVVWTSPLSLPVTLGQPASISCKSSQSLDSDGKTFLEWPFQQRPGSGPRRLIYLVSKLD 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      134  EIVLTQSLPVTLGQPASISCRSSQNLVYSDGNTVLSWFQQRPGSGPRRLIYKVSNRD 193

Qy      61  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCWQGHF-PYTFGQTRLRIK 112

Db      194  SGVPDRFSGSGSGTDFTLKISRVEREDIGVYCMQGHWPRTFGQGVKRIK 246

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RESULT 15
US-11-054-669-122
; Sequence 122, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 122
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-122

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[illegible]

Search completed: January 28, 2006, 10:12:13  
Job time : 6.72673 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 61.3108 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVGNGVGGTILVTSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	4	Aae06954 Humanised
2	620	100.0	117	4	Aau09927 Humanised
3	620	100.0	117	5	Abg75536 Humanised
4	620	100.0	117	5	Aaol14980 Humanised
5	620	100.0	117	5	Adf98240 Humanised
6	620	100.0	117	8	Adq89239 Humanised
7	620	100.0	117	9	Aeb09512 Humanised
8	620	100.0	119	4	Aae07034 Humanised
9	620	100.0	119	8	Adq89326 Humanised
10	620	100.0	119	9	Aeb09599 Humanised
11	613	98.9	117	4	Aae06955 Humanised
12	613	98.9	117	5	Abg75537 Humanised
13	613	98.9	117	5	Aaol14981 Humanised
14	613	98.9	117	5	Adf98241 Humanised
15	613	98.9	117	8	Adq89240 Humanised
16	613	98.9	117	9	Aeb09513 Humanised
17	604	97.4	117	4	Aae06956 Humanised
18	604	97.4	117	4	Aau09929 Humanised
19	604	97.4	117	4	Aau09928 Humanised
20	604	97.4	117	5	Abg75538 Humanised
21	604	97.4	117	5	Aaol14982 Humanised
22	604	97.4	117	5	Adf98242 Humanised
23	604	97.4	117	8	Adq89241 Humanised
24	604	97.4	117	9	Aeb09514 Humanised

25	599	96.6	117	4	Aae06957	Aae06957 Humanised
26	599	96.6	117	4	Aau09930	Aau09930 Humanised
27	599	96.6	117	5	Abg75539	Abg75539 Humanised
28	599	96.6	117	5	Adf98243	Adf98243 Humanised
29	599	96.6	117	8	Adq89242	Adq89242 Humanised
30	599	96.6	117	9	Aeb09515	Aeb09515 Humanised
31	588.5	94.9	118	5	Aaol14983	Aaol14983 Humanised
32	548	88.4	117	4	Aae06947	Aae06947 Murine ID
33	548	88.4	117	4	Aau09919	Aau09919 Murine mAb
34	548	88.4	117	5	Abg75528	Abg75528 Murine mAb
35	548	88.4	117	5	Adf98238	Adf98238 Murine mAb
36	548	88.4	117	8	Adq89232	Adq89232 Mouse imm
37	548	88.4	117	9	Aeb09505	Aeb09505 Murine ID
38	548	88.4	125	8	Adj95988	Adj95988 Immunoglo
39	548	88.4	148	4	Aae07033	Aae07033 Murine an
40	548	88.4	148	8	Adq89322	Adq89322 Mouse imm
41	548	88.4	148	9	Aeb09595	Aeb09595 Murine ID
42	539	86.9	117	5	Aaol14978	Aaol14978 Mouse hea
43	505.5	81.5	452	9	Adx01863	Adx01863 SARS coro
44	505	81.5	120	9	Adv86726	Adv86726 Anti-FLJ3
45	502	81.0	120	9	Adv86731	Adv86731 Anti-PLJ3

ALIGNMENTS

RESULT 1  
AAE06954  
ID AAE06954 standard; protein; 117 AA.  
XX AC AAE06954;

DT 11-SEP-2003 (revised)  
DT 16-OCT-2001 (first entry)  
XX

DE Humanised murine ID9 antibody heavy chain variable region, ID9RHA.

XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW multiple sclerosis; atherosclerosis; arteriosclerosis; stenosis; asthma;  
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
KW inflammatory glomerulopathy; vascular intervention; ID9 antibody;  
KW neonatal hyperplasia; VH; heavy chain variable region; ID9RHA.

XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.

Key Location/Qualifiers  
Region 27..35 /label= CDR1  
Region 50..68 /note= "Complementarity determining region 1"  
Region /label= CDR2  
Region /note= "Complementarity determining region 2"  
Region 101..106 /label= CDR3  
Region /note= "Complementarity determining region 3"

WO200157226-A1.

09-AUG-2001.

02-FEB-2001; 2001WO-US003537.

03-FEB-2000; 2000US-00497625.

(MILL-) MILLENNIUM PHARM INC.

Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;





RESULT 3  
 ID ABG75536 standard; protein; 117 AA.  
 AC  
 AC ABG75536;  
 DT  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Humanised mouse mAb 1D9 heavy chain variable region, 1D9RHAVH.  
 XX  
 KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
 KW antigen binding fragment; cellular adhesion molecule; adhesion;  
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
 KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
 KW endovascular disease; prosthetic valve; transplantation;  
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
 KW chronic bronchitis; asthma; graft-versus-host disease;  
 KW chronic inflammatory disease; hypersensitivity pneumonitis;  
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HP-21/28;  
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
 KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RHAVH;  
 KW heavy chain variable region; VH; complementarity determining region; CDR;  
 KW mutant; mutein.  
 XX  
 XX Mus sp.  
 OS  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 31..35  
 FT /note="Mouse complementarity determining region 1  
 FT (CDR1)"  
 FT Region 50..68  
 FT /note="Mouse complementarity determining region 2  
 FT (CDR2)"  
 FT Region 101..106  
 FT /note="Mouse complementarity determining region 3  
 FT (CDR3)"  
 XX  
 PN US2002106369-A1.  
 XX  
 XX 08-AUG-2002.  
 XX  
 XX 15-MAR-2001; 2001US-00809739.  
 XX  
 XX 17-MAR-2000; 2000US-00528267.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Horvath CJ, Rao PE;  
 XX  
 XX WPI; 2002-697861/75.  
 XX  
 XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
 PT administering first and second agents that inhibit adhesion and/or  
 PT recruitment of neutrophils and mononuclear cells, respectively to site of  
 PT vascular injury.  
 XX  
 XX Claim 32; Fig 18; 59pp; English.  
 XX  
 CC The invention discloses a method for inhibiting stenosis or restenosis of  
 CC a blood vessel following vascular injury in a subject. The method  
 CC involves administering to the subject a first therapeutic agent, which  
 CC comprises an antibody or its antigen binding fragment which binds a  
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
 CC of neutrophils to a site of vascular injury and a second therapeutic  
 CC agent, which comprises an antagonist of CCR2 function, that inhibits  
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
 CC injury. The vascular injury arises from a vascular intervention procedure  
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty

CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
 CC stenting, insertion of a prosthetic valve and transplantation of organs,  
 CC tissues or cells. The method is also useful for treating inflammatory  
 CC diseases or conditions mediated by early neutrophil activity and later  
 CC mononuclear cell activity. Preferably, the method is useful for treating  
 CC asthma and graft-versus-host disease, cholecystitis, chronic bronchitis,  
 CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
 CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
 CC mellitus. The method is also useful for treating inflammatory bowel  
 CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy  
 CC chain variable region (VH), 1D9RHAVH, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human 4B4'CL  
 CC mAb VH regions  
 XX  
 SQ Sequence 117 AA;  
 Query Match 100.0%; Score 620; DB 5; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYANMWVRQAPGKGLVWGRIRTKNNYAT 60  
 DB 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYANMWVRQAPGKGLVWGRIRTKNNYAT 60  
 QY 61 YYADSVKDRPTISRDDSKNTLYLQWNSLKTEDTAVYCTTFFGNGVWGOGTLVTVSS 117  
 DB 61 YYADSVKDRPTISRDDSKNTLYLQWNSLKTEDTAVYCTTFFGNGVWGOGTLVTVSS 117  
 RESULT 4  
 AA014980  
 ID AA014980 standard; protein; 117 AA.  
 XX  
 AC AA014980;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE Humanised murine heavy chain variable region (1D9RHa Vh).  
 XX  
 KW Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
 KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
 KW bowel transplant; heart transplant; graft versus host disease;  
 KW chronic graft rejection; antibody heavy chain variable region; 1D9RHa Vh.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 XX US2002042370-A1.  
 XX  
 XX 11-APR-2002.  
 XX  
 XX 13-APR-2001; 2001US-00835087.  
 XX  
 XX 14-APR-2000; 2000US-00549448.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Hancock WW;  
 XX  
 XX WPI; 2002-351265/38.  
 XX  
 XX Inhibiting graft rejection, graft versus host disease or chronic

PT rejection of a transplanted graft, involves administering a CCR2  
PT antagonist.

XX Claim 26; Fig 2; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
CC versus host disease or chronic rejection of a transplanted graft. The  
CC method involves administering an antagonist of CC chemokine receptor 2  
CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
CC complementarity determining regions from various non-human origins). CCR2  
CC is known to be involved in the rejection of transplanted grafts. The  
CC method of the invention is useful for inhibiting graft rejection -  
CC particularly allografts such as kidney, liver, lung, heart-lung,  
CC pancreas, bowel and heart. The method of the invention is also useful for  
CC inhibiting graft versus host disease and for inhibiting chronic rejection  
CC of a transplanted graft. The present amino acid sequence represents a  
CC humanised murine antibody heavy chain variable region (1D9RHa Vh)

XX Sequence 117 AA;

Query Match 100.0%; Score 620; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 5

ADP98240

ID ADP98240 standard; protein; 117 AA.

XX ADP98240;

XX 26-FEB-2004 (first entry)

XX Humanised 1D9 heavy chain variable region, 1D9RHA VH, SEQ ID 10.

XX Immunosuppressive; CCR2 function inhibitor; graft rejection;

KW graft versus host disease; CC chemokine receptor 2; CCR2;

KW anti-CCR2 antibody.

XX Synthetic.

OS Mus musculus.

OS Homo sapiens.

XX WO200178653-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US012139.

XX 14-APR-2000; 2000US-00549448.

PA (MILL-) MILLENNIUM PHARM INC.

XX Hancock WW;

XX WPI; 2002-017543/02.

XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
PT involves use of CC chemokine receptor 2 inhibitor.

XX Claim 26; Fig 2; 44pp; English.

XX The present invention relates to a method for inhibiting graft rejection  
CC or graft versus host diseases. The method comprises administration of a

CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
CC recipient of a transplanted graft. The CCR2 function antagonist is an  
CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
CC ADP98240-ADP98249). The method is useful for inhibiting rejection,  
CC particularly chronic rejection of a graft, particularly an allograft of  
CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
CC inhibiting graft versus host disease for a bone marrow graft.

XX Sequence 117 AA;

Query Match 100.0%; Score 620; DB 5; Length 117;

Best Local Similarity 100.0%; Pred. No. 8.1e-48;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 6

ADQ89239

ID ADQ89239 standard; protein; 117 AA.

XX ADQ89239;

XX 21-OCT-2004 (first entry)

XX Humanised immunoglobulin protein #5.

XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;

KW inflammatory disease; autoimmune disorder; graft rejection;

KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;

KW anti-HIV; virucide; antiarteriosclerotic.

XX Synthetic.

XX US2004151721-A1.

XX 05-AUG-2004.

XX 10-DEC-2003; 2003US-00733563.

XX 19-OCT-2001; 2001US-0350166P.

PR 26-JUN-2002; 2002US-0392364P.

PR 17-OCT-2002; 2002US-00272899.

XX (OKEE/) O'KEEFE T.

PA (PONA/) PONAETH P.

XX O'Keefe T, Ponath P;

XX WPI; 2004-580175/56.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.

XX Claim 1; SEQ ID NO 17; 129pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised

immunoglobulin protein of the invention.

Sequence 117 AA;

Query Match 100.0%; Score 620; DB 8; Length 117;  
Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60  
1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60

61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYCTTFFGNGVWGQGLTVTVSS 117  
61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYCTTFFGNGVWGQGLTVTVSS 117

RESULT 7  
AEB09512  
ID AEB09512 standard; protein; 117 AA.  
AC AEB09512;  
DT 08-SEP-2005 (first entry)  
DE Humanized 1D9 heavy chain variable region SEQ ID NO 17.  
KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
KW antibody engineering; therapeutic; diagnosis; inflammation;  
KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
KW heavy chain variable region.  
OS Synthetic.  
XX WO2005060368-A2.  
PN 07-JUL-2005.  
PD 10-DEC-2003; 2003WO-US039599.  
PF 10-DEC-2003; 2003WO-US039599.  
PR (MILL-) MILLENNIUM PHARM INC.  
PA Okeefe T, Ponath P;  
PI WPI; 2005-488561/49.  
DR New humanized immunoglobulin or its antigen binding portion having  
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
PT diseases.  
XX Claim 1; SEQ ID NO 17; 192pp; English.

The invention describes a humanized immunoglobulin (I) or its antigen  
binding portion having binding specificity for CC-chemokine receptor 2  
(CCR2) and having a heavy chain and a light chain, where the heavy chain  
comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
sequence, given in specification or its portion, and the light chain  
comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
in specification. Also described are: a humanized immunoglobulin heavy  
chain, or its antigen binding fragment, having binding specificity for  
CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
immunoglobulin light chain, or its antigen binding fragment, having  
binding specificity for CCR2 and comprising the amino acid sequence of  
(SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
sequence, given in specification. The following are disclosed: isolated  
nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
construct comprising nucleic acid molecule encoding (I); and host cell  
comprising the nucleic acid molecule. (I) is useful as a therapeutic

agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
reducing inflammatory response, for use in the treatment of diseases  
associated with leukocyte infiltration of tissue, e.g. in the treatment  
of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
fluid), and for modulating binding function and/or leukocyte trafficking  
modulated by CCR2. This is the amino acid sequence of a humanized 1D9  
heavy chain variable region used in the creation of a humanized anti-CCR2  
-antibody.

Sequence 117 AA;

Query Match 100.0%; Score 620; DB 9; Length 117;  
Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60  
1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60

61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYCTTFFGNGVWGQGLTVTVSS 117  
61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYCTTFFGNGVWGQGLTVTVSS 117

RESULT 8  
AEB07034  
ID AEB07034 standard; protein; 119 AA.  
XX AAE07034;  
XX 11-SEP-2003 (revised)  
DT 16-OCT-2001 (first entry)  
DE Humanised murine antibody heavy chain 1D9RHA protein.  
XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW multiple sclerosis; atherosclerosis; atherosclerosis; stenosis; asthma;  
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
KW inflammatory glomerulopathy; vascular intervention;  
KW neointimal hyperplasia; antibody 1D9 heavy chain; 1D9RHA.  
XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX WO200157226-A1.  
PN 09-AUG-2001.  
PD 02-FEB-2001; 2001WO-US003537.  
PF 03-FEB-2000; 2000US-00497625.  
PR (MILL-) MILLENNIUM PHARM INC.  
PA Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
PI WPI; 2001-488888/53.  
DR N-PSDB; AAD13179.  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
PT disorder in a patient, comprises a binding specificity for CCR2, and a  
PT non-human antigen binding region and human immunoglobulin.  
XX Disclosure; Fig 23; 183pp; English.

CC The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
 CC comprising an antigen binding region of non-human origin and at least a  
 CC portion of an immunoglobulin of human origin. The humanised antibodies  
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
 CC are useful for inhibiting or treating HIV infection. The proteins of the  
 CC invention are useful for inhibiting leukocyte trafficking, for treating  
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
 CC disorders such as rheumatoid arthritis and multiple sclerosis,  
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
 CC are useful in therapy or diagnosis, and in the manufacture of a  
 CC medicament for treating CCR-2 mediated disease. They are also useful for  
 CC treating allergy, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and IgE-mediated allergic reaction, shock,  
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
 CC associated with vascular intervention, including angioplasty and/or stent  
 CC placement in a mammal. Humanised antibodies are also useful for  
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
 CC with vascular intervention. The present sequence is humanised murine  
 CC antibody heavy chain region, 1D9RHA. 1D9RHA sequence consist of the  
 CC complementarity determining regions (CDRs) of the murine 1D9 antibody  
 CC heavy chain variable (VH) region genetically inserted into the framework  
 CC regions (FRs) of the human 4B4'CL antibody VH region. (Updated on 11-SEP-  
 CC 2003 to standardise OS field)

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 620; DB 4; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60  
 Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
 Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 9

ID AQ89326 standard; protein; 119 AA.

XX AC AQ89326;

XX DT 21-OCT-2004 (first entry)

XX DE Humanised immunoglobulin protein #9.

XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
 KW inflammatory disease; autoimmune disorder; graft rejection;  
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 KW anti-HIV; virucide; antiarteriosclerotic.

XX OS Synthetic.

XX PN US2004151721-A1.

XX PD 05-AUG-2004.

XX PF 10-DEC-2003; 2003US-00733563.

XX PR 19-OCT-2001; 2001US-0350166P.

XX PR 26-JUN-2002; 2002US-0392364P.

XX PR 17-OCT-2002; 2002US-00272899.

XX FA (OKEE/) O'KEEFE T.

XX FA (PONA/) PONAETH P.

XX PI O'Keefe T, Ponath P;

XX WPI; 2004-580175/56.  
 DR N-PSDB; ADQ89319.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
 PT useful for diagnosing and/or treating inflammatory or autoimmune  
 PT diseases, and HIV infection.

XX Disclosure; SEQ ID NO 104; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a humanised  
 CC immunoglobulin protein of the invention.

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 620; DB 8; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60  
 Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
 Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 10

ID AEB09599 standard; protein; 119 AA.

XX AC AEB09599;

XX DT 08-SEP-2005 (first entry)

XX DE Humanized heavy chain 1D9RHA.

XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW heavy chain variable region.

XX OS Synthetic.

XX PN WO2005060368-A2.

XX PD 07-JUL-2005.

XX PF 10-DEC-2003; 2003WO-US039599.

XX PR 10-DEC-2003; 2003WO-US039599.

XX FA (MILL-) MILLENNIUM PHARM INC.

XX PI Okeefe T, Ponath P;

XX WPI; 2005-488561/49.

DR N-PSDB; AEB09592.

XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune

PT diseases.  
PS Disclosure; SEQ ID NO 104; 192pp; English.  
XX  
CC The invention describes a humanized immunoglobulin (I) or its antigen  
CC binding portion having binding specificity for CC-chemokine receptor 2  
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
CC sequence, given in specification or its portion, and the light chain  
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
CC in specification. Also described are: a humanized immunoglobulin heavy  
CC chain, or its antigen binding fragment, having binding specificity for  
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
CC immunoglobulin light chain, or its antigen binding fragment, having  
CC binding specificity for CCR2 and comprising the amino acid sequence of  
CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
CC sequence, given in specification. The following are disclosed: isolated  
CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
CC construct comprising nucleic acid molecule encoding (I); and host cell  
CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic  
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
CC reducing inflammatory response for use in the treatment of diseases  
CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
CC infection and monocyte-mediated disorders such as atherosclerosis. (I) Is  
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
CC fluid), and for modulating binding function and/or leukocyte trafficking  
CC modulated by CCR2. This is the amino acid sequence of humanized heavy  
CC chain 1D9RHA.  
XX  
SQ Sequence 119 AA;  
Query Match 100.0%; Score 620; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 8.3e-48;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60  
DB 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60  
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGQGLTVTVSS 117  
DB 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGQGLTVTVSS 117  
RESULT 11  
AAE06955  
ID AAE06955 standard; protein; 117 AA.  
XX  
AC AAE06955;  
XX  
DT 11-SEP-2003 (revised)  
DT 16-OCT-2001 (first entry)  
XX  
XX Humanised murine 1D9 antibody heavy chain variable region, 1D9RHB.  
DE  
DE  
XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma;  
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody;  
KW neonatal hyperplasia; VH; heavy chain variable region; 1D9RHB.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
XX Key Location/Qualifiers  
XX

FT Region 27..35  
FT /label= CDR1  
FT /note= "Complementarity determining region 1"  
FT 50..68  
FT /label= CDR2  
FT /note= "Complementarity determining region 2"  
FT 101..106  
FT /label= CDR3  
FT /note= "Complementarity determining region 3"  
XX  
PN WO200157226-A1.  
XX  
XX 09-AUG-2001.  
XX  
XX 02-FEB-2001; 2001WO-US003537.  
XX  
XX 03-FEB-2000; 2000US-00497625.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;  
XX WPI; 2001-488888/53.  
XX  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
XX disorder in a patient, comprises a binding specificity for CCR2, and a  
XX non-human antigen binding region and human immunoglobulin.  
XX  
XX Claim 62; Fig 12; 183pp; English.  
XX  
XX The patent discloses a humanized antibody or its antigen-binding  
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
XX comprising an antigen binding region of non-human origin and at least a  
XX portion of an immunoglobulin of human origin. The humanised antibodies  
XX are useful for inhibiting the interaction of a cell expressing CCR2. They  
XX are useful for inhibiting or treating HIV infection. The proteins of the  
XX invention are useful for inhibiting leukocyte trafficking, for treating  
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune  
XX disorders such as rheumatoid arthritis and multiple sclerosis,  
XX atherosclerosis and atherosclerosis, and for inhibiting restenosis. They  
XX are useful in therapy or diagnosis, and in the manufacture of a  
XX medicament for treating CCR-2 mediated disease. They are also useful for  
XX treating allergy, anaphylaxis, malignancy, allergic reaction, shock,  
XX inflammation, histamine and Ige-mediated allergic disease, inflammatory  
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
XX associated with vascular intervention, including angioplasty and/or stent  
XX placement in a mammal. Humanised antibodies are also useful for  
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
XX neointimal hyperplasia of a vessel in a mammal, preferably associated  
XX with vascular intervention. The present sequence is humanised murine 1D9  
XX antibody heavy chain variable (VH) region, 1D9RHB. (Updated on 11-SEP-  
XX 2003 to standardise OS field)  
SQ Sequence 117 AA;  
Query Match 98.9%; Score 613; DB 4; Length 117;  
Best Local Similarity 98.3%; Pred. No. 3.4e-47;  
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60  
DB 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60  
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGQGLTVTVSS 117  
DB 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGQGLTVTVSS 117  
RESULT 12  
ABG75537  
ID ABG75537 standard; protein; 117 AA.  
XX



PT Inhibiting graft rejection, graft versus host disease or chronic  
 PT rejection of a transplanted graft, involves administering a CCR2  
 antagonist.

PS Claim 26; Fig 2; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
 CC versus host disease or chronic rejection of a transplanted graft. The  
 CC method involves administering an antagonist of CC chemokine receptor 2  
 CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
 CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
 CC complementarity determining regions from various non-human origins). CCR2  
 CC is known to be involved in the rejection of transplanted grafts. The  
 CC method of the invention is useful for inhibiting graft rejection -  
 CC particularly allografts such as kidney, liver, lung, heart-lung,  
 CC pancreas, bowel and heart. The method of the invention is also useful for  
 CC inhibiting graft versus host disease and for inhibiting chronic rejection  
 CC of a transplanted graft. The present amino acid sequence represents a  
 CC humanised murine antibody heavy chain variable region (1D9RHB VH)

XX Sequence 117 AA;

Query Match 98.9%; Score 613; DB 5; Length 117;

Best Local Similarity 98.3%; Pred. No. 3.4e-47;  
 Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGSRLRLSCAASGFTPSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

DB 1 EVQLVESGGGLVKPGSRLRLSCAASGFTPSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGNVGWGQGLTLVTSS 117

DB 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGNVGWGQGLTLVTSS 117

RESULT 14

ADP98241

ID ADP98241 standard; protein; 117 AA.

AC ADP98241;

DT 26-FEB-2004 (first entry)

DE Humanised ID9 heavy chain variable region, 1D9RHB VH, SEQ ID 11.

KW Immunosuppressive; CCR2 function inhibitor; graft rejection;

KW graft versus host disease; CC chemokine receptor 2; CCR2;

KW anti-CCR2 antibody.

OS Synthetic.

OS Mus musculus.

OS Homo sapiens.

FN WO200178653-A2.

XX 25-OCT-2001.

PF 13-APR-2001; 2001WO-US012139.

XX 14-APR-2000; 2000US-00549448.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hancock WW;

XX WPI; 2002-017543/02.

XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
 PT involves use of CC chemokine receptor 2 inhibitor.

PS Claim 26; Fig 2; 44pp; English.

XX The present invention relates to a method for inhibiting graft rejection

CC or graft versus host diseases. The method comprises administration of a  
 CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
 CC recipient of a transplanted graft. The CCR2 function antagonist is an  
 CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
 CC ADP98240-ADP98249). The method is useful for inhibiting rejection,  
 CC particularly chronic rejection of a graft, particularly an allograft of  
 CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
 CC inhibiting graft versus host disease for a bone marrow graft.

XX Sequence 117 AA;

Query Match 98.9%; Score 613; DB 5; Length 117;

Best Local Similarity 98.3%; Pred. No. 3.4e-47;

Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGSRLRLSCAASGFTPSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

DB 1 EVQLVESGGGLVKPGSRLRLSCAASGFTPSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGNVGWGQGLTLVTSS 117

DB 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGNVGWGQGLTLVTSS 117

RESULT 15

ADQ89240

ID ADQ89240 standard; protein; 117 AA.

AC ADQ89240;

DT 21-OCT-2004 (first entry)

DE Humanised immunoglobulin protein #6.

KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;

KW inflammatory disease; autoimmune disorder; graft rejection;

KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;

KW anti-HIV; virucide; antiarteriosclerotic.

OS Synthetic.

XX US2004151721-A1.

XX 05-AUG-2004.

XX 10-DEC-2003; 2003US-00733563.

XX 19-OCT-2001; 2001US-0350166P.

PR 26-JUN-2002; 2002US-0392364P.

PR 17-OCT-2002; 2002US-00272899.

XX (OKEE/) O'KEEFE T.

XX (PONA/) PONATH P.

XX O'keefe T, Ponath P;

XX WPI; 2004-580175/56.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
 PT useful for diagnosing and/or treating inflammatory or autoimmune  
 PT diseases, and HIV infection.

XX Example 2; SEQ ID NO 18; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV

CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.

XX  
SQ Sequence 117 AA;

Query Match 98.9%; Score 613; DB 8; Length 117;  
Best Local Similarity 98.3%; Pred. No. 3.4e-47;  
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EVQLVESGGGLVKGPGSLRLSCAASGFTFSAYAMNWVROAPGKGLEWVGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVKGPGSLRLSCAASGFTFSAYAMNWVROAPGKGLEWVGRIRTKNNYAT 60  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNQVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNQVWGQGLTVTVSS 117

Search completed: January 28, 2006, 09:38:13  
Job time : 62.3108 secs



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:23:14 ; Search time 11.9459 Seconds  
(without alignments)  
942.358 Million cell updates/sec

Title: US-10-733-563-17  
Perfect score: 620  
Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVGNGGTLVTVSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: Piri.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492.5	79.4	137	2 S42467	Ig heavy chain V r
2	490	79.0	121	2 S31106	Ig heavy chain - h
3	485	78.2	127	2 S58213	Ig heavy chain V r
4	483	77.9	121	2 H36005	Ig heavy chain V r
5	482	77.7	117	2 S31109	Ig heavy chain V r
6	480	77.4	121	2 A41940	Ig heavy chain V r
7	479.5	77.3	141	2 I32513	Ig heavy chain pre
8	478	77.1	123	2 A36006	Ig heavy chain V r
9	477	76.9	138	2 A30561	Ig heavy chain pre
10	474	76.5	139	2 S31678	Ig heavy chain V r
11	472.5	76.2	126	2 S44107	Ig heavy chain V-D
12	467	75.3	160	2 S05271	Ig heavy chain pre
13	463.5	74.8	122	2 S30533	Ig heavy chain V r
14	463.5	74.8	147	2 I37780	Ig variable region
15	463	74.7	123	2 S26794	Ig heavy chain V r
16	463	74.7	140	2 S31588	Ig heavy chain V r
17	461	74.4	119	2 C36005	Ig heavy chain V r
18	460	74.2	115	1 AVMS06	Ig heavy chain V r
19	460	74.2	119	2 S31107	Ig heavy chain V-I
20	459.5	74.1	120	2 B49590	Ig heavy chain - h
21	458	73.9	138	2 S31666	Ig heavy chain V r
22	457.5	73.8	120	2 S48798	Ig heavy chain V r
23	456	73.5	119	2 S31108	Ig heavy chain - h
24	456	73.5	143	2 S23624	Ig heavy chain V r
25	454.5	73.3	122	2 E36005	Ig heavy chain V r
26	454.5	73.3	124	2 S20775	Ig heavy chain V r
27	454.5	73.3	124	2 S20782	Ig heavy chain V r
28	454	73.2	119	2 D36005	Ig heavy chain V r
29	454	73.2	123	2 S34009	Ig heavy chain V r

30	454	73.2	140	2 S31686	Ig heavy chain V r
31	453.5	73.1	114	2 S46390	Ig heavy chain V r
32	453	73.1	134	2 S31699	Ig heavy chain V r
33	452	72.9	133	2 S34010	Ig heavy chain V r
34	450	72.6	113	1 AVMSAB	Ig heavy chain V-I
35	450	72.6	113	1 AVMSB7	Ig heavy chain V-I
36	450	72.6	115	1 AVMS82	Ig heavy chain V-I
37	450	72.6	123	2 S31114	Ig heavy chain - h
38	448.5	72.3	140	2 S70442	Ig heavy chain pre
39	448	72.3	125	2 S30531	Ig heavy chain V r
40	448	72.3	135	2 S31598	Ig heavy chain V r
41	447.5	72.2	118	2 S31116	Ig heavy chain - h
42	447	72.1	134	2 S31679	Ig heavy chain V r
43	446.5	72.0	122	2 S20772	Ig heavy chain V r
44	446	71.9	121	2 S31113	Ig heavy chain - h
45	445.5	71.9	114	2 S46391	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S42467  
Ig heavy chain V region precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S42467  
R:Shiyonov, P.A.; Bepalov, I.A.; Terletskaya, H.N.; Deyev, S.M.  
submitted to the EMBL Data Library, March 1994  
A:Reference number: S42466  
A:Accession: S42467  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-137 <SH1>  
A:Cross-references: UNIPARC:UPI00001161DB; EMBL:X78107; NID:G460798; PIDN:CAAS4997.1; PII  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match	79.4%	Score	492.5	DB	2	Length	137
Best Local Similarity	79.2%	Pred. No.	3.9e-37				
Matches	95	Conservative	11	Mismatches	9	Indels	5
Gaps	2						
QY	1	EVQLVESGGGLVPGGSLRLSCAASGFTFSYAMNWVRQAPGKLEWYGRITKNNYAT	60				
DB	20	EVQLVESGGELVQPGKSLKLSAASGFTFTYAMNWVRQAPGKLEWVARIRSKNNTAT	79				
QY	61	YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGN--GVWGGGTLVTVSS	117				
DB	80	YYGNSVKDRFTISRDDSQSMLYLQWNLKTEDTAMYYCV--YGNFGPAYWGQGLTVTVSA	137				

RESULT 2

S31106  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31106  
R:Kaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Bur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31106  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-121 <RAA>  
A:Cross-references: UNIPARC:UPI0000176C8E; EMBL:X62954  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 490; DB 2; Length 121;

```
Best Local Similarity 81.0%; Pred. No. 5.8e-37;
Matches 98; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKDGGTT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-----FYGNVGWQGLTVTVS 116
Db 61 DYAAPVKGRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTIDYYIGMDVWGQGLTVTVS 120
Qy 117 S 117
Db 121 S 121

RESULT 3
S58213
Ig heavy chain V region (anti-F(ab')2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 23-Jul-1999
C:Accession: S58213; S58212
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebe, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58213
A:Molecule type: mRNA
A:Residues: 1-127 <WEL>
A:Cross-references: UNIPARC:UPI000003PEA8; EMBL:X89055; NID:G929638; PIDN:CAA61442.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 485; DB 2; Length 127;
Best Local Similarity 75.6%; Pred. No. 1.7e-36;
Matches 96; Conservative 7; Mismatches 14; Indels 10; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNSYAT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-----FYGNVGWQGL 110
Db 61 AYASVKGKFTISRDDSENTAYLQWNSLKIEDTAVYYCTTGRSSWVRGVNGYGMVWGQGL 120
Qy 111 TLTVSS 117
Db 121 TTVTVSS 127

RESULT 4
H36005
Ig heavy chain V region (M85) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: H36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: H36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: UNIPARC:UPI0000176C28; GB:M34032
C:Genetics:
A:Gene: GDB:IGH@; IGHY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
```

```
Query Match 77.9%; Score 483; DB 2; Length 121;
Best Local Similarity 82.0%; Pred. No. 2.4e-36;
Matches 98; Conservative 3; Mismatches 16; Indels 4; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKDGGTT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTTFYGNVGWQGLTVTVS 116
Db 61 DYAAPVKGRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTDRGGSSQGDYWGQGLTVTVS 120
Qy 117 S 117
Db 121 S 121

RESULT 5
S31109
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31109
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31109
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <RAA>
A:Cross-references: UNIPARC:UPI0000176DCA; EMBL:X62960
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 77.7%; Score 482; DB 2; Length 117;
Best Local Similarity 82.1%; Pred. No. 2.9e-36;
Matches 96; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKDGGTT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTTFYGNVGWQGLTVTVSS 117
Db 61 DYAAPVKGRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTATYYFDYWGQGLTVTVSS 117

RESULT 6
A41940
Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment)
A:Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C:Accession: A41940; PL0201
R:Herion, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss J.;
Proteins 11, 159-175, 1991
A:Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional str
A:Reference number: A41940; MUID:92086633; PMID:1749770
A:Accession: A41940
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-121 <HER>
A:Cross-references: UNIPARC:UPI0000176D34
A:Note: sequence extracted from NCBI backbone (NCBIP:70715)
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from M
A:Reference number: PL0198; MUID:90309768; PMID:2114528
A:Accession: PL0201
```

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Query Match          77.3%; Score 479.5; DB 2; Length 141;
Best Local Similarity 75.4%; Pred. No. 5.8e-36;
Matches 92; Conservative 12; Mismatches 13; Indels 5; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLISCAASGTTFAAYANWVRQAPGKLEWVGRIPTKNRYAT 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVETGGGLVOPKGSKLISCPASGFSFTNANWVRQAPGKLEWVARIRSKSNRYAT 79
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMNLSKTEDTAVYYCTTFYGN-----GVWGQGLTAVTV 115
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 YYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRDAANWSAFAFYWGQGLTAVTV 139
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 116 SS 117
      ||:
Db 140 SA 141

RESULT 8
A36006
Ig heavy chain V region (M26) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: A36006
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

```

RESULT 8  
A36006  
IG heavy chain V region (M26) - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C/Accession: A36006  
R/Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-138 <SAN>  
A;Cross-references: UNIPARC:UPT0000176C80  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A;Reference number: S26885; MUID:93021117; PMID:1404388  
A;Accession: S26931  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 20-119 <TOM>  
A;Cross-references: UNIPARC:UPT000011640B; EMBL:Z12338; NID:932896; PIDN:CAA78208.1; PID:  
R;Mariette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A;Reference number: S34001; MUID:93209281; PMID:7681398  
A;Accession: S34008  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 20-119 <MAR>  
A;Cross-references: UNIPARC:UPT000011640B  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 477; DB 2; Length 138;  
Best Local Similarity 81.5%; Pred. No. 9.5e-36;  
Matches 97; Conservative 5; Mismatches 15; Indels 2; Gaps 1;

Query Match 76.9%; Score 477; DB 2; Length 138;  
Best Local Similarity 81.5%; Pred. NO. 9.5e-36;  
Matches 97; Conservative 5; Mismatches 15; Indels 2; Gaps 1;

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Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVROAPGKGLVWVGRIRTKNNYAT 60
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFSANMSWVRQAPGKGLVWVGRIRKSTDGGTT 79
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTDATVYYCTT--FYGNGVWGQGLVTVSS 117
Db 80 DYAAPVKGRFTISRDDSKNTLYLQWNSLKTDATVYYCTTDSLPPHRVWGQGLVTVSS 138

RESULT 10
S31678
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31678
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
submitted to the EMBL Data Library, June 1992
A:Reference number: S31585
A:Accession: S31678
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CU>
A:Cross-references: UNIPARC:UPI0000116456; EMBL:Z14169; NID:G31003; PIDN:CAA78538.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-116/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 474; DB 2; Length 139;
Best Local Similarity 77.2%; Pred. No. 1.8e-35;
Matches 95; Conservative 6; Mismatches 16; Indels 6; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVROAPGKGLVWVGRIRTKNNYAT 60
Db 17 EVQLVESGGGLVPGGSLRLSCAASGFTFSANMSWVRQAPGKGLVWVARIKSTDGGTT 76
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTDATVYYCTTFYNG-----VWGQGLTVT 114
Db 77 DYAAPVKGRFTISRDDSKNTLYLQWNSLKTDATVYYCTTDSIQGNLLAFDIWGGTMTV 136
Qy 115 VSS 117
Db 137 VSS 139

RESULT 11
S44107
Ig heavy chain V-D-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44107
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
submitted to the EMBL Data Library, March 1994
A:Reference number: S44105
A:Accession: S44107
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <HAW>
A:Cross-references: UNIPARC:UPI0000116634; EMBL:Z31394; NID:9472961; PIDN:CAA83269.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:115-100/Domain: immunoglobulin homology <IMM>

Query Match 76.2%; Score 472.5; DB 2; Length 126;
Best Local Similarity 74.6%; Pred. No. 2.2e-35;
Matches 94; Conservative 6; Mismatches 13; Indels 13; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVROAPGKGLVWVGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAGSMHWVRQASGKGLVWVGRIRSKANSYAT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTDATVYYCTT-----FYGNGV 107
```

```
Db 61 AYAAASVKGRTISRDDSKNTAYLQWNSLKTDATVYYCTTRHVNDFWSGYPTLYYIGMDVW 120
Qy 108 GQGTLV 113
Db 121 GQGPTV 126

RESULT 12
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: S05271; S04602
R:Kishimoto, T.
A:Submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <KIS1>
A:Cross-references: UNIPROT:Q96BB9; UNIPARC:UPI0000176B50; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of e
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <KIS2>
A:Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 467; DB 2; Length 160;
Best Local Similarity 73.2%; Pred. No. 8.7e-35;
Matches 93; Conservative 8; Mismatches 14; Indels 12; Gaps 2;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVROAPGKGLVWVGRIRTKNNYAT 60
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWVSAI--SGSGGST 77
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTDATVYYCTT-----FYGNGVWGQ 110
Db 78 YYADSVKGRFTISRDDSKNTLYLQWNSLRADTAVYYCAKAVVRGVISYYYIGMDVWGQ 137
Qy 111 TLTVVSS 117
Db 138 TTVTVSS 144

RESULT 13
S30533
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C:Accession: S30533
R:Marlette, X.
A:Submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <MAR>
A:Cross-references: UNIPROT:Q9UL88; UNIPARC:UPI0000176C2E; EMBL:Z18319
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 463.5; DB 2; Length 122;
Best Local Similarity 77.9%; Pred. No. 1.4e-34;
Matches 95; Conservative 7; Mismatches 15; Indels 5; Gaps 2;
```

```
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EQVQVESGGGLVQPGGSLRLSCAASRFTFTNAWMSVVRQAPGKLEWVGRIKSKTDGGTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YYADSVKORFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-FYNG-----VWGQGTLVTV 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DYAAPVKGRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFTFSADGDYVRYWGQGTLVTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 SS 117
   ||
Db 121 SS 122
   ||

RESULT 14
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C:Accession: I37780; S25474
R:Demailson, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
A:Reference number: A38876; MUID:94119917; PMID:8290556
A:Accession: I37780
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <RES>
A:Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:G33578; PIDN:CAA48130.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 463.5; DB 2; Length 147;
Best Local Similarity 73.8%; Pred. No. 1.5e-34;
Matches 93; Conservative 7; Mismatches 15; Indels 11; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVANI--KQDGSEK 71
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YYADSVKORFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-----FYNGVWGQGT 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 YYADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAKGEGWGLYYYYGMDVWGQGT 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 112 LTVSS 117
   ||||
Db 132 TTVSS 137
   ||||

RESULT 15
S26794
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S26794
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26794
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MOR>
A:Cross-references: UNIPARC:UPI0000176C2B; EMBL:X61011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.7%; Score 463; DB 2; Length 123;
Best Local Similarity 72.8%; Pred. No. 1.5e-34;
Matches 91; Conservative 11; Mismatches 13; Indels 10; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
```

```
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVSYISSSS--TI 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YYADSVKORFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-----TFYNGVWGQGT 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLRDEDTAVYYCARSIKYYDENTYYGMDVWGQGT 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 VTVSS 117
   ||||
Db 119 VTVSS 123
   ||||
```

Search completed: January 28, 2006, 09:45:38  
Job time : 11.9459 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:21:24 ; Search time 62.0135 Seconds  
(without alignments)  
1331.110 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVGQGLVTVSS 117

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	477.5	77.0	471	2	Q66K04_MOUSE	Q66K04 mus musculus
2	463	74.7	464	2	Q6MZU6_HUMAN	Q6MZU6 homo sapien
3	460	74.2	115	1	HV32_MOUSE	P01801 mus musculus
4	453	73.1	113	2	Q9UL90_HUMAN	Q9UL90 homo sapien
5	453	73.1	131	2	Q9UL88_HUMAN	Q9UL88 homo sapien
6	452	72.9	240	2	Q65ZC9_HUMAN	Q65ZC9 homo sapien
7	450	72.6	113	1	HV27_MOUSE	P01796 mus musculus
8	450	72.6	113	1	HV30_MOUSE	P01799 mus musculus
9	450	72.6	115	1	HV33_MOUSE	P01802 mus musculus
10	447	72.1	597	2	Q96BB9_HUMAN	Q96BB9 homo sapien
11	446.5	72.0	494	2	Q96K68_HUMAN	Q96K68 homo sapien
12	446.5	72.0	613	2	Q8WUK3_HUMAN	Q8WUK3 homo sapien
13	446	71.9	121	1	HV28_MOUSE	Q9UL71 homo sapien
14	444	71.6	113	1	HV28_MOUSE	Q80Z17 mouse
15	444	71.6	487	2	Q9UL93_HUMAN	Q9UL93 homo sapien
16	443	71.5	116	2	Q9UL93_HUMAN	Q80Z17 mus musculus
17	442.5	71.4	606	2	Q6GMV2_HUMAN	Q6GMV2 homo sapien
18	442	71.3	113	1	HV31_MOUSE	P01800 mus musculus
19	440.5	71.0	118	2	Q9UL91_HUMAN	Q9UL91 homo sapien
20	440	71.0	113	1	HV29_MOUSE	P01798 mus musculus
21	439	70.8	468	2	Q569B4_RAT	Q569B4 rattus norv
22	437	70.5	458	2	Q65ZQ1_HUMAN	Q65ZQ1 homo sapien
23	436.5	70.4	469	2	Q569P4_HUMAN	Q569P4 homo sapien
24	436	70.3	472	2	Q6N089_HUMAN	Q569F4 homo sapien
25	434	70.0	478	2	HV31_MOUSE	Q6N089 homo sapien
26	432.5	69.8	122	1	HV33_MOUSE	Q6P181 homo sapien
27	432.5	69.8	573	2	Q8WU38_HUMAN	P01768 homo sapien
28	431	69.5	470	2	Q6PJA4_HUMAN	Q8WU38 homo sapien
29	429	69.2	142	1	HV01_RAT	Q6PJA4 homo sapien
30	429	69.2	464	2	Q6P1F8_MOUSE	P01805 rattus norv
31	429	69.2	493	2	Q6GMX2_HUMAN	Q6P1F8 mus musculus
						Q6GMX2 homo sapien

32	426.5	68.8	465	2	Q6P6C4_HUMAN	Q6P6C4 homo sapien
33	426	68.7	120	1	HV3E_HUMAN	P01766 homo sapien
34	424.5	68.5	473	2	Q6MZV7_HUMAN	Q6MZV7 homo sapien
35	424	68.4	466	2	Q6IN78_HUMAN	Q6IN78 homo sapien
36	423	68.2	113	1	HV34_MOUSE	P01803 mus musculus
37	422.5	68.1	119	2	Q5F2I8_MOUSE	Q5F2I8 mus musculus
38	422.5	68.1	475	2	Q6MZQ6_HUMAN	Q6MZQ6 homo sapien
39	418	67.4	119	2	Q920E7_MOUSE	Q920E7 mus musculus
40	417.5	67.3	122	1	HV21_MOUSE	P01790 mus musculus
41	416.5	67.2	465	2	Q5IOJ0_RAT	Q5IOJ0 rattus norv
42	416.5	67.2	475	2	Q6GMW7_HUMAN	Q6GMW7 homo sapien
43	415.5	67.0	112	2	Q9HCC1_HUMAN	Q9HCC1 homo sapien
44	415.5	67.0	114	1	HV3B_HUMAN	P01763 homo sapien
45	415.5	67.0	467	2	Q4VBH1_RAT	Q4VBH1 rattus norv

ALIGNMENTS

RESULT 1  
Q66K04\_MOUSE PRELIMINARY; PRT; 471 AA.  
AC Q66K04\_25-OCT-2004 (Tremblrel. 28, Created)  
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
DE Hypothetical protein.  
GN Name=Igh-1a;  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH II;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,  
RA Scheraga A., Schein J.E., Jones S.J.N., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH II;  
RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RA TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RA Director MGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC080671; AAH80671.1; -; mRNA.  
DR SMR; Q66K04; 20-467.  
DR MGI; MGI:96443; Igh-1a.  
DR GO; GO:0003823; F-antigen binding; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.V.





```

OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Rasphorst F.M., Timmers B., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RL immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07P CRC64;

Query Match 73.1%; Score 453; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 5.5e-40;
Matches 91; Conservative 7; Mismatches 15; Indels 4; Gaps 2;

QY 1 EVQLVESGGLVKPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLVWGRITRTKNNYAT 60
Db 1 EVQLVESGGVVPQGGSLRLSCAASGFTFSYGMHWVRQAPGKGLVWAFIRYDGSN--K 58

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAK--DLNFWGQGLTVTVSS 113

RESULT 5
Q9UL88 HUMAN
ID Q9UL88 HUMAN PRELIMINARY; PRT; 131 AA.
AC Q9UL88
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DS (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.B., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; PDCFD3645F64B373 CRC64;

Query Match 72.9%; Score 452; DB 2; Length 240;
Best Local Similarity 74.8%; Pred. No. 1.7e-39;
Matches 89; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

QY 1 EVQLVESGGLVKPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLVWGRITRTKNNYAT 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLVWAVISYDGSN--K 58

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGV--WGQGLTVTVSS 117
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCARDWGDGLDPWGKGLTVTVSS 117

RESULT 6
Q55ZC9 HUMAN
ID Q55ZC9 HUMAN PRELIMINARY; PRT; 240 AA.
AC Q55ZC9
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.B., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; PDCFD3645F64B373 CRC64;

Query Match 72.9%; Score 452; DB 2; Length 240;
Best Local Similarity 74.8%; Pred. No. 1.7e-39;
Matches 89; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

QY 1 EVQLVESGGLVKPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLVWGRITRTKNNYAT 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLVWAVISYDGSN--K 58

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGV--WGQGLTVTVSS 117
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCARDWGDGLDPWGKGLTVTVSS 117
```

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RESULT 7
HV27 HV27 MOUSE STANDARD; PRT; 113 AA.
AC P01796;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

PROTEIN SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC
DR PIR; A93818; AVMSAB.
DR HSSP; P01783; IIGC.
DR SMR; P01796; 1-113.
DR Ensembl; ENSMUSG000000045097; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 >113 Ig-like.
FT DISULFID 22 98 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRITRKNNTAT 60
Db 1 EVKLEESGGGLVPGGSKLSCLVASGFTFSNWNVRQSPKGLVWVAEIRLASHNAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTV 115
Db 61 HYAESVKGRTISRDDSKSSVYLQNNLRAEDTGIYCTT--GPAFYWGQGLTVTV 113

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRITRKNNTAT 60
Db 1 EVKLEESGGGLVPGGSKLSCLVASGFTFSNWNVRQSPKGLVWVAEIRLASHNAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTV 115
Db 61 HYAESVKGRTISRDDSKSSVYLQNNLRAEDTGIYCTT--GPAFYWGQGLTVTV 113

RESULT 8
HV30 MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region ABB-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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PROTEIN SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
protein.";
RL Biochemistry 16:1170-1175(1977).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2PBJ.
DR SMR; P01799; 1-113.
DR Ensembl; ENSMUSG000000045097; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 >113 Ig-like.
FT DISULFID 22 98 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 16; Mismatches 13; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRITRKNNTAT 60
Db 1 EVKLEESGGGLVPGGSKLSCLVASGFTFSNWNVRQSPKGLVWVAEIRLASHNAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTV 115
Db 61 HYAESVKGRTISRDDSKSSVYLQNNLRAEDTAVYYCTT--GPAFYWGQGLTVTV 113

RESULT 9
HV33 MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

PROTEIN SEQUENCE.
RX MEDLINE=82099361; PubMed=679811;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC

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CC PIR; D92811; AVMS82.
DR HSP; P01852; INF.
DR SMR; P01802; 1-115.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114 Ig-like.
FT DISULPID 22 98 By similarity.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 72.6%; Score 450; DB 1; Length 115;
Best Local Similarity 71.8%; Pred. NO. 1.2e-39;
Matches 84; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFTFSAYAMNVRQAPGKGLGWGRIRTKNNYAT 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVKLEESGGGLVQPGSMKLSVASGFTFSNTYMNVRQSPKGLGWAEIRLKSHNYAT 60

QY 61 YYADSVKDRFTISRDRSKNTLYLQWNSLKTEDTAVYCTTFTYGVNGVWGQGLTLVTSS 117
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 HYAESVKGKFTISRDRSKSVYLRMNLRPEDTGIYCTT--GFAYWGQGLTLVTVSA 115

RESULT 10
Q96BB9 HUMAN
ID Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
RT chains of a human monoclonal antibody with broad reactivity to
RT malignant tumor cells.";
RL Nucleic Acids Res. 17:4385-0 (1989).
DR EMBL; BC015760; AAH15760.1; -; mRNA.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSP; P01861; IADQ.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 72.1%; Score 447; DB 2; Length 597;
Best Local Similarity 70.1%; Pred. NO. 1.7e-38;
Matches 89; Conservative 11; Mismatches 15; Indels 12; Gaps 2;

QY 1 EVLVESGGGLVKPGSLRLSCAASGFTFSAYAMNVRQAPGKGLGWGRIRTKNNYAT 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EVQLLESGGGLVQPGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVSAT--SGSGGT 77

QY 61 YYADSVKDRFTISRDRSKNTLYLQWNSLKTEDTAVYCTTFTYGVNGVWGQGL 110
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 YYADSVKGRFTISRDRSKNTLYLQWNSLRAEDTAVYCAKDPGRGYSASGNTYREDYWGQ 137

QY 111 TLVTSS 117
Db |||:|||||
138 TLVTSS 144

RESULT 11
Q96K68 HUMAN
ID Q96K68 HUMAN PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ14473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Okeyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

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Matches 83; Conservative 15; Mismatches 15; Indels 2; Gaps 1;  
QY 1 EVQLVESGGGLVQPGGSLRLSAAAGTFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60  
DB 1 EVKLEESGGGLVQPGGSMKLSAAAGTFTFSYNNWVRQSPKGLVWVGRIRLRSNNYAT 79  
QY 61 YYADSVKDRFTISRDDSKNTLYLQMNLSLKTEDTAVYYCT-TFYGN-----GVWGQGLTAVT 114  
DB 61 HYAESVKGRTISRDDSKSSVYLQMNLRADDTGIYYCTT--GFAYWGQGLTPVP 113

RESULT 15

Q802I7\_MOUSE PRELIMINARY; PRT; 487 AA.  
AC Q802I7;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Igh-VJ558 protein.  
GN Name=Igh-VJ558;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RG NIH MGC Project;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC049143; AAH49143.1; -, mRNA.  
DR HSP; P01789; IMCP.  
DR SMR; Q802I7; 20-242.  
DR MGI; MGI:96486; Igh-VJ558.  
DR GO; GO:0003823; F-antigen binding; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; CI-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 487 AA; 31F2C893900A4D80 CRC64;

Query Match 71.6%; Score 444; DB 2; Length 487;  
Best Local Similarity 69.1%; Pred. No. 2.8e-38;  
Matches 85; Conservative 17; Mismatches 15; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSAAAGTFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60  
DB 20 EVKLEESGGGLVQPGGSMKLSAAAGTFTFSYNNWVRQSPKGLVWVGRIRLRSNNYAT 79  
QY 61 YYADSVKDRFTISRDDSKNTLYLQMNLSLKTEDTAVYYCT-TFYGN-----GVWGQGLTAVT 114  
DB 80 HYAESVKGRTISRDDSKSSVYLQMNLRADDTGIYYCTT--GFAYWGQGLTPVP 113  
QY 115 VSS 117  
DB 140 VSS 142

Search completed: January 28, 2006, 09:44:18  
Job time : 62.0135 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 17.2162 Seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-17  
Perfect score: 620  
Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVGVGQGLTVTVSS 117

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	2	US-09-809-739-20
2	620	100.0	117	2	US-09-840-459-17
3	620	100.0	117	2	US-09-497-625A-17
4	620	100.0	119	2	US-09-840-459-104
5	620	100.0	119	2	US-09-497-625A-104
6	613	98.9	117	2	US-09-809-739-21
7	613	98.9	117	2	US-09-840-459-18
8	613	98.9	117	2	US-09-497-625A-18
9	604	97.4	117	2	US-09-809-739-22
10	604	97.4	117	2	US-09-840-459-19
11	604	97.4	117	2	US-09-497-625A-19
12	599	96.6	117	2	US-09-809-739-23
13	599	96.6	117	2	US-09-840-459-20
14	599	96.6	117	2	US-09-497-625A-20
15	548	88.4	117	2	US-09-809-739-12
16	548	88.4	117	2	US-09-840-459-10
17	548	88.4	117	2	US-09-497-625A-10
18	548	88.4	148	2	US-09-840-459-100
19	548	88.4	148	2	US-09-497-625A-100
20	486.5	78.8	116	1	US-08-428-197-10
21	486.5	78.8	116	4	PCT-US93-10555-10
22	487	78.5	123	2	US-09-097-055B-87
23	487	78.5	123	2	US-09-893-615-87
24	485	78.2	125	1	US-08-428-197-9
25	485	78.2	125	4	PCT-US93-10555-9
26	485	78.2	127	2	US-09-840-459-71
27	485	78.2	127	2	US-09-497-625A-71

28	483.5	78.0	126	2	US-09-840-459-74	Sequence 74, Appl
29	483.5	78.0	126	2	US-09-497-625A-74	Sequence 74, Appl
30	482	77.7	115	2	US-08-767-128-36	Sequence 36, Appl
31	482	77.7	117	2	US-09-840-459-83	Sequence 83, Appl
32	482	77.7	117	2	US-09-497-625A-83	Sequence 83, Appl
33	480.5	77.5	126	2	US-09-840-459-73	Sequence 73, Appl
34	480.5	77.5	126	2	US-09-497-625A-73	Sequence 73, Appl
35	480.5	77.5	130	1	US-08-478-039-70	Sequence 70, Appl
36	480.5	77.5	130	1	US-08-478-039-93	Sequence 93, Appl
37	480.5	77.5	130	1	US-08-476-349A-70	Sequence 70, Appl
38	480.5	77.5	130	1	US-08-476-349A-93	Sequence 93, Appl
39	480	77.4	332	2	US-09-133-121B-7	Sequence 7, Appl
40	478	77.1	123	2	US-09-840-459-94	Sequence 94, Appl
41	478	77.1	123	2	US-09-497-625A-94	Sequence 94, Appl
42	477	76.9	119	1	US-08-428-197-11	Sequence 11, Appl
43	477	76.9	119	2	US-09-809-739-19	Sequence 19, Appl
44	477	76.9	119	2	US-09-840-459-16	Sequence 16, Appl
45	477	76.9	119	2	US-09-840-459-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1  
US-09-809-739-20  
; Sequence 20, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-20

Query Match	100.0%	Score 620;	DB 2;	Length 117;
Best Local Similarity	100.0%	Pred. No. 1.1e-54;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPKGLEWVGRITKNNYAT 60		
Db	1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPKGLEWVGRITKNNYAT 60		
QY	61	YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVGVGQGLTVTVSS 117		
Db	61	YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVGVGQGLTVTVSS 117		

RESULT 2  
US-09-840-459-17  
; Sequence 17, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; METHODS OF USE THEREFOR

FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Humanized sequence  
US-09-840-459-17

Query Match 100.0%; Score 620; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.1e-54;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117

RESULT 3  
US-09-497-625A-17  
Sequence 17, Application US/09497625A  
Patent No. 6727349  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-004  
CURRENT APPLICATION NUMBER: US/09/497,625A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Humanized sequence  
US-09-497-625A-17

Query Match 100.0%; Score 620; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.1e-54;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117  
RESULT 4  
US-09-840-459-104  
Sequence 104, Application US/09840459  
Patent No. 6696550  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 104  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Humanized heavy chain  
US-09-840-459-104

Query Match 100.0%; Score 620; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.1e-54;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117

RESULT 5  
US-09-497-625A-104  
Sequence 104, Application US/09497625A  
Patent No. 6727349  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-004  
CURRENT APPLICATION NUMBER: US/09/497,625A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0



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; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
US-09-497-625A-104

Query Match
Best Local Similarity 100.0%; Score 620; DB 2; Length 119;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117

RESULT 6
US-09-809-739-21
; Sequence 21, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-21

Query Match
Best Local Similarity 98.9%; Score 613; DB 2; Length 117;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117

RESULT 7
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459

Query Match
Best Local Similarity 98.3%; Score 613; DB 2; Length 117;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117

RESULT 8
US-09-497-625A-18
; Sequence 18, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-18

Query Match
Best Local Similarity 98.9%; Score 613; DB 2; Length 117;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117
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```

US-09-809-739-22
; Sequence 22, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-22

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 10
US-09-840-459-19
; Sequence 19, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-19

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 11
US-09-497-625A-19
; Sequence 19, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-19

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 12
US-09-809-739-23
; Sequence 23, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-23
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```

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 11
US-09-497-625A-19
; Sequence 19, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-19

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKLEWVGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 12
US-09-809-739-23
; Sequence 23, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-23
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```
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-23

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.4e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGNGWGQGLVTVSS 117
Db 61 YYADSVKDRYTIISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGNGWGQGLVTVSS 117

RESULT 13
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-20

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.4e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGNGWGQGLVTVSS 117
Db 61 YYADSVKDRYTIISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGNGWGQGLVTVSS 117

RESULT 14
US-09-497-625A-20
; Sequence 20, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
```

```
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-20

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.4e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGNGWGQGLVTVSS 117
Db 61 YYADSVKDRYTIISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGNGWGQGLVTVSS 117

RESULT 15
US-09-809-739-12
; Sequence 12, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
; NAME/KEY: SITE
; LOCATION: (31)...(35)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (50)...(68)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (101)...(106)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-12
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 49.8919 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVKPGSURL.....CTTFYGVNGVWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	3	US-09-835-087-10
2	620	100.0	117	3	US-09-809-739-20
3	620	100.0	117	3	US-09-840-459-17
4	620	100.0	117	4	US-10-766-773-17
5	620	100.0	117	4	US-10-766-610-17
6	620	100.0	117	4	US-10-733-563-17
7	620	100.0	117	5	US-10-662-061-20
8	620	100.0	119	3	US-09-840-459-104
9	620	100.0	119	4	US-10-766-773-104
10	620	100.0	119	4	US-10-766-610-104
11	620	100.0	119	4	US-10-733-563-104
12	613	98.9	117	3	US-09-835-087-11
13	613	98.9	117	3	US-09-809-739-21
14	613	98.9	117	3	US-09-840-459-18
15	613	98.9	117	4	US-10-766-773-18
16	613	98.9	117	4	US-10-766-610-18
17	613	98.9	117	4	US-10-733-563-18
18	613	98.9	117	5	US-10-662-061-21
19	604	97.4	117	3	US-09-835-087-12
20	604	97.4	117	3	US-09-809-739-22
21	604	97.4	117	3	US-09-840-459-19
22	604	97.4	117	4	US-10-766-773-19
23	604	97.4	117	4	US-10-766-610-19
24	604	97.4	117	4	US-10-733-563-19
25	604	97.4	117	5	US-10-662-061-22
26	599	96.6	117	3	US-09-835-087-13
27	599	96.6	117	3	US-09-809-739-23

28	599	96.6	117	3	US-09-840-459-20	Sequence 20, Appl
29	599	96.6	117	4	US-10-766-773-20	Sequence 20, Appl
30	599	96.6	117	4	US-10-766-610-20	Sequence 20, Appl
31	599	96.6	117	4	US-10-733-563-20	Sequence 20, Appl
32	599	96.6	117	5	US-10-662-061-23	Sequence 23, Appl
33	548	88.4	117	3	US-09-835-087-8	Sequence 8, Appl
34	548	88.4	117	3	US-09-809-739-12	Sequence 12, Appl
35	548	88.4	117	3	US-09-840-459-10	Sequence 10, Appl
36	548	88.4	117	4	US-10-766-773-10	Sequence 10, Appl
37	548	88.4	117	4	US-10-766-610-10	Sequence 10, Appl
38	548	88.4	117	4	US-10-733-563-10	Sequence 10, Appl
39	548	88.4	117	5	US-10-662-061-12	Sequence 12, Appl
40	548	88.4	125	4	US-10-272-899A-84	Sequence 84, Appl
41	548	88.4	148	3	US-09-840-459-100	Sequence 100, App
42	548	88.4	148	4	US-10-766-773-100	Sequence 100, App
43	548	88.4	148	4	US-10-766-610-100	Sequence 100, App
44	548	88.4	148	4	US-10-733-563-100	Sequence 100, App
45	499.5	80.6	120	5	US-10-920-899-1779	Sequence 1779, Ap

ALIGNMENTS

RESULT 1

US-09-835-087-10  
; Sequence 10, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; FILE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-10

Query Match	100.0%	Score 620;	DB 3;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 1.7e-49;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EVQLVESGGGLVKPGSURLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT	60	
Db	1	EVQLVESGGGLVKPGSURLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT	60	
Qy	61	YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS	117	
Db	61	YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS	117	

RESULT 2

US-09-809-739-20  
; Sequence 20, Application US/09809739  
; Patent No. US20020106369A1  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-20

Query Match          100.0%; Score 620; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIRTKNNYAT 60
    |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIRTKNNYAT 60
    |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
    |||||
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
    |||||

RESULT 3
US-09-840-459-17
; Sequence 17, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-17

Query Match          100.0%; Score 620; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIRTKNNYAT 60
    |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIRTKNNYAT 60
    |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
    |||||
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
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RESULT 4
US-10-766-773-17
; Sequence 17, Application US/10766773
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```
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-17

Query Match          100.0%; Score 620; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIRTKNNYAT 60
    |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIRTKNNYAT 60
    |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
    |||||
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117
    |||||

RESULT 5
US-10-766-610-17
; Sequence 17, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-610-17

Query Match      100.0%; Score 620; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 6
US-10-733-563-17
; Sequence 17, Application US/107333563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-17

Query Match      100.0%; Score 620; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 7
US-10-662-061-20
; Sequence 20, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: Restenosis
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15

Query Match      100.0%; Score 620; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 8
US-09-840-459-104
; Sequence 104, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
US-09-840-459-104

Query Match      100.0%; Score 620; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 9
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US-10-766-773-104  
; Sequence 104, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-028  
; CURRENT APPLICATION NUMBER: US/10/766,773  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-10-766-773-104

Query Match 100.0%; Score 620; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60  
  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 10  
US-10-766-610-104  
; Sequence 104, Application US/10766610  
; Publication No. US20040132980A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-029  
; CURRENT APPLICATION NUMBER: US/10/766,610  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/840,459  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104

; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-10-766-610-104  
  
Query Match 100.0%; Score 620; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60  
  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 11  
US-10-733-563-104  
; Sequence 104, Application US/10733563  
; Publication No. US20040151721A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa  
; APPLICANT: Ponath, Paul  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 10448-213001  
; CURRENT APPLICATION NUMBER: US/10/733,563  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: US 10/272,899  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized heavy chain  
US-10-733-563-104

Query Match 100.0%; Score 620; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60  
  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 12  
US-09-835-087-11  
; Sequence 11, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448



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; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-11

Query Match      98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||

RESULT 13
US-09-809-739-21
; Sequence 21, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-21

Query Match      98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||

RESULT 14
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
```

```
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-18

Query Match      98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||

RESULT 15
US-10-766-773-18
; Sequence 18, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-18

Query Match      98.9%; Score 613; DB 4; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
        |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
        |||
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Db	1	EVQLVESGGGLVQPGGSLRLSCAASGSPSFNAYAMNWVRQAPGKGLEWVGRIRTKNNYAT	60
Qy	61	YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYNGVWGQGTILVTVSS	117
Db	61	YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYNGVWGQGTILVTVSS	117

Search completed: January 28, 2006, 10:11:22  
Job time : 50.8919 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 7.02703 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGLVKPGSRL.....CTTFYNGVWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	7	US-11-075-184A-8
2	613	98.9	117	7	US-11-075-184A-9
3	604	97.4	117	7	US-11-075-184A-10
4	599	96.6	117	7	US-11-075-184A-11
5	548	88.4	117	7	US-11-075-184A-2
6	487	78.5	123	7	US-11-193-440-87
7	478.5	77.2	251	7	US-11-054-515-997
8	478.5	77.2	251	7	US-11-054-515-1346
9	476.5	76.9	139	7	US-11-125-837-24
10	475	76.6	257	7	US-11-054-515-958
11	474	76.5	244	7	US-11-054-515-1991
12	473.5	76.4	258	7	US-11-054-515-1841
13	471.5	76.0	120	6	US-10-834-397-38
14	471.5	76.0	120	6	US-10-834-397-63
15	471.5	76.0	256	7	US-11-054-515-1209
16	471.5	76.0	281	6	US-10-834-397-178
17	471	76.0	250	7	US-11-054-515-1179
18	470	75.8	253	7	US-11-054-515-1650
19	469.5	75.7	256	7	US-11-054-515-843
20	468	75.5	115	7	US-11-127-903-33
21	468	75.5	470	7	US-11-144-248-46
22	468	75.5	470	7	US-11-144-222-46
23	467.5	75.4	116	6	US-10-925-366A-1
24	467.5	75.4	240	6	US-10-925-366A-219
25	467	75.3	117	7	US-11-127-903-32

26	466.5	75.2	256	7	US-11-054-515-872
27	466	75.2	125	7	US-11-144-248-16
28	466	75.2	125	7	US-11-144-222-16
29	465.5	75.1	120	6	US-10-925-366A-235
30	465.5	75.1	250	7	US-11-054-515-1325
31	465	75.0	248	7	US-11-054-515-913
32	465	75.0	248	7	US-11-054-515-2070
33	465	75.0	472	7	US-11-086-289-2
34	464	74.8	117	6	US-10-834-397-24
35	464	74.8	117	7	US-11-127-903-29
36	464	74.8	117	7	US-11-127-903-30
37	464	74.8	117	7	US-11-127-903-37
38	463.5	74.8	254	7	US-11-054-515-1701
39	463.5	74.8	254	7	US-11-054-515-1735
40	463	74.7	117	7	US-11-127-903-36
41	463	74.7	119	7	US-11-127-903-31
42	462.5	74.6	248	7	US-11-054-515-921
43	462.5	74.6	248	7	US-11-054-515-1456
44	462.5	74.6	248	7	US-11-054-515-1974
45	462	74.5	113	6	US-10-665-658-6

ALIGNMENTS

RESULT 1

US-11-075-184A-8  
; Sequence 8, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE  
US-11-075-184A-8

Query Match	100.0%	Score 620;	DB 7;	Length 117;
Best Local Similarity	100.0%	Pred. No. 4.7e-47;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EVQLVESGGLVKPGSRLSCAASGFTFSAYANWVQAQPGKLEWVGRIRTKNNYAT 60		
Db	1	EVQLVESGGLVKPGSRLSCAASGFTFSAYANWVQAQPGKLEWVGRIRTKNNYAT 60		
QY	61	YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117		
Db	61	YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLTVTVSS 117		

RESULT 2

US-11-075-184A-9  
; Sequence 9, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669

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; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine Ig9 a
US-11-075-184A-9

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Query Match 98.9%; Score 613; DB 7; Length 117;  
 Best Local Similarity 98.3%; Pred. No. 1.9e-46;  
 Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EVQLVESGGGLVPGGSLRLS	CAASGTFPS	YAMNVRQ	APGKGL	EWVGR	IRTKNN	NYAT	60
			:	:	:	:	:	:	
Db	1	EVQLVESGGGLVPGGSLRLS	CAASGFS	NAYAMNVRQ	APGKGL	EWVGR	IRTKNN	NYAT	60
Qy	61	YYADSVKDRFTIS	DDSKNTLYL	QWNSLKT	EDTAY	YCTTFY	GNVGW	CGGLTV	117
			:	:	:	:	:	:	
Db	61	YYADSVKDRFTIS	DDSKNTLYL	QWNSLKT	EDTAY	YCTTFY	GNVGW	CGGLTV	117

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RESULT 3
US-11-075-184A-10
; Sequence 10, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 10
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody heavy chain variable region, 1D9
US-11-075-184A-10

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Query Match	97.4%	Score 604;	DB 7;	Length 117;
Best Local Similarity	96.6%;	Pred. No. 1.le-45;		
Matches 113; Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0;

  

Qy	1	EVLVPSGGGLVPGGSLRLSCAASGFTTSPAYAMNVRQAPGKLEBWGRIRTKNNYAT	60
		:           :	
Dd	1	EVLVPSGGGLVPGGSLRLSCAASGFSPNAYAMNVRQAPGKLEWVARIRTKNNYAT	60
		:           :	
Qy	61	YYADSVKDRTIISRDSDKNLYLQMLSLKTEDTAIVYCTTFYGNGVWGQTLVTSS	117
		:           :	
Dd	61	YYADSVKDRTIISRDSDKNLYLQMLSLKTEDTAIVYCTTFYGNGVWGQTLVTSS	117
		:           :	

RESULT 4  
US-11-075-184A-11  
; Sequence 11, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2 Receptor Antagonists

```

; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine IgD9 a
US-11-075-184A-11

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Query Match	96.6%	Score 599;	DB 7;	Length 117;
Best Local Similarity	95.7%;	Pred. No. 2.9e-45;		
Matches 112;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;
Qy 1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRI	RTKNNYAT 60		
	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRI	RTKNNYAT 60		
Db 1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRI	RTKNNYAT 60		
Qy 61	YYADSVKDRITISRDSDNTLYIQMNSLKTEDTAVYYCTTFYGNVGWGQGL	FLTVSS 117		
	YYADSVKDRITISRDSDNTLYIQMNSLKTEDTAVYYCTTFYGNVGWGQGL	FLTVSS 117		
Db 61	YYADSVKDRITISRDSDNTLYIQMNSLKTEDTAVYYCTTFYGNVGWGQGL	FLTVSS 117		

RESULT 5  
 US-11-075-184A-2  
 ; Sequence 2, Application US/11075184A  
 ; Publication No. US20050260139A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boshringer Ingelhiem International GmbH  
 ; APPLICANT: PAIRET, Michel  
 ; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
 ; TITLE OF INVENTION: Receptor Antagonists  
 ; FILE REFERENCE: 1/1669  
 ; CURRENT APPLICATION NUMBER: US/11/075,184A  
 ; CURRENT FILING DATE: 2005-03-08  
 ; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
 ; PRIOR FILING DATE: 2004-03-30  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 2  
 ; LENGTH: 117  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Murine antibody 1D9 heavy chain variable region; presumably Mur  
 ; OTHER INFORMATION: musculus  
 ; US-11-075-184A-2

	Query Match	88.4%;	Score 548;	DB 7;	Length 117;	
	Best Local Similarity	86.3%;	Pred. No. 6.8e-41;			
	Matches 101;	Conservative 10;	Mismatches 6;	Indels 0;	Gaps 0;	
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Qy	1	EVQLVDSGGGLVPKGSRLRLSCAASGFTFSAYAMNVRQAPKGKLEWVGRIIRTKNNYAT	60			
		:           :           :				
		:           :           :				
Dd	1	EVQLVESGGGLVQP KGS LKLS CAAS GSF S FNA YAMN VRQA PGK LEW VARI RTKN NYAT	60			
<hr/>						
Qy	61	YYADSVKDRTIISRDSDSKNTLYIQMSLKTEDTAIVYCCTTFYGNVGWGQGLTVTVSS	117			
		:           :           :				
		:           :           :				
Dd	61	YYADSVKDRVTIISRDSDSESMFLQMNNLKTEDTAMYCVTFYGNVGWGTGTTTVTVSS	117			
		:           :           :				
		:           :           :				

RESULT 6  
US-11-193-440-87  
; Sequence 87, Application US/11193440  
; Publication No. US2006000293A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Gerald W.  
; Schuman, Richard F.  
;

```

Query Match      78.5%; Score 487; DB 7; Length 123;
Best Local Similarity 75.6%; Pred. No. 1.2e-35;
Matches 93; Conservative 13; Mismatches 11; Indels 6; Gaps 1;

QY      1  EVQLVSGGGLVPGGSLRLSQAASGTFPSAYAMNWVRQAPGKLEWVGRIPTKNNYAT 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       1  EVMLVSGGGLVQPKGSLKLSQAASGTFPNYAMNWVRQAPGKLEWVARIRSKSNYYAT 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61  YYADSVKDRFTISRDTSKNTLYIQMNSLKTEDTAVYYCTTFYGNV-----WGQGTLT 114
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       61  FYADSVKDRFTISRDTSQSMLYIQMNLKTEDTAVYYCVRGASGIDYAMDYWGQGTSLT 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      115  VSS 117
      |||
Db       121  VSS 123

RESULT 7
US-11-054-515-997
; Sequence 997, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418

```

```
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1346

Query Match          77.2%; Score 478.5; DB 7; Length 251;
Best Local Similarity 73.4%; Pred. No. 1.2e-34;
Matches 94; Conservative 10; Mismatches 13; Indels 11; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLTKTEDTAVYYCT-----TFYGNQVWGQ 109
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EYAASVGRFTISRDDSKNSLFLQWNSLTKTEDTAVYYCARAPYDILTGYSDYGMVNGR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 110 GTLVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GTLVTVSS 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Query Match          76.9%; Score 476.5; DB 7; Length 139;
Best Local Similarity 75.0%; Pred. No. 1.1e-34;
Matches 90; Conservative 15; Mismatches 12; Indels 3; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVETGGGLVQPGKSLKLSCAASGFTFNTAMNVRQAPGKGLVWVARIRSKNNYAT 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLTKTEDTAVYYCT---TFYGNQVWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 YYADSVKDRFTISRDDTQSMYQLQWNSLTKTEDTGMTCYVGRGSYFDFVWGAGITTVTVSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-11-054-515-958
; Sequence 958, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1991
```

```
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 958
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-958

Query Match          76.6%; Score 475; DB 7; Length 257;
Best Local Similarity 73.3%; Pred. No. 2.5e-34;
Matches 96; Conservative 7; Mismatches 14; Indels 14; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSANMNSWVRQAPGKGLVWGRIRKSDGGTT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLTKTEDTAVYYCTT-----FYGNQV 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DYAAPVGRFTISRDDSKNTLYLQWNSLTKTEDTAVYYCTTQAHYDILTGYVLWSYGMVDV 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 107 WGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 WGRGLTVTVSS 131
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-11-054-515-1991
; Sequence 1991, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1991
```



GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Fack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION NUMBER: US/10/834,397  
FILING DATE: 29-Apr-2004  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 63:  
US-10-834-397-63

Query Match 76.0%; Score 471.5; DB 6; Length 120;  
Best Local Similarity 77.0%; Pred. No. 2.5e-34;  
Matches 94; Conservative 9; Mismatches 12; Indels 7; Gaps 2;  
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIIRTKNNYAT 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVSAL--SGSGGST 58  
Qy 61 YYADSVKDRPTISRDDSKNTLYLQMSLKTEDTAVYYCTFYGNG-----VWGQGLTVTV 115  
Db 59 YYADSVKGRFTISRDNKNTLYLQMSLKRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTV 118  
Qy 116 SS 117  
Db 119 SS 120

RESULT 15  
US-11-054-515-1209  
Sequence 1209, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
FILE REFERENCE: PF523P3  
CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 1209  
LENGTH: 256  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-1209  
Query Match 76.0%; Score 471.5; DB 7; Length 256;  
Best Local Similarity 70.0%; Pred. No. 5e-34;  
Matches 91; Conservative 11; Mismatches 15; Indels 13; Gaps 1;  
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIIRTKNNYAT 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVSAL--SGSGGST 60  
Qy 61 YYADSVKDRPTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----FYGNGVW 107  
Db 61 YYADSVKGRFTISRDNKNTLYLQMSLKRAEDTAVYYCARDPGNYDILTGYYYTYGMDVW 120  
Qy 108 GQGTLVTVSS 117  
Db 121 GQGTLVTVSS 130  
Search completed: January 28, 2006, 10:12:14  
Job time : 8.02703 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using franklin's n2p model  
Run on: January 28, 2006, 08:12:21 ; Search time 54.8108 Seconds  
(without alignments)  
5627.428 Million cell updates/sec

Title: US-10-733-563-108  
Perfect score: 631  
Sequence: 1 gagggtcaattggttgagtc.....ccctggtcaccgcagctca 351

Scoring table:  
BLOSUM62 Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 4886326  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cpn2\_1/USPTO\_spool\_p/US10733563/runat\_27012006\_180005\_4773/app\_query.fasta\_1.2716  
-DB=A\_Geneseq -QFWT=facian -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosom62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CNC 1.1 624 @runat\_27012006\_180005\_4773 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq 21:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003ba:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	4	Aae06954 Humanised
2	620	98.3	117	4	Aau09927 Humanised
3	620	98.3	117	5	Abg75536 Humanised
4	620	98.3	117	5	Aao14980 Humanised
5	620	98.3	117	5	Adf98240 Humanised
6	620	98.3	117	8	Adq99239 Humanised
7	620	98.3	117	9	Aeb09512 Humanised
8	620	98.3	119	4	Aae07034 Humanised
9	620	98.3	119	8	Adq89326 Humanised

10	620	98.3	119	9	AEB09599	Aeb09599 Humanised
11	613	97.1	117	4	AAE06955	Aae06955 Humanised
12	613	97.1	117	5	ABG75537	Abg75537 Humanised
13	613	97.1	117	5	AAO14981	Aao14981 Humanised
14	613	97.1	117	5	ADF98241	Adf98241 Humanised
15	613	97.1	117	8	ADQ89240	Adq89240 Humanised
16	613	97.1	117	9	AEB09513	Aeb09513 Humanised
17	604	95.7	117	4	AAE06956	Aae06956 Humanised
18	604	95.7	117	4	AAU09929	Aau09929 Humanised
19	604	95.7	117	4	AAU09928	Aau09928 Humanised
20	604	95.7	117	5	ABG75538	Abg75538 Humanised
21	604	95.7	117	5	AAO14982	Aao14982 Humanised
22	604	95.7	117	5	ADF98242	Adf98242 Humanised
23	604	95.7	117	8	ADQ89241	Adq89241 Humanised
24	604	95.7	117	9	AEB09514	Aeb09514 Humanised
25	599	94.9	117	4	AAE06957	Aae06957 Humanised
26	599	94.9	117	4	AAU09930	Aau09930 Humanised
27	599	94.9	117	5	ABG75539	Abg75539 Humanised
28	599	94.9	117	5	ADF98243	Adf98243 Humanised
29	599	94.9	117	8	ADQ89242	Adq89242 Humanised
30	599	94.9	117	9	AEB09515	Aeb09515 Humanised
31	588.5	93.3	118	5	AAO14983	Aao14983 Humanised
32	548	86.8	117	4	AAE06947	Aae06947 Murine 1D
33	548	86.8	117	4	AAU09919	Aau09919 Murine MA
34	548	86.8	117	5	ABG75528	Abg75528 Mouse mAb
35	548	86.8	117	5	ADF98238	Adf98238 Murine mAb
36	548	86.8	117	8	ADQ89232	Adq89232 Mouse imm
37	548	86.8	117	9	AEB09505	Aeb09505 Murine 1D
38	548	86.8	125	8	ADJ95988	Adj95988 Immunoglo
39	548	86.8	148	4	AAE07033	Aae07033 Murine an
40	548	86.8	148	8	ADQ89322	Adq89322 Mouse imm
41	548	86.8	148	9	AEB09595	Aeb09595 Murine 1D
42	539	85.4	117	5	AAO14978	Aao14978 Mouse hea
43	505.5	80.1	452	9	ADX01863	Adx01863 SARS coro
44	505	80.0	120	9	ADV86726	Adv86726 Anti-FLJ3
45	502	79.6	120	9	ADV86731	Adv86731 Anti-FLJ3

ALIGNMENTS

RESULT 1  
AAE06954  
ID AAE06954 standard; protein; 117 AA.  
XX  
AC AAE06954;  
XX  
DT 11-SEP-2003 (revised)  
DT 16-OCT-2001 (first entry)  
XX  
DE Humanised murine 1D9 antibody heavy chain variable region, 1D9RHA.

Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neonatal hyperplasia; VH; heavy chain variable region; 1D9RHA.

OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX	Key	Location/Qualifiers
FT	Region	27..35
FT		/label= CDR1
FT		/note= "Complementarity determining region 1"
FT	Region	50..68
FT		/label= CDR2
FT		/note= "Complementarity determining region 2"
FT	Region	101..106

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FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US003537.
XX 03-FEB-2000; 2000US-00497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX WPI; 2001-488888/53.
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
FT disorder in a patient, comprises a binding specificity for CCR2, and a
XX non-human antigen binding region and human immunoglobulin.
XX Claim 62; Fig 12; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
XX comprising an antigen binding region of non-human origin and at least a
XX portion of an immunoglobulin of human origin. The humanised antibodies
XX are useful for inhibiting the interaction of a cell expressing CCR2. They
XX are useful for inhibiting or treating HIV infection. The proteins of the
XX invention are useful for inhibiting leukocyte trafficking, for treating
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune
XX disorders such as rheumatoid arthritis and multiple sclerosis,
XX atherogenesis and atherosclerosis, and for inhibiting restenosis. They
XX are useful in therapy or diagnosis, and in the manufacture of a
XX medicament for treating CCR-2 mediated disease. They are also useful for
XX treating allergy, anaphylaxis, malignancy, chronic and acute
XX inflammation, histamine and IgE-mediated allergic reaction, shock,
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
XX associated with vascular intervention, including angioplasty and/or stent
XX placement in a mammal. Humanised antibodies are also useful for
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
XX neointimal hyperplasia of a vessel in a mammal, preferably associated
XX with vascular intervention. The present sequence is humanised murine 1D9
XX antibody heavy chain variable (VH) region, 1D9RHA. (Updated on 11-SEP-
XX 2003 to standardise OS field)
XX SQ Sequence 117 AA;

Alignment Scores:
Pred. No.: 1.75e-59 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x AA06954 (1-117)

QY 1 GAGGTGCAATGGTGGTGGAGGAGGATGGTGAAGCTGGGGGTGATTGAGATC 60
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCGAGCTCTGGATTCACTTTCAGTGCCTACGCGCATGAGTGGTCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTGGATGGGTCGCCGCATAGAACTAAATAATTAATATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 191 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAACACG 240
DB 191 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAACACG 240

Db 61 TyrTyrAlaAspSerValLysAspArgPheThrLysSerArgAspSerLysAsnThr 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGACACAGCCGTGTTACTGTACCAACC 300
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCCACGTCAGTCA 351
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 2
AAU09927
ID AAU09927 standard; protein; 117 AA.
XX AC AAU09927;
XX 18-JUN-2002 (first entry)
XX Humanised 1D9 heavy chain variable region, 1D9RHA protein sequence.
XX Human; mouse; 4B4'CL heavy chain variable region; vasotropic;
XX antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;
XX insulin-dependent diabetes mellitus; inflammatory bowel disease;
XX ulcerative colitis; 1D9RHA; graft rejection; allergic disease;
XX antipsoriatic; antiarthritic; nephrotropic; antithyroid; restenosis;
XX dermatological; anaphylaxis; cell adhesion inhibitor; vascular injury;
XX autoimmune disease; immunoglobulin; complementarity determining region;
XX CDR; CD18; CCR2; atherosclerosis; mutant; mutein.
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FT Region 27..30
FT /note= "Part of H1 structure loop"
FT Region 31..35
FT /note= "Complementarity determining region 1 (CDR1),
FT grafted from mouse mAb 1D9 heavy chain sequence
FT (AAU09919)"
FT Region 50..68
FT /note= "Complementarity determining region 2 (CDR2),
FT grafted from mouse mAb 1D9 heavy chain sequence
FT (AAU09919)"
FT Region 101..108
FT /note= "Complementarity determining region 3 (CDR3),
FT grafted from mouse mAb 1D9 heavy chain sequence
FT (AAU09919)"
XX WO200170266-A2.
XX 27-SEP-2001.
XX 15-MAR-2001; 2001WO-US008266.
XX 17-MAR-2000; 2000US-00528267.
XX (MILL-) MILLENNIUM PHARM INC.
XX Horvath CJ, Rao PE;
XX WPI; 2001-607511/69.
XX Inhibiting stenosis or restenosis of a blood vessel following vascular
XX injury or angioplasty in a subject by administering agent which inhibits
XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.
XX Claim 32; Fig 18; 108pp; English.
XX The present invention relates to a new method of inhibiting stenosis or
XX restenosis of a blood vessel following vascular injury in a subject. The
XX new method comprises administering to the subject agents which inhibit
```

CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a  
 CC site of vascular injury by binding CD18 or CCR2. The method of the  
 CC invention inhibits stenosis or restenosis of a blood vessel following  
 CC vascular injury arising from a vascular intervention procedure such as  
 CC vascular by-pass or transplantation surgery. The method is also useful  
 CC for treating a subject having an inflammatory disease or condition  
 CC mediated by neutrophil and mononuclear cell activity e.g. asthma and  
 CC graft versus host disease. Chronic inflammatory diseases of the lung,  
 CC collagen diseases, and insulin-dependent diabetes mellitus can also be  
 CC treated. The method is further useful for treating inflammatory bowel  
 CC diseases, such as ulcerative colitis. Additional diseases or conditions  
 CC include inflammatory or allergic diseases and conditions, including  
 CC systemic anaphylaxis of hypersensitivity responses, drug allergies,  
 CC psoriasis and inflammatory dermatoses, autoimmune diseases such as  
 CC arthritis, graft rejection and other diseases including atherosclerosis.  
 CC This sequence represents the variable region of one of several humanised  
 CC 1D9 heavy chains (AAU09927-AAU09930). These heavy chains were used in the  
 CC invention for the production of anti-CCR2 antibody or antigen-binding  
 CC fragment

XX Sequence 117 AA;

Alignment Scores:  
 Pred. No.: 1,75e-59 Length: 117  
 Score: 620.00 Matches: 117  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.26% Indels: 0  
 DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x AAU09927 (1-117)

QY 1 GAGGTGCAATTGTTGAGTCTGGAGGAGGATTGGTGAAGCTGGGGGTCATTGAGACTC 60  
 DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValValProGlyGlySerLeuArgLeu 20  
 QY 61 TCATGTGCGACTCTGGATTCACTTTTCAGTGGCTACGCCATGAATGGTGGCCAGGCT 120  
 DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
 QY 121 CCAGGAAGGGTTTGAAGTGGTGGCCGATAGAACTAAAATAATATTATGCAACA 180  
 DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60  
 QY 181 TATTATGCGGATTCAGTGAAGACAGATTCAACATCTCCAGAGATGATTCACAAAACACG 240  
 DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
 QY 241 CTCTATCTGCAATGAACACAGCTTGAAACTGAGGACACACGCCGTGTATTACTGTACCAC 300  
 DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
 QY 301 TTTTACGGTAACGGTCTCTGGGGCGAGGGACCGCTGGTCACCGTCAGCTCA 351  
 DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 3

ABG75536

ID ABG75536 standard; protein; 117 AA.

XX AC ABG75536;

XX 16-APR-2003 (first entry)

XX Humanised mouse mAb 1D9 heavy chain variable region, 1D9RHAVH.

XX Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
 KW antigen binding fragment; cellular adhesion molecule; adhesion;  
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
 KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
 KW endovascular stenting; prosthetic valve; transplantation;  
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;

KW chronic bronchitis; asthma; graft-versus-host disease;  
 KW chronic inflammatory disease; hypersensitivity pneumonitis;  
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HP-21/28;  
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
 KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RHAVH;  
 KW heavy chain variable region; VH; complementarity determining region; CDR;  
 KW mutant; mutein.

XX Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.

XX Location/Qualifiers

31..35  
 /note="Mouse complementarity determining region 1  
 (CDR1)"  
 50..68  
 /note="Mouse complementarity determining region 2  
 (CDR2)"  
 101..106  
 /note="Mouse complementarity determining region 3  
 (CDR3)"

US2002106369-A1.

08-AUG-2002.

15-MAR-2001; 2001US-00809739.

17-MAR-2000; 2000US-00528267.

(MILL-) MILLENNIUM PHARM INC.

Horvath CJ, Rao PE;

WPI; 2002-697861/75.

PT Inhibiting (re)stenosis of blood vessel following vascular injury, by  
 PT administering first and second agents that inhibit adhesion and/or  
 PT recruitment of neutrophils and mononuclear cells, respectively to site of  
 PT vascular injury.

Claim 32; Fig 18; 59pp; English.

CC The invention discloses a method for inhibiting stenosis or restenosis of  
 CC a blood vessel following vascular injury in a subject. The method  
 CC involves administering to the subject a first therapeutic agent, which  
 CC comprises an antibody or its antigen binding fragment which binds a  
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
 CC of neutrophils to a site of vascular injury and a second therapeutic  
 CC agent, which comprises an antagonist of CCR2 function, that inhibits  
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
 CC injury. The vascular injury arises from a vascular intervention procedure  
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
 CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
 CC stenting, insertion of a prosthetic valve and transplantation of organs,  
 CC tissues or cells. The method is also useful for treating inflammatory  
 CC diseases or conditions mediated by early neutrophil activity and later  
 CC mononuclear cell activity. Preferably, the method is useful for treating  
 CC asthma and graft-versus-host disease, chronic inflammatory disease of  
 CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
 CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
 CC mellitus. The method is also useful for treating inflammatory bowel  
 CC disease. Crohn's disease, inflammatory or allergic diseases (such as  
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition

CC of mononuclear cell participation, and thus provides superior therapy for  
CC inhibiting stenosis or restenosis following vascular injury. The sequence  
CC presented is the humanised mouse monoclonal antibody (mab), 1D9, heavy  
CC chain variable region (VH), 1D9RHAVH, which is comprised of the mouse 1D9  
CC mAb complementarity determining regions (CDR's) linked by human 4B4'CL  
CC mAb VH regions  
XX

SQ Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1.75e-59 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-108 (1-351) x ABG75536 (1-117)

QY 1 GAGTGCATTTGGTTGAGTCTGGAGAGGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCTCTGGATTCACTTTCAGTGCCTACGCATCAACTGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGAAAGGGTTTGGATTGGTTCGGCGCATTAAGAACTAAATAATTAATTATCAACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGCAACAGCTTGAAGAGGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 4

AAO14980  
ID AAO14980 standard; protein; 117 AA.

AC AAO14980;

XX 05-SEP-2002 (first entry)

XX Humanised murine heavy chain variable region (1D9RHa VH).

DE Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
KW bowel transplant; heart transplant; graft versus host disease;  
KW chronic graft rejection; antibody heavy chain variable region; 1D9RHa VH.  
XX

OS Mus musculus.

OS Synthetic.

XX US2002042370-A1.

XX 11-APR-2002.

XX 13-APR-2001; 2001US-00835087.

XX 14-APR-2000; 2000US-00549448.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hancock WH;

PI

XX WPI; 2002-351265/38.  
DR Inhibiting graft rejection, graft versus host disease or chronic  
XX rejection of a transplanted graft, involves administering a CCR2  
PT antagonist.  
PT

XX Claim 26; Fig 2; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
CC versus host disease or chronic rejection of a transplanted graft. The  
CC method involves administering an antagonist of CC chemokine receptor 2  
CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
CC complementarity determining regions from various non-human origins). CCR2  
CC is known to be involved in the rejection of transplanted grafts. The  
CC method of the invention is useful for inhibiting graft rejection -  
CC particularly allografts such as kidney, liver, lung, heart-lung,  
CC pancreas, bowel and heart. The method of the invention is also useful for  
CC inhibiting graft versus host disease and for inhibiting chronic rejection  
CC of a transplanted graft. The present amino acid sequence represents a  
CC humanised murine antibody heavy chain variable region (1D9RHa VH)

XX Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1.75e-59 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-108 (1-351) x AAO14980 (1-117)

QY 1 GAGTGCATTTGGTTGAGTCTGGAGAGGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 60

DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCTCTGGATTCACTTTCAGTGCCTACGCATCAACTGGTCCGCCAGGCT 120

DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGATTGGTTCGGCGCATTAAGAACTAAATAATTAATTATCAACA 180

DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240

DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCATCTGCAATGCAACAGCTTGAAGAGGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 300

DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351

DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 5

ADF98240

ID ADF98240 standard; protein; 117 AA.

XX ADF98240;

XX 26-FEB-2004 (first entry)

XX Humanised 1D9 heavy chain variable region, 1D9RHa VH, SEQ ID 10.

XX Immunosuppressive; CCR2 function inhibitor; graft rejection;

XX graft versus host disease; CC chemokine receptor 2; CCR2;

XX anti-CCR2 antibody.

XX





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PR 03-FEB-2000; 2000US-00497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX WPI; 2001-488888/53.
DR N-PSDB; AAD13179.
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.
XX
PS Disclosure; Fig 23; 183pp; English.
XX
CC The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE- mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is humanised murine
CC antibody heavy chain region, 1D9RHA. 1D9RHA sequence consist of the
CC complementarity determining regions (CDRs) of the murine 1D9 antibody
CC heavy chain variable (VH) region genetically inserted into the framework
CC regions (FRs) of the human 4B4'CL antibody VH region. (Updated on 11-SEP-
CC 2003 to standardise OS field)
XX
SQ Sequence 119 AA;

Alignment Scores:
Pred. No.: 1,76e-59 Length: 119
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x AAE07034 (1-119)

QY 1 GAGTGCATTTGGTTCGAGCTCGAGAGGATTGGTGAAGCCCTGGGGGTTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLeuValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCTCTGGATTCTTCATCTTCAGTGCCTAGCCATCACTGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGGAAGGGTTTGGATTGGGTTCGCCCATAGAACTAAATAATTAATTATCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgLleArgThrLysAsnAsnAsnTrpAlaThr 60

QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCATAAAACACG 240
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80

QY 241 CTCATATCGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCACC 300
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCCACCGTCAGCTCA 351
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 9
ADQ89326
ID ADQ89326 standard; protein; 119 AA.
XX
XX AC ADQ89326;
XX
XX 21-OCT-2004 (first entry)
XX
XX Humanised immunoglobulin protein #9.
XX
XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;
KW inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW anti-HIV; virucide; antiarteriosclerotic.
XX
OS Synthetic.
PN US2004151721-A1.
PD 05-AUG-2004.
XX
PF 10-DEC-2003; 2003US-00733563.
PR 19-OCT-2001; 2001US-0350166P.
PR 26-JUN-2002; 2002US-0392364P.
PR 17-OCT-2002; 2002US-00272899.
XX
PA (OKEE/) O'KEEFE T.
PA (PONA/) PONATH P.
XX
XX O'keefe T, Ponath P;
XX
XX WPI; 2004-580175/56.
DR N-PSDB; ADQ89319.
XX
PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
XX
PS Disclosure; SEQ ID NO 104; 128pp; English.
XX
CC The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of the CCR2 polypeptide,
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents a humanised
CC immunoglobulin protein of the invention.
XX
SQ Sequence 119 AA;

Alignment Scores:
Pred. No.: 1,76e-59 Length: 119
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 8 Gaps: 0

US-10-733-563-108 (1-351) x ADQ89326 (1-119)

QY 1 GAGTGCATTTGGTTCGAGCTCGAGAGGATTGGTGAAGCCCTGGGGGTTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLeuValProGlyGlySerLeuArgLeu 20
```

QY 61 TCATGTGAGCGCTCTGGATTCACTTTTCAGTGCCTACGCGCATGCACTGGTCCGCCAGGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
 QY 121 CCAGGAAAGGTTTGGATGGTGGCCGCATAGCACTAAATAAATAATTATGCAACA 180  
 Db 41 ProGlyLySgLyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
 QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAAACAG 240  
 Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
 QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGCGTGTATTACTGTACCACC 300  
 Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
 QY 301 TTTTACGGTAAAGCTGTCTGGGGCCAGGGGACCTGGTCACCGTCAGCTCA 351  
 Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 10

AEB09599

ID AEB09599 standard; protein; 119 AA.

XX AC AEB09599;

XX XX

XX 08-SEP-2005 (first entry)

XX Humanized heavy chain 1D9RHA.

XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW heavy chain variable region.

XX Synthetic.  
 OS

XX WO2005060368-A2.  
 PN

XX 07-JUL-2005.  
 PD

XX 10-DEC-2003; 2003WO-US039599.  
 PF

XX 10-DEC-2003; 2003WO-US039599.  
 PR

XX (MILL-) MILLENNIUM PHARM INC.  
 PA

XX Okeefe T, Ponath P;  
 PI

XX WPI; 2005-488561/49.  
 DR

XX N-PSDB; AEB09592.  
 DR

XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.

XX Disclosure; SEQ ID NO 104; 192pp; English.  
 PS

XX The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for  
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of

CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
 CC construct comprising nucleic acid molecule encoding (I); and host cell  
 CC comprising the nucleic acid molecule. (I) is useful as a therapeutic  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of humanized heavy  
 CC chain 1D9RHA.

XX SQ Sequence 119 AA;  
 SQ

## Alignment Scores:

Pred. No.: 1.76e-59 Length: 119  
 Score: 620.00 Matches: 117  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.26% Indels: 0  
 DB: 9 Gaps: 0

US-10-733-563-108 (1-351) x AEB09599 (1-119)

QY 1 GAGGTGCANNTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
 Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCGCTCTGGATTCACTTTTCAGTGCCTACGCGCATGCACTGGTCCGCCAGGCT 120

Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGGAAAGGTTTGGATGGTGGCCGCATAGCACTAAATAAATAATTATGCAACA 180

Db 41 ProGlyLySgLyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAAACAG 240

Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGCGTGTATTACTGTACCACC 300

Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100

QY 301 TTTTACGGTAAAGCTGTCTGGGGCCAGGGGACCTGGTCACCGTCAGCTCA 351

Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 11

AEB09595

ID AEB09595 standard; protein; 117 AA.

XX AC AAE06955;  
 XX

XX 11-SEP-2003 (revised)  
 DT 16-OCT-2001 (first entry)  
 XX

XX Humanised murine 1D9 antibody heavy chain variable region, 1D9RHB.  
 DE

XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody;  
 KW neonatal hyperplasia; VH; heavy chain variable region; 1D9RHB.





XX 17-MAR-2000; 2000US-00528267.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Horvath CJ, Rao PE;  
XX WPI; 2002-697861/75.  
XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
PT administering first and second agents that inhibit adhesion and/or  
PT recruitment of neutrophils and mononuclear cells, respectively to site of  
PT vascular injury.

XX Claim 32; Fig 18; 59pp; English.

XX The invention discloses a method for inhibiting stenosis or restenosis of  
CC a blood vessel following vascular injury in a subject. The method  
CC involves administering to the subject a first therapeutic agent, which  
CC comprises an antibody or its antigen binding fragment which binds a  
CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
CC of neutrophils to a site of vascular injury and a second therapeutic  
CC agent, which comprises an antagonist of CCR2 function, that inhibits  
CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
CC injury. The vascular injury arises from a vascular intervention procedure  
CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
CC stenting, insertion of a prosthetic valve and transplantation of organs,  
CC tissues or cells. The method is also useful for treating inflammatory  
CC diseases or conditions mediated by early neutrophil activity and later  
CC mononuclear cell activity. Preferably, the method is useful for treating  
CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
CC asthma and graft-versus-host disease, chronic inflammatory disease of  
CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
CC disease. The method is also useful for treating inflammatory bowel  
CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
CC (such as arthritis and multiple sclerosis), graft rejection,  
CC atherosclerosis and myositis. The method enables simultaneous inhibition  
CC of neutrophil and mononuclear cell participation in response to vascular  
CC injury or inhibition of neutrophil participation followed by inhibition  
CC of mononuclear cell participation, and thus provides superior therapy for  
CC inhibiting stenosis or restenosis following vascular injury. The sequence  
CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy  
CC chain variable region (VH), 1D9RHBVH, which is comprised of the mouse 1D9  
CC mAb complementarity determining regions (CDR's) linked by human 4B4'CL  
CC mAb VH regions with a mouse derived Thr at position 28 and Ser at  
CC position 30

XX Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1,04e-58 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-108 (1-351) x ABG75537 (1-117)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATGGTGAAGCCCTGGGGGTCTATTGAGCTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCATCTTTCAGTGCCTACGCCATGAACCTGGTCCGCGAGCT 120  
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGTTTGGATGGTTCGGCGCATAGCACTTAAATAATAATATATGCAACA 180

Db 41 ProGlyIysGlyLeuGluTrpValGlyArgIleArgThrIysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTTCAAAAAACAG 240  
DB 61 TyrTyrAlaAspSerValIysAspArgPheThrIleSerArgAspAspSerIysAsnThr 80  
QY 241 CTCATCTGCAAAATGAACAGCTTGAAACTGAGACACAGCCGTGTATTACTGTACCA 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuIysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGTTACGTTCTCTGCGGCGGACCCCTGGTCCAGCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 13

AAO14981

ID AAO14981 standard; protein; 117 AA.

XX AC AAO14981;

XX DT 05-SEP-2002 (first entry)

XX DE Humanised murine heavy chain variable region (1D9RHB VH).

XX KW Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
KW bowel transplant; heart transplant; graft versus host disease;  
KW chronic graft rejection; antibody heavy chain variable region; 1D9RHB VH.

XX OS Mus musculus.

XX OS Synthetic.

XX PN US2002042370-A1.

XX PD 11-APR-2002.

XX PF 13-APR-2001; 2001US-00835087.

XX PR 14-APR-2000; 2000US-00549448.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Hancock WW;

XX WPI; 2002-351265/38.

XX PT Inhibiting graft rejection, graft versus host disease or chronic

XX PT rejection of a transplanted graft, involves administering a CCR2

XX PS Claim 26; Fig 2; 16pp; English.

XX CC The invention comprises a method of inhibiting graft rejection, graft  
CC versus host disease or chronic rejection of a transplanted graft. The  
CC method involves administering an antagonist of CC chemokine receptor 2  
CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
CC complementarity determining regions from various non-human origins). CCR2  
CC is known to be involved in the rejection of transplanted grafts. The  
CC method of the invention is useful for inhibiting graft rejection -  
CC particularly allografts such as kidney, liver, lung, heart-lung,  
CC pancreas, bowel and heart. The method of the invention is also useful for  
CC inhibiting graft versus host disease and for inhibiting chronic rejection  
CC of a transplanted graft. The present amino acid sequence represents a  
CC humanised murine antibody heavy chain variable region (1D9RHB VH)

XX SQ Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1,04e-58 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 98.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-108 (1-351) x AAO14981 (1-117)

QY 1 GAGTGCATTTGGTTCAGCTGAGGAGGATTGGTGAAGCCTGGGGGGTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCCTCTCGATTTCATTTCACTTCAGTGCCTACGCATCACTGAACCTGGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGGTTTGAATGGTTCGCCGCATAGAAGCTAAATAATAATATGTCACACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgGlyLeuValLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAACACG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCTATCTCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTCTCTGGGGCCAGGGGACCCTGCTCACCCTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 14

ADP98241  
ID ADF98241 standard; protein; 117 AA.  
AC ADF98241;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Humanised ID9 heavy chain variable region, ID9RHB VH, SEQ ID 11.  
XX  
KW Immunosuppressive; CCR2 function inhibitor; graft rejection;  
KW graft versus host disease; CC chemokine receptor 2; CCR2;  
KW anti-CCR2 antibody.  
OS Synthetic.  
OS Mus musculus.  
OS Homo sapiens.  
XX  
PN WO200178653-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 13-APR-2001; 2001WO-US012139.  
XX  
PR 14-APR-2000; 2000US-00549448.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Hancock WW;  
XX  
XX WPI; 2002-017543/02.  
XX  
XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
XX involves use of CC chemokine receptor 2 inhibitor.  
XX  
XX Claim 26; Fig 2; 44pp; English.  
XX  
XX The present invention relates to a method for inhibiting graft rejection  
XX or graft versus host diseases. The method comprises administration of a  
XX CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
XX CC recipient of a transplanted graft. The CCR2 function antagonist is an  
XX anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
XX ADF98240-ADP98249). The method is useful for inhibiting rejection,

CC particularly chronic rejection of a graft, particularly an allograft of  
CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
CC inhibiting graft versus host disease for a bone marrow graft.  
XX  
SQ Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1.04e-58 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-108 (1-351) x ADF98241 (1-117)

QY 1 GAGTGCATTTGGTTCAGCTGAGGAGGATTGGTGAAGCCTGGGGGGTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCCTCTCGATTTCATTTCACTTCAGTGCCTACGCATCACTGAACCTGGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGGTTTGAATGGTTCGCCGCATAGAAGCTAAATAATAATATGTCACACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgGlyLeuValLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAACACG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCTATCTCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTCTCTGGGGCCAGGGGACCCTGCTCACCCTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 15

ADQ89240  
ID ADQ89240 standard; protein; 117 AA.  
XX  
AC ADQ89240;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Humanised immunoglobulin protein #6.  
XX  
KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX  
OS Synthetic.  
XX  
XX US2004151721-A1.  
XX  
XX 05-AUG-2004.  
XX  
XX 10-DEC-2003; 2003US-00733563.  
XX  
XX 19-OCT-2001; 2001US-0350166P.  
XX 26-JUN-2002; 2002US-0392364P.  
XX 17-OCT-2002; 2002US-00272899.  
XX  
XX (OKEE/) O'KEEFE T.  
XX (PONA/) PONAATH P.  
XX  
XX O'keefe T, Ponath P;  
XX  
XX WPI; 2004-580175/56.  
XX

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX  
PS Example 2; SEQ ID NO 18; 128pp; English.  
XX  
CC The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.  
XX  
SQ Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1.04e-58 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 99.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-108 (1-351) x ADQ89240 (1-117)

QY	1	GAGGTGCAATTGTTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGTCATTGAGACTC	60
Db	1	GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu	20
QY	61	TCATGTGAGCCCTCTGGATTCACTTTCAGTGCCTAGCCCATGAACCTGGTCCGCCAGGCT	120
Db	21	SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla	40
QY	121	CCAGGAAAGGGTTTGGATTGGGTGGCCGATAGAACTAAAAATAATATTATCAACA	180
Db	41	ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr	60
QY	181	TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG	240
Db	61	TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr	80
QY	241	CTCTATCTGCRAATGACAGCTTGAAACTGAGGACACAGCCGCTGTATTACTGTACCACC	300
Db	81	LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr	100
QY	301	TTTTACGGTAACGGTCTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA	351
Db	101	PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer	117

Search completed: January 28, 2006, 08:33:31  
Job time : 57.8108 secs



```
Db 60 ProGlyLysGlyLeuGluTrpValAlaArgIleArgSerLysSerAsnAsnTyrAlaThr 79
Qy 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 80 TyrTyrGlyAsnSerValLysAspArgPheThrIleSerArgAspAspSerGlnSerMet 99
Qy 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGGTGTATTACTGTACACACC 300
Db 100 LeuTyrLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrCysVal--- 118
Qy 301 TTTTACGGTAAC-----GGTCTCTGGGGCCAGGGGACCTCGTCCAGCTCAGCTCA 351
Db 119 ---TyrGlyAsnPheGlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 137

RESULT 2
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31106
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:9211633; PMID:173252
A:Accession: S31106
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <RAA>
A:Cross-references: UNIPARC:UPI0000176C8E; EMBL:X62954
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,156-40 Length: 121
Score: 490.00 Matches: 98
Percent Similarity: 85.12% Conservative: 5
Best Local Similarity: 80.99% Mismatches: 14
Query Match: 77.65% Indels: 4
Gaps: 2

US-10-733-563-108 (1-351) x S31106 (1-121)

Qy 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
Qy 61 TCATGTGACGCTCTGGATTCACTTTCAGTGCCTACGCCATGAACCTGGGTCGCCAGGCT 120
Db 21 SerCysAlaIleSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40
Qy 121 CCAGAAAGGGTTTGGAAATGGTGGCCGATAGAACTAAATAATATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleLysSerLysThrAspGlyThrThr 60
Qy 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 21 SerCysAlaIleSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40
Qy 121 CCAGAAAGGGTTTGGAAATGGTGGCCGATAGAACTAAATAATATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleLysSerLysThrAspGlyThrThr 60
Qy 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80
Qy 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGGTGTATTACTGTACACACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
Qy 301 -----TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTCGTCCAGCTCAGC 348
Db 101 ValIleAspTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThrThrValThrValSer 120
Qy 349 TCA 351
Db 121 Ser 121

RESULT 3
```

```
S58213
Ig heavy chain V region (anti-F(ab')2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 23-Jul-1999
C:Accession: S58213; S58212
R:Weischof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58213
A:Molecule type: mRNA
A:Residues: 1-127 <WE>
A:Cross-references: UNIPARC:UPI000003FEA8; EMBL:X89055; NID:G929638; PIDN:CAA61442.1; P
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 6,66e-40 Length: 127
Score: 485.00 Matches: 96
Percent Similarity: 81.10% Conservative: 7
Best Local Similarity: 75.59% Mismatches: 14
Query Match: 76.86% Indels: 10
Gaps: 1

US-10-733-563-108 (1-351) x S58213 (1-127)

Qy 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuLysLeu 20
Qy 61 TCATGTGACGCTCTGGATTCACTTTCAGTGCCTACGCCATGAACCTGGGTCGCCAGGCT 120
Db 21 SerCysAlaIleSerGlyPheThrPheSerGlySerThrMetHisTrpValArgGlnAla 40
Qy 121 CCAGAAAGGGTTTGGAAATGGTGGCCGATAGAACTAAATAATATTATGCAACA 180
Db 41 SerGlyLysGlyLeuGluTrpValGlyArgIleArgAsnLysAspAsnSerTyrAlaThr 60
Qy 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 61 AlaTyrAlaAlaSerValLysGlyArgPheThrIleSerArgAspAspSerGluAsnThr 80
Qy 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGGTGTATTACTGTACACACC 300
Db 81 AlaTyrLeuGlnMetAsnSerLeuLysIleGluAspThrAlaValTyrTyrCysThrArg 100
Qy 301 -----TTTTACGGTAACGGTGTCTGGGGCCAGGGG 330
Db 101 GlySerSerMetValArgGlyValAsnGlyTyrTyrGlyMetAspValTrpGlyGlnGly 120
Qy 331 ACCCTGGTCACCGTCAGCTCA 351
Db 121 ThrThrValThrValSerSer 127

RESULT 4
H36005
Ig heavy chain V region (W85) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: H36005
R:Schröder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: H36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: UNIPARC:UPI0000176C28; GB:M34032
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
```

A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.05e-39 Length: 121  
Score: 483.00 Matches: 98  
Percent Similarity: 83.47% Conservative: 3  
Best Local Similarity: 80.99% Mismatches: 16  
Query Match: 76.55% Indels: 4  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x H36005 (1-121)

```
QY 1 GAGGTGCAATTGGTTCAGTCTGGAGGAGGATTGGTGAAGCTGGGGGGTCATTGAGACTC 60
  |||
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlySerLeuArgLeu 20
  |||
QY 61 TCATGTGCAGCTCTCGATTCACTTTTCAGTGCCTACGCCATGAACCTGGGTCCGCCAGGCT 120
  |||
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetAsnTrpValArgGlnAla 40
  |||
QY 121 CCAGGAAGCGTTTGAATGGTTGGCCGCATGAAGAACTAAATAATATTATGCAACA 180
  |||
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgGlyLeuSerLysThrAspGlyGlyThrThr 60
  |||
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCANAAAAACAGC 240
  |||
Db 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80
  |||
QY 241 CTCTATCTCAATGAACAGCTTTGAAACTGAGGACACAGCCCTGTATTACTGTACACC 300
  |||
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
  |||
QY 301 TTTTACGGTAACGGT-----GTCGGGGCCAGGGACCTCGTCCACCGTCAGC 348
  |||
Db 101 AspArgGlyGlySerSerGlnGlyAspTyrTrpGlyGlnGlyThrLeuValThrValSer 120
  |||
QY 349 TCA 351
  |||
Db 121 Ser 121
```

RESULT 5  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31109  
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31109  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-117 <RAA>  
A:Cross-references: UNIPARC:UPI0000176DCA; EMBL:X62960  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.33e-39 Length: 117  
Score: 482.00 Matches: 96  
Percent Similarity: 85.47% Conservative: 4  
Best Local Similarity: 82.05% Mismatches: 17  
Query Match: 76.39% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x S31109 (1-117)

```
QY 1 GAGGTGCAATTGGTTCAGTCTGGAGGAGGATTGGTGAAGCTGGGGGGTCATTGAGACTC 60
  |||
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlySerLeuArgLeu 20
  |||
QY 61 TCATGTGCAGCTCTCGATTCACTTTTCAGTGCCTACGCCATGAACCTGGGTCCGCCAGGCT 120
  |||
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40
  |||
QY 121 CCAGGAAGCGTTTGAATGGTTGGCCGCATGAAGAACTAAATAATATTATGCAACA 180
  |||
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgGlyLeuSerLysThrAspGlyGlyThrThr 60
  |||
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCANAAAAACAGC 240
  |||
Db 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80
  |||
QY 241 CTCTATCTCAATGAACAGCTTTGAAACTGAGGACACAGCCCTGTATTACTGTACACC 300
  |||
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrAla 100
  |||
QY 301 TTTTACGGTAACGGTCTCTGGGGCCAGGGACCTCGTCCACCGTCAGCTCA 351
  |||
Db 101 ThrTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 117
```

#### RESULT 6

A41940  
Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment)  
N:Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-May-1999  
C:Accession: A41940; PL0201  
R:Herron, J.N.; He, X.M.; Ballard, D.W.; Bliler, P.R.; Pace, P.E.; Bothwell, A.L.; Voss  
Proteins 11, 159-175, 1991  
A:Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional st  
A:Reference number: A41940; MUID:92086633; PMID:1749770  
A:Accession: A41940  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-121 <HER>  
A:Cross-references: UNIPARC:UPI0000176D34  
A:Note: sequence extracted from NCBI backbone (NCBIP:70715)  
R:Smith, R.G.; Voss Jr., E.W.  
Mol. Immunol. 27, 463-470, 1990  
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from:  
A:Reference number: PL0198; MUID:90309768; PMID:2114528  
A:Accession: PL0201  
A:Molecule type: mRNA  
A:Residues: 1-118 <SMI>  
A:Cross-references: UNIPARC:UPI0000176D35  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:50-68/Region: complementarity-determining 2  
F:101-110/Region: complementarity-determining 3  
F:101-106/Region: D region  
F:107-115/Region: JH region

#### Alignment Scores:

Pred. No.: 2.08e-39 Length: 121  
Score: 480.00 Matches: 93  
Percent Similarity: 86.18% Conservative: 13  
Best Local Similarity: 75.61% Mismatches: 9  
Query Match: 76.07% Indels: 8  
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x A41940 (1-121)

```
QY 1 GAGGTGCAATTGGTTCAGTCTGGAGGAGGATTGGTGAAGCTGGGGGGTCATTGAGACTC 60
  |||
Db 1 GluValGlnProValGluThrGlyGlyLeuValGlnProGlySerLeuArgLeu 20
  |||
QY 61 TCATGTGCAGCTCTGGATTCTTCTAGTGCCTACGCCATGAACCTGGGTCCGCCAGGCT 120
```

Db 21 SerCysAlaAlaSerGlyPheSerPheAsnThrAsnAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGTTTGGATGGGTCGCATAGAACTAAATAATAATTATCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleAArgSerLysSerAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerGlnAsnMet 80  
QY 241 CTCTATCTGCAATCAAGACAGCTTGAATACTGAGGACACAGCGGTGTATTAAGTGT 294  
Db 81 LeuTyrLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValArg 100  
QY 295 -----ACCACCTTTTACGGTAACGGTGTCTGGGGCCAGGACCTGTGTACCC 342  
Db 101 AspGlnThrGlyThrAlaTrpPhe-----AlaTyrTrpGlyGlnGlyThrLeuValThr 118  
QY 343 CTCAGCTCA 351  
Db 119 ValSerAla 121

## RESULT 7

Ig heavy chain precursor V region (MRL4) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 23-Jul-1999  
C:Accession: I32513  
R:Kofler, R.; Strohal, R.; Baldaras, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
J. Clin. Invest. 82, 852-860, 1988  
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A:Reference number: A94689; MUID:8831394; PMID:3138286  
C:Accession: I32513  
A:Molecule type: DNA  
A:Residues: 1-141 <KOF>  
A:Cross-references: UNIPARC:UPI0000114D98; GB:M20829; NID:gl96951; PIDN:AAA38849.1; PID:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2,3e-39 Length: 141  
Score: 479.50 Matches: 92  
Percent Similarity: 85.25% Conservative: 12  
Best Local Similarity: 75.41% Mismatches: 13  
Query Match: 75.95% Indels: 5  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x I32513 (1-141)

QY 1 GAGGTGCAATTGGTTGAGTCTCGAGAGGAGGATTGGTGAAGCCCTGGGGGGTCATTGAGACTC 60  
Db 20 GluValGlnLeuValGluThrGrGlyGlyLeuValGlnProLysGlySerLeuLysLeu 39  
QY 61 TCATGTGCGCCTCTGGATTCATTTTCAGTGCCTACGCCATGAATCGGTCGCCAGGCT 120  
Db 40 SerCysProAlaSerGlyPheSerPheAsnThrAsnAlaMetAsnTrpValArgGlnAla 59  
QY 121 CCAGGAAAGGTTTGGATGGTGGCGCATAGAACTAAATAATAATTATCAACA 180  
Db 60 ProGlyLysGlyLeuGluTrpValAlaArgIleAArgSerLysSerAsnAsnTyrAlaThr 79  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
Db 80 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerGlnSerMet 99  
QY 241 CTCTATCTGCAATCAAGACAGCTTGAATACTGAGGACACAGCGGTGTATTAAGTGTACCC 300  
Db 100 LeuTyrLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValArg 119  
QY 301 TTTTACGGTAAC-----GGTGTCTGGGGCCAGGACCTGTGTACCGTCC 345

Db 120 AspAlaAlaAsnTrpSerAlaTrpPheAlaTyrTrpGlyGlnGlyThrLeuValThrVal 139  
QY 346 AGCTCA 351  
Db 140 SerAla 141  
RESULT 8  
A36006  
Ig heavy chain V region (M26) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C:Accession: A36006  
R:Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A36005; MUID:90349571; PMID:2117273  
C:Accession: A36006  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <SCH>  
A:Cross-references: UNIPARC:UPI000003PEBD; GB:M34023  
C:Genetics:  
A:Gene: GDB:IGH@; IGHDI1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 3,28e-39 Length: 123  
Score: 478.00 Matches: 97  
Percent Similarity: 82.11% Conservative: 4  
Best Local Similarity: 78.86% Mismatches: 16  
Query Match: 75.75% Indels: 6  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x A36006 (1-123)

QY 1 GAGGTGCAATTGGTTGAGTCTCGAGAGGAGGATTGGTGAAGCCCTGGGGGGTCATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGCGCCTCTGGATTCATTTTCAGTGCCTACGCCATGAATCGGTCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGTTTGGATGGTGGCGCATAGAACTAAATAATAATTATCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleLysSerLysThrAspGlyGlyThrThr 60  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATGAACAGCTTGAATACTGAGGACACAGCGGTGTATTAAGTGTACCC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 -----TTTACGGTAACCGTGTCTGGGGCCAGGACCTGTGTACCC 342  
Db 101 SerIleProGlyIleAlaValAlaGlyThrAspTyrTrpGlyGlnGlyThrLeuValThr 120  
QY 343 CTCAGCTCA 351  
Db 121 ValSerSer 123

## RESULT 9

A30561  
Ig heavy chain precursor V-III region (4B4) - human (fragment)  
N:Alternate names: Ig heavy chain V region (DP-38)  
C:Species: Homo sapiens (man)  
C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 23-Jul-1999



C:Accession: A30561; S26931; S34008  
R:Sanz, I.; Dang, H.; Takei, M.; Talal, N.; Capra, J.D.  
J. Immunol. 142, 883-887, 1989  
A:Title: V-H sequence of a human anti-Sm autoantibody. Evidence that autoantibodies can  
A:Reference number: A30561; MUID:89110065; PMID:2492331  
A:Accession: A30561  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-138 <SAN>  
A:Cross-references: UNIPARC:UPI0000176C80  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A:Reference number: S26885; MUID:93021117; PMID:1404388  
A:Accession: S26931  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 20-119 <TOM>  
A:Cross-references: UNIPARC:UPI000011640B; EMBL:Z12338; NID:G32896; PIDN:CAA78208.1; PIDN:  
R:Marlette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A:Reference number: S34001; MUID:93209281; PMID:7681398  
A:Accession: S34008  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 20-119 <MAR>  
A:Cross-references: UNIPARC:UPI000011640B  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 4,07e-39 Length: 138  
Score: 477.00 Matches: 97  
Percent Similarity: 85.71% Conservatives: 5  
Best Local Similarity: 81.51% Mismatches: 15  
Query Match: 75.59% Indels: 2  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x A30561 (1-138)

QY 1 GAGGTGCAATGTTGAGTCTGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
|||||  
Db 20 GluValGlnLeuValGluSerGlyGlyLeuValValGlyProGlyGlySerLeuArgLeu 39  
|||||

QY 61 TCATGTGCAGCCTCTGGATTCACTTTCACTGCTGCTAGCCCATGACTGGGTCCGCCAGGCT 120  
|||||  
Db 40 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 59  
|||||

QY 121 CCAGGAAAGGGTTTGGAAATGGGTTGGCGCATAGAAGCTAAATAATAATTATGCAACA 180  
|||||  
Db 60 ProGlyLysGlyLeuGluTrpValGlyArgLysSerLysThrAspGlyThrThr 79  
|||||

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
|||||  
Db 80 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspSerLysAsnThr 99  
|||||

QY 241 CTCTATCTGCAATGACAGCTTGAAGACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
|||||  
Db 100 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 119  
|||||

QY 301 -----TTTTACGGTAACGGTGTCTGGGGCCAGGGACCTGGTCAACCGTCAGCTCA 351  
|||||  
Db 120 AspSerLeuProHisArgValTrpGlyGlnGlyThrLeuValThrValSerSer 138  
|||||

RESULT 10  
S31678  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31678  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.

submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31678  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CUI>  
A:Cross-references: UNIPARC:UPI0000116456; EMBL:Z14169; NID:G31003; PIDN:CAA78538.1; P1:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 8,04e-39 Length: 139  
Score: 474.00 Matches: 95  
Percent Similarity: 82.11% Conservatives: 6  
Best Local Similarity: 77.24% Mismatches: 16  
Query Match: 75.12% Indels: 6  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x S31678 (1-139)

QY 1 GAGGTGCAATGTTGAGTCTGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
|||||  
Db 17 GluValGlnLeuValGluSerGlyGlyLeuValValGlyProGlyGlySerLeuArgLeu 36  
|||||

QY 61 TCATGTGCAGCCTCTGGATTCACTTTCACTGCTGCTAGCCCATGAACTATAATAATTATGCAACA 180  
|||||  
Db 57 ProGlyLysGlyLeuGluTrpValAlaArgLysSerLysThrAspGlyThrThr 76  
|||||

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
|||||  
Db 77 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspSerLysAsnThr 96  
|||||

QY 241 CTCTATCTGCAATGACAGCTTGAAGACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
|||||  
Db 97 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 116  
|||||

QY 301 TTTTACGGTAACGGT-----GTCTGGGGCCAGGGACCTGGTGGTCAACC 342  
|||||  
Db 117 AspLysSerGlnGlyAsnLeuLeuAlaPheAspLysThrGlyGlnGlyThrMetValThr 136  
|||||

QY 343 GTCAGCTCA 351  
|||||  
Db 137 ValSerSer 139  
|||||

RESULT 11

S44107

Ig heavy chain V-D-J region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001

C:Accession: S44107

R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, P.K.

submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable

A:Reference number: S44105

A:Accession: S44107

A:Molecule type: DNA

A:Residues: 1-126 <HAW>

A:Cross-references: UNIPARC:UPI0000116634; EMBL:Z31394; NID:G472961; PIDN:CAA83269.1; P1:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1.14e-38 Length: 126

Score: 472.50 Matches: 94

Percent Similarity: 79.37% Conservatives: 6

```
Best Local Similarity: 74.60% Mismatches: 13
Query Match: 74.88% Indels: 13
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x S44107 (1-126)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGGTCAATTGAGACTC 60
D 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuLeuVal 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGTGCTACGCGCATGCAATCGGCTGGCGGCT 120
D 21 SerCysAlaAlaSerGlyPheThrPheSerGlySerAlaMetHisTrpValArgGlnAla 40
QY 121 CCAGAAAGGGTTTGGAAATGGTGGCCGCAATAAGAACTAAATAATAATAATATGCAACA 180
D 60 ProGlyLysGlyLeuGluTrpValSerAlaAla-----SerGlySerGlyGlySerThr 77
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAAACACG 240
D 78 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 97
QY 241 CTCTATCTGCAAAATGAAACAGCTTGAATACTGAGGACACAGCCGCTGATTACTGTACCACC 300
D 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 117
QY 301 -----TTTACGGTAACGGTGTCTGGGGCCAGGG 330
D 118 AlaValValArgGlyValIleSerTyrTyrTyrGlyMetAspValTrpGlyGlnGly 137
QY 331 ACCCTGGTCAACCGTCAGCTCA 351
D 138 ThrThrValThrValSerSer 144

RESULT 13
S30533
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C:Accession: S30533
R:Marlette, X.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <MAR>
A:Cross-references: UNIPROT:Q9UL88; UNIPARC:UPI0000176C2E; EMBL:Z18319
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 8.84e-38 Length: 122
Score: 463.50 Matches: 95
Percent Similarity: 83.61% Conservative: 7
Best Local Similarity: 77.87% Mismatches: 15
Query Match: 73.45% Indels: 5
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x S30533 (1-122)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGGTCAATTGAGACTC 60
D 1 GluValGlnValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGTGCTACGCGCATGCAATCGGCTGGCGGCT 120
D 21 SerCysAlaAlaSerArgPheThrPheThrAsnAlaTrpMetSerTrpValArgGlnAla 40
QY 121 CCAGAAAGGGTTTGGAAATGGTGGCCGCAATAAGAACTAAATAATAATAATATGCAACA 180
D 41 ProGlyLysGlyLeuGluTrpValGlyArgIleLysSerLysThrAspGlyGlyThrThr 60
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAAACACG 240
D 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAAAATGAAACAGCTTGAATACTGAGGACACAGCCGCTGATTACTGTACCACC 300
D 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

Best Local Similarity: 74.60% Mismatches: 13
Query Match: 74.88% Indels: 13
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x S44107 (1-126)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGGTCAATTGAGACTC 60
D 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuLeuVal 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGTGCTACGCGCATGCAATCGGCTGGCGGCT 120
D 21 SerCysAlaAlaSerGlyPheThrPheSerGlySerAlaMetHisTrpValArgGlnAla 40
QY 121 CCAGAAAGGGTTTGGAAATGGTGGCCGCAATAAGAACTAAATAATAATAATATGCAACA 180
D 41 SerGlyLysGlyLeuGluTrpValGlyArgIleArgSerLysAlaAsnSerTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAAACACG 240
D 61 AlaTyrAlaAlaSerValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAAAATGAAACAGCTTGAATACTGAGGACACAGCCGCTGATTACTGTACCACC 300
D 81 AlaTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrArg 100
QY 301 -----TTTACGGTAACGGTGTCTGG 321
D 101 HisValAsnAspPheTyrSerGlyTyrProThrLeuTyrTyrTyrGlyMetAspValTrp 120
QY 322 GCCCAGGGGACCTCGTGC 339
D 121 GlyGlnGlyProThrVal 126

RESULT 12
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: S05271; S04602
R:Kishimoto, T.
Submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <KIS1>
A:Cross-references: UNIPROT:Q96BB9; UNIPARC:UPI0000176B50; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
F:20-160/Product: Ig heavy chain (fragment) #status predicted <SIG>
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <KIS2>
A:Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.9e-38 Length: 160
Score: 467.00 Matches: 93
Percent Similarity: 79.53% Conservative: 8
Best Local Similarity: 73.23% Mismatches: 14
Query Match: 74.01% Indels: 12
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x S05271 (1-160)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGGTCAATTGAGACTC 60
```

QY 301 -----TTTTACGGTAACGGT-----GTCCTGGGGCCAGGGACCTGCTGTCACCGTC 345  
Db 101 GluPheSerAlaAspGlyAspTyrValArgTyrTrpGlyGlnGlyThrLeuValThrVal 120  
QY 346 AGCTCA 351  
Db 121 SerSer 122  
RESULT 14  
Ig variable region (VDJ) (clone T20-11) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #Sequence\_revision 16-Feb-1996 #text\_change 23-Jul-1999  
C:Accession: I37780; S25474  
R:Demaison, C.; Chaetagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by B  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37780  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <RES>  
A:Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:G33578; PIDN:CAA48130.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:28-111/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 8 7e-38 Length: 147  
Score: 463.50 Matches: 93  
Percent Similarity: 79.37% Conservative: 7  
Best Local Similarity: 73.81% Mismatches: 15  
Query Match: 73.45% Indels: 11  
Gaps: 2  
US-10-733-563-108 (1-351) x I37780 (1-147)  
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60  
Db 14 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 33  
QY 61 TCATGTGCAGCTCTGGATTCACTTTCAGTGGCTAGCCATGAACCTGGTCCGCCAGGCT 120  
Db 34 SerCysAlaAlaSerGlyPheThrPheSerSerTyrTrpMetSerTrpValArgGlnAla 53  
QY 121 CCAGGAAAGGGTTTGAATGGTGGCCGCATGAAGAACTAAATAATAATTATGCAACA 180  
Db 54 ProGlyLysGlyLeuGluTrpValAlaAlaSerLeu-----LysGlnAspGlySerGluLys 71  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAAACACG 240  
Db 72 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 91  
QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCAACC 300  
Db 92 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 111  
QY 301 -----TTTTACGGTAAACGGTGTCTGGGGCCAGGGGACC 333  
Db 112 AspGlyGluGlyTrpGlyLeuTyrTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThr 131  
QY 334 CTGGTCACCGTCAGCTCA 351  
Db 132 ThrValThrValSerSer 137  
RESULT 15  
S26794  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #Sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
C:Accession: S26794  
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992

A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami  
A:Reference number: S26786; MUID:92111632; PMID:1730251  
A:Accession: S26794  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <MOR>  
A:Cross-references: UNIPARC:UPI0000176C2B; EMBL:X61011  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 9 9e-38 Length: 123  
Score: 463.00 Matches: 91  
Percent Similarity: 81.60% Conservative: 11  
Best Local Similarity: 72.80% Mismatches: 13  
Query Match: 73.38% Indels: 10  
Gaps: 2  
US-10-733-563-108 (1-351) x S26794 (1-123)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCTCTGGATTCACTTTCAGTGGCTAGCCATGAACCTGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrSerMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGGTTTGAATGGTGGCCGCATGAAGAACTAAATAATAATTATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValSerTyrIleSerSerSerSer-----ThrIle 58  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAAACACG 240  
Db 59 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 78  
QY 241 CTCATCTGCAATGAACAGCTTGAAAACTCGAGGACACAGCCGTGTATTACTGTACCC--- 297  
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAspGluAspThrAlaValTyrTyrCysAlaArg 98  
QY 298 -----ACCTTTTACGGTAAACGGTGTCTGGGGCCAGGGGACCCCTG 336  
Db 99 SerIleLysTyrTyrAspGluAsnTyrTyrGlyMetAspValTrpGlyGlnGlyThrThr 118  
QY 337 CTCACCGTCAGCTCA 351  
Db 119 ValThrValSerSer 123

Search completed: January 28, 2006, 08:45:55  
Job time : 11.5743 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 ; Search time 53.8446 Seconds  
(without alignments)  
9198.340 Million cell updates/sec

Title: US-10-733-563-108

Perfect score: 631

Sequence: 1 gagggtcaattggttgagtc.....ccctgggtcacogtcagctca 351

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool.p/US10733563/runat.27012006.180005.4782/app.query.fasta\_1.2716  
-DB=UniProt -QFMT=fastn -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CGN 1.1.632 @runat.27012006.180005.4782 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80.\*

- 1: uniprot\_sprot.\*
- 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	477.5	75.7	471	2	Q66K04_MOUSE
2	463	73.4	464	2	Q6MZU6_HUMAN
3	460	72.9	115	1	HV33_MOUSE
4	453	71.8	113	2	Q9UL90_HUMAN
5	453	71.8	131	2	Q9UL88_HUMAN
6	452	71.6	240	2	Q65ZC9_HUMAN
7	450	71.3	113	1	HV27_MOUSE
8	450	71.3	113	1	HV30_MOUSE
9	450	71.3	115	1	HV33_MOUSE
10	447	70.8	597	2	Q96BB9_HUMAN
11	446.5	70.8	494	2	Q96K68_HUMAN
12	446.5	70.8	613	2	Q8WU1_HUMAN
13	446	70.7	121	2	Q9UL71_HUMAN
14	444	70.4	113	1	HV28_MOUSE
15	444	70.4	487	2	Q80Z17_MOUSE
16	443	70.2	116	2	Q9UL93_HUMAN

17	442.5	70.1	606	2	Q6GMY2_HUMAN
18	442	70.0	113	1	HV31_MOUSE
19	440.5	69.8	118	2	Q9UL91_HUMAN
20	440	69.7	113	1	HV29_MOUSE
21	439	69.6	468	2	Q569B4_RAT
22	437	69.3	458	2	Q65ZQ1_HUMAN
23	436.5	69.2	469	2	Q569F4_HUMAN
24	436	69.1	472	2	Q6N089_HUMAN
25	434	68.8	478	2	Q6PI81_HUMAN
26	432.5	68.5	122	1	HV3G_HUMAN
27	432.5	68.5	573	2	Q8WU38_HUMAN
28	431	68.3	470	2	Q6FUA4_HUMAN
29	429	68.0	142	1	HV01_RAT
30	429	68.0	464	2	Q6PIB8_MOUSE
31	429	68.0	493	2	Q6GMY2_HUMAN
32	426.5	67.6	465	2	Q6P6C4_HUMAN
33	426	67.5	120	1	HV3E_HUMAN
34	424.5	67.3	473	2	Q6MZV7_HUMAN
35	424	67.2	466	2	Q6IN78_HUMAN
36	423	67.0	113	1	HV34_MOUSE
37	422.5	67.0	119	2	Q5F2I8_MOUSE
38	422.5	67.0	475	2	Q6WZQ6_HUMAN
39	418	66.2	119	2	Q920E7_MOUSE
40	417.5	66.2	122	1	HV21_MOUSE
41	416.5	66.0	465	2	Q5I0J0_RAT
42	416.5	66.0	475	2	Q6GMW7_HUMAN
43	415.5	65.8	112	2	Q9HCC1_HUMAN
44	415.5	65.8	114	1	HV3B_HUMAN
45	415.5	65.8	467	2	Q4VBH1_RAT

ALIGNMENTS

RESULT 1

Q66K04_MOUSE	Q66K04_MOUSE PRELIMINARY;	PRT;	471 AA.
AC	Q66K04;		
DT	25-OCT-2004 (Tremblrel. 28, Created)		
DT	25-OCT-2004 (Tremblrel. 28, Last sequence update)		
DT	25-OCT-2004 (Tremblrel. 28, Last annotation update)		
DE	Hypothetical protein.		
GN	Name=Igh-1a;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridea; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CZECH II;		
RC	TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;		
EX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,		
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		

RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=CZECH 11;
RC	TISSUE=Wammary tumor metastasized to lung. Tumor arose spontaneously;
RAL	Director MGC Project;
RA	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC080671; AAH80671.1; -; mRNA.
DR	SMR; Q68K04; 20-467.
DR	MGI; MGI:96443; Igh-1a.
DR	GO; GO:0003823; F:antigen binding; IEA.
DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003597; IG-cl
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF07654; Cl-set; 3.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; Igcl; 3.
DR	SMART; SM00406; Igv; 1.
DR	PROSITE; PS08335; IG_LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; 1.
KW	Hypothetical protein.
SQ	SEQUENCE 471 AA; 52259 MW; 81BB7C322E315AC2 CRC64;

Alignment Scores:		
Pred. No.:	2,418-45	471
Score:	477.50	92
Percent Similarity:	85.25%	Conservative: 12
Best Local Similarity:	75.41%	Mismatches: 13
Query Match:	75.67%	Indels: 5
DB:	2	Gaps: 1

US-10-733-563-108 (1-351) x Q66K04 MOUSE (1-471)

QY	1	GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC	60
Db	20	GluaValGlnLeuValGluThrGlyGlyLeuValGlnProIysGlySerLeuLysLeu	39
QY	61	TCATGTGCAGCCCTCTGGATTCACTTTCACTGCCCTACGCCATGAACTCGGTCCGCCAGGCT	120
Db	40	SerCysAlaAlaSerGlyPheSerPheAsnThrAsnAlaMetAsnTrpValArgGlnAla	55
QY	121	CCAGGAAAGGGTTTGGAAATGGGTCGCGCATAAAGACTAAAAATAATAATTATGCAACA	180
Db	60	ProGlyLysGlyLeuGluTrpValAlaArgIleArgSerLysSerAsnAsnTrpAlaThr	79
QY	181	TATTATGCGGATTCAGTGAAGACAGATTCCATCCAGAGATGATTCAAAAACACG	240
Db	80	TyrTyrrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerGlnSerMet	99
QY	241	CNCTATCTGCAATCAACAGCTTGAAACTCAGACACACGCGTGATTACTCTACCAACC	300
Db	100	LeuTyrLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrrCysValLys	119
QY	301	TTT-----TAGCGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTC	345
Db	120	GlucGlyGlnLeuGlyProTyrTyrrPheAspTyrTrpGlyGlnGlyThrThrIleThrVal	139
QY	346	AGCTCA	351
Db	140	SerSer	141

RESULT 2	Q6MZU6 HUMAN	Q6MZU6 HUMAN	PRELIMINARY;	PRT;	464 AA.
ID	Q6MZU6;	Q6MZU6;			
AC	Q6MZU6;	Q6MZU6;			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)			
DE	Hypothetical protein DKFZp686C15213.				
GN	Name=DKFZp686C15213;				
OS	Homo sapiens (Human).				
OC	Eumaryota; Metazoa; Chordata; Craniata; Vertebrata;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora;				

```

OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Rectum tumor;
RC The German cDNA Consortium;
RG Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wienann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAB45931.1; --; mRNA.
DR HSSP; P01861; 1AQQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR DR PROSITE; PS50835; IG LIKE; 4.
DR DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Alignment Scores:
Pred. No.: 1,09e-43 Length: 464
Score: 463.00 Matches: 90
Percent Similarity: 85.00% Conservative: 12
Best Local Similarity: 75.00% Mismatches: 14
Query Match: 73.38% Indels: 4
DB: 2 Gaps: 2

```

US-10-733-563-108 (1-351) X O6MZU6 HUMAN (1-464)

QY	1	GAGGTGCAATTGGTTGAGTCTGTGAGGAGGATTGGTGAAGCCTCGGGGGTCAATTGAGACTC	60
Db	20	GLuValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu	39
QY	61	TCATGTGCAGCCTCTGGATTCACTTCAGTGGCCCTAGCCCATGAACCTGGTGGCCCGCCAGGCT	120
Db	40	SerCySAIaIaSerGlyPheThrPheSerSerTyrSerMetAsnTrpValArgGlnAla	59
QY	121	CCAGGAAAGGGTTTGGATGGGTTGGCGCATGAAGATAAAAAATAATATATGCAACA	180
Db	60	ProGlyLysGlyLeuGluTrpValSerSerPheSerSerArgGlyGlySerTyr---Glu	78
QY	181	TATTATGCGGATTCAGTGAAGACAGATTACCATCTCCAGAGATGATTCAAAAACACG	240
Db	79	TyTrpAlaAspSerValLysGlyArgPheThrIleSerArgAspAlaLysAsnSer	98
QY	241	CTCTATCTGCAAAATGAACAGCTTGAAACCTGAGGACACAGCCGTATTACTGTACCA	300
Db	99	LeuTyLeuGlnMetAsnSerLeuArgAlaGluAsnThrAlaValTyTrpCySAIaArg	118
QY	301	-----TTTTTCAGTAACGGTGTCTGGGGCCAGGGGACCTCTGGTACCGTCAGCTCA	351
Db	119	AspLeuGlyTrpPheGlyLeuAspTyTrpGlyGlnGlyThrLeuValThrValSerSer	138
RESULT 3			
HV32_MOUSE			
ID	HV32_MOUSE	STANDARD;	PRT; 115 AA.
AC	P01801;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	10-MAY-2005	(Rel. 47, Last annotation update)	
DE	Ig heavy chain V-III region J606.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;		
OC	Muroidea; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		

RP PROTEIN SEQUENCE.  
RX MEDLINE=82099361; PubMed=6798111;  
RA Johnson N., Slankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-  
binding proteins.";  
RL J. Immunol. 128:302-307(1982).  
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
CC binds inulin.  
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR PIR; C92811; AVMS06.  
DR HSP; P01852; INFD.  
DR Ensembl; ENSMUSG00000045097; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IG\_V.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT DOMAIN 1 114 Ig-like.  
FT DISULFID 22 98 By similarity.  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Alignment Scores:  
Pred. No.: Length: 115  
Score: 460.00  
Percent Similarity: 86.32%  
Best Local Similarity: 73.50%  
Query Match: 72.90%  
DB: 1  
Gaps: 1

US-10-733-563-108 (1-351) x HV32\_MOUSE (1-115)

QY 1 GAGGTGCAATGTTGAGTCTGAGGAGGATGGTGAAGCCCTGGGGGTTCATTGAGACTC 60  
DB 1 GluValLeuGluGluSerGlyGlyLeuValGlnProGlySerMetLysLeu 20  
QY 61 TCATGTGACGCTCTGGATTCACTTTTCAGTGTGCTAGCCATCACTGAGTGGTCCGCCAGGCT 120  
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40  
QY 121 CAGGAAGGGTTGGATGGTGGCCGCATCAAGAACTATAAATAATTAATTAATCAACA 180  
DB 41 ProGluLysGlyLeuGluTrpValAlaGluIleArgLeuLysSerAsnAsnTyrAlaThr 60  
QY 181 TATTATCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAACAACAG 240  
DB 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSer 80  
QY 241 CTCATCTCAATGAACAGCTTGAATGGTGGCCGCATCAAGAACTATAAATAATTAATTAATCAACA 300  
DB 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCCAGCTCACTCA 351  
DB 101 -----GlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 115

RESULT 4

Q9UL90\_HUMAN  
ID Q9UL90\_HUMAN PRELIMINARY; PRT; 113 AA.  
AC Q9UL90;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
(Fragment).

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1730252;  
RA Raaphorst F.M.; Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
RA Schuurman R.K.;  
RT "Restricted utilization of germ-line VH3 genes and short diverse third  
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte  
RT immunoglobulin heavy chain rearrangements.";  
RL Eur. J. Immunol. 22:247-251(1992).  
DR EMBL; AF035024; AAD56260.1; -; mRNA.  
DR PIR; S78486; S78486.  
DR HSP; P01772; 2F84.  
DR SMR; Q9UL90; 1-113.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IG\_V; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
FT NON\_TER 1 113  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Alignment Scores:  
Pred. No.: Length: 113  
Score: 453.00  
Percent Similarity: 83.76%  
Best Local Similarity: 77.78%  
Query Match: 71.79%  
DB: 2  
Gaps: 2

US-10-733-563-108 (1-351) x Q9UL90\_HUMAN (1-113)

QY 1 GAGGTGCAATGTTGAGTCTGAGGAGGATGGTGAAGCCCTGGGGGTTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyValValGlnProGlySerLeuArgLeu 20  
QY 61 TCATGTGACGCTCTGGATTCACTTTTCAGTGTGCTAGCCATCAAGAACTATAAATAATTAATTAATCAACA 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40  
QY 121 CAGGAAGGGTTGGATGGTGGCCGCATCAAGAACTATAAATAATTAATTAATTAATCAACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValAlaPheIleArgTyrAspGlySerAsn-----Lys 58  
QY 181 TATTATCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAACAACAG 240  
DB 59 TyrTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 78  
QY 241 CTCATCTCAATGAACAGCTTGAATGGTGGCCGCATCAAGAACTATAAATAATTAATTAATTAATCAACA 300  
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 98  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCCAGCTCACTCA 351  
DB 99 -----AspLeuAsnTyrTrpGlyGlnGlyThrLeuValThrValSerSer 113

RESULT 5

Q9UL90\_HUMAN  
ID Q9UL90\_HUMAN PRELIMINARY; PRT; 131 AA.  
AC Q9UL90;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345(1992).
DR EMBL; AF05026; AAD56262.1; -; mRNA.
DR PIR; S21205; S21205.
DR PIR; S30533; S30533.
DR HSSP; P01852; INFED.
DR SMR; Q9UL88; 1-131.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Alignment Scores:
Pred. No.: 1,266-42 Length: 131
Score: 453.00 Matches: 131
Percent Similarity: 94
Best Local Similarity: 74.07% Conservative: 6
Query Match: 69.63% Mismatches: 13
DB: 71.79% Indels: 22
Gaps: 2

US-10-733-563-108 (1-351) x Q9UL88_HUMAN (1-131)
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTCACTGCTACGCGCATGAACCTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerLysAlaTrpMetSerTrpValArgGlnAla 40
QY 121 CCAGAAAGGGTTTGGATTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyPheThrPheSerLysAlaTrpMetSerTrpValArgGlnAla 40
QY 181 TATTATGCGGATTCACTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 AspTrpAlaAlaProValLysGlyArgLeuThrLysSerLysLeuThrAspGlyThrThr 60
QY 241 CTCATCTGCAAAATGAACAGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
Db 81 LeuTrpAlaAlaProValLysGlyArgLeuThrLysSerLysLeuThrAspGlyThrThr 80
QY 301 TTTTACGGTACGGTGTC-----TGCGGCGAGGGACCTGGTCACCGTCAGCTCA 351
Db 101 -----GlyIleThrMetIleValValIleThrThrSerSerLysArgThr 116
QY 319 -----TGCGGCGAGGGACCTGGTCACCGTCAGCTCA 351
Db 117 -----GlyIleThrMetIleValValIleThrThrSerSerLysArgThr 116

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Db 117 SerPheGluTrpTrpGlyGlnGlyThrLeuValThrValSerSer 131
RESULT 6
Q65ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
CN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1G/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD03645F64B373 CRC64;

Alignment Scores:
Pred. No.: 1,796-42 Length: 240
Score: 452.00 Matches: 89
Percent Similarity: 84.87% Conservative: 12
Best Local Similarity: 74.79% Mismatches: 14
Query Match: 71.63% Indels: 4
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q65ZC9_HUMAN (1-240)
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTCACTGCTACGCGCATGAACCTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTrpGlyMetHisTrpValArgGlnAla 40
QY 121 CCAGAAAGGGTTTGGATTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaValLysSerTrpAspGlySerAsn-----Lys 58
QY 181 TATTATGCGGATTCACTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 59 TyrTrpAlaAspSerValLysGlyArgPheThrLysSerArgAspAsnSerLysAsnThr 78
QY 241 CTCATCTGCAAAATGAACAGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
Db 79 LeuTrpAlaAlaProValLysGlyArgLeuThrLysSerLysLeuThrAspGlyThrThr 98
QY 301 TTTTACGGTACGGTGTC-----TGCGGCGAGGGACCTGGTCACCGTCAGCTCA 351
Db 99 AspTrpGlyAspSerLeuAspProTrpGlyLysGlyThrLeuValThrValSerSer 117

RESULT 7
HV27_MOUSE
ID HV27_MOUSE STANDARD; PRT; 113 AA.
AC P01796;
DT 21-JUL-1986 (Rel. 01, Created)

```



DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V-II region A4.  
 OS Mus musculus (Mouse).  
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR PIR; A93818; AVMSAB.  
 DR HSSP; P01783; 1IGC.  
 DR SMR; P01796; 1-113.  
 DR Ensembl; ENSMUSG00000045097; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 >113 Ig-like.  
 FT DISULFID 22 98 By similarity.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;  
 Alignment Scores:  
 Pred. No.: 2,71e-42 Length: 113  
 Score: 450.00 Matches: 84  
 Percent Similarity: 86.09% Conservative: 15  
 Best Local Similarity: 73.04% Mismatches: 14  
 Query Match: 71.32% Indels: 2  
 DB: 1 Gaps: 1  
 US-10-733-563-108 (1-351) x HV27\_MOUSE (1-113)  
 QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCTGGGGGGTCATTGAGACTC 60  
 Db 1 GluValLysLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
 QY 61 TCATGTGACCTCTCGATTCACTTTTCAGTGCTACGCCATGACCTGGTCCGCCAGGCT 120  
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40  
 QY 121 CCAGGAAGGTTTGAAGTGGTTGGCCCATAGACTAAATAATTAATTATGCAACA 180  
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60  
 QY 181 TATTATGCGGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAACACG 240  
 Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80  
 QY 241 CTCATCTGCAATGCAATGAGTGGTGGCCGCATAGAACTTAAATAATTAATTATGCAACA 300  
 Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrCysThrThr 100  
 QY 301 TTTTACGGTAACGGTCTCTGGGCGCCAGGGACCTGGTCACCGTC 345  
 Db 101 -----GlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrVal 113

RESULT 8  
 HV30\_MOUSE STANDARD; PRT; 113 AA.  
 ID HV30\_MOUSE  
 AC P01799;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V-II region ABB-47N.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=77134726; PubMed=402936;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Heavy-chain variable-region sequence from an inulin-binding myeloma  
 protein.";  
 RL Biochemistry 16:1170-1175(1977).  
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
 binds inulin.  
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
 CC -----  
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 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR PIR; A90400; AVMSB7.  
 DR HSSP; P01810; 2FBJ.  
 DR SMR; P01799; 1-113.  
 DR Ensembl; ENSMUSG00000045097; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 >113 Ig-like.  
 FT DISULFID 22 98 By similarity.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;  
 Alignment Scores:  
 Pred. No.: 2,71e-42 Length: 113  
 Score: 450.00 Matches: 84  
 Percent Similarity: 86.96% Conservative: 16  
 Best Local Similarity: 73.04% Mismatches: 13  
 Query Match: 71.32% Indels: 2  
 DB: 1 Gaps: 1  
 US-10-733-563-108 (1-351) x HV30\_MOUSE (1-113)  
 QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCTGGGGGGTCATTGAGACTC 60  
 Db 1 GluValLysLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20  
 QY 61 TCATGTGACCTCTCGATTCACTTTTCAGTGCTACGCCATGACCTGGTCCGCCAGGCT 120  
 Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40  
 QY 121 CCAGGAAGGTTTGAAGTGGTGGCCGCATAGAACTTAAATAATTAATTATGCAACA 180  
 Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLeuLysSerHisAsnTyrAlaThr 60  
 QY 181 TATTATGCGGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAACACG 240  
 Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSerSer 80  
 QY 241 CTCATCTGCAATGCAATGAGTGGTGGCCGCATAGAACTTAAATAATTAATTATGCAACC 300

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Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrAlaIleTyrTyrCysSerThr 100
      ::::::::::::::::::::::::::::
Qy 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTC 345
      |||
Db 101 -----GlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrVal 113
      |||
RESULT 9
HV33 MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
DR PIR; D92811; AVMS82.
DR HSSP; P01852; 1NFD.
DR SMR; P01802; 1-115.
DR Ensembl; ENSMUSG0000045097; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114 Ig-like.
FT DISULFID 22 98 By similarity.
FT NON_TER 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Alignment Scores:
Pred. No.: 2,728-42 Length: 115
Score: 450.00 Matches: 84
Percent Similarity: 86.32% Conservative: 17
Best Local Similarity: 71.79% Mismatches: 14
Query Match: 71.32% Indels: 2
DB: 1 Gaps: 1

US-10-733-563-108 (1-351) x HV33_MOUSE (1-115)
Qy 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATGGTGAAGCCCTGGGGGTCATTGAGACTC 60
      ::::::::::::::::::::::::::::
Db 1 GluValTyrLeuGluSerGlyGlyLeuValGlnProGlyGlySerMetTyrLeu 20
      |||
Qy 61 TCATGTGCGACCTCTGGATTCATCTTACGTGCTACGCCATGAATCGGTCCGCCAGGCT 120
      |||
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 40
      |||
Qy 121 CCAGGAAAGGGTTTGGATGGTGGCCGCATACAACTAAATAATATATATCAACA 180
      |||
Db 41 ProGluTyrGlyLeuGluTrpValAlaGluIleArgLeuTyrSerHisAsnTyrAlaThr 60
      |||
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Qy 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAACACG 240
      ::::::::::::::::::::::::::::
Db 61 HisTyrAlaGluSerValTyrGlyArgPheThrIleSerArgAspSerTyrSer 80
      |||
Qy 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGGTGTATTACTGTACAC 300
      ::::::::::::::::::::::::::::
Db 81 ValTyrLeuArgMetAsnLeuArgProGluAspThrGlyIleTyrTyrCysThrThr 100
      |||
Qy 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCACGTC 351
      |||
Db 101 -----GlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 115
      |||
RESULT 10
Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
chains of a human monoclonal antibody with broad reactivity to
malignant tumor cells.";
RL Nucleic Acids Res. 17:4385-0(1989).
DR EMBL; BC015760; AAHL5760.1; -, mRNA.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; 1ADQ.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```

Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Immunoglobulin domain  
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Alignment Scores:  
 Pred. No.: 7,69e-42 Length: 597  
 Score: 447.00 Matches: 89  
 Percent Similarity: 78.74% Conservative: 11  
 Best Local Similarity: 70.84% Mismatches: 15  
 Query Match: 70.84% Indels: 12  
 DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q96B9\_HUMAN (1-597)

QY 1 GAGGTGCAATGTTGAGTCTGGAGGAGGATGGTGAACCTGGGGGTCAATGAGACTC 60  
 Db 20 GluValGlnLeuLeuGluSerGlyGlyLeuValGlnProGlySerLeuArgLeu 39

QY 61 TCATGTGACGCTCTGGATTCTACTTTCAGTGTGCTACGCCATGAACCTGGGTCCGCCAGGCT 120  
 Db 40 SerCysAlaAlaSerGlyPheSerPheSerThrAlaMetAsnTrpValArgGlnAla 59

QY 121 CCAGGAAGGGTTTGAATGGTGGCCGCTAAGAACTAAATAATTAATTTATGCAACA 180  
 Db 60 ProGlyLysGlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThr 77

QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACATCTCAGAGATGATTCAAAACACG 240  
 Db 78 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThr 97

QY 241 CTCTATCTCAATGAACAGCTTGAAGTGGTGGCCGCTAAGAACTAAATAATTAATTTATGCAACA 180  
 Db 60 ProGlyLysGlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThr 77

QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACATCTCAGAGATGATTCAAAACACG 240  
 Db 78 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThr 97

QY 241 CTCTATCTCAATGAACAGCTTGAAGTGGTGGCCGCTAAGAACTAAGAGCACAGCGTGTATTACTGTACC--- 297  
 Db 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 117

QY 298 -----ACCTTTCAGTGAACGCTGTCTGGCGCCAGGGG 330  
 Db 118 AspProArgGlyTyrSerAlaSerGlyAsnTyrThrArgGluAspTyrTrpGlyGlnGly 137

QY 331 ACCCTGGTCACGCTGAGCTCA 351  
 Db 138 ThrLeuValThrValSerSer 144

RESULT 11  
 Q96K68 HUMAN  
 ID Q96K68\_HUMAN PRELIMINARY; PRT; 494 AA.  
 AC Q96K68;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein FLJ14473.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RX PubMed=14702039; DOI=10.1038/ngl1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 RA Omura Y., Abe K., Kamiyama M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,  
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotuta T.,

Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
 RA Imose N., Mutsaers K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RL cDNAs";  
 RL Nat. Genet. 36:40-45 (2004).  
 RN [2]  
 RP PROTEIN SEQUENCE.  
 RX PubMed=1555592;  
 RA Makiya R., Stigbrand T.;  
 RT "Placental alkaline phosphatase has a binding site for the human  
 RT immunoglobulin-G Fc portion.";  
 RL Eur. J. Biochem. 205:341-345 (1992).  
 DR EMBL; AK027379; BAB55072.1; -, mRNA.  
 DR PIR; S21205; S21205.  
 DR HSSP; P01876; IOWO.  
 DR SMR; Q96K68; 264-472.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Immunoglobulin domain  
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AB5A5B4C0E CRC64;

Alignment Scores:  
 Pred. No.: 8.53e-42 Length: 494  
 Score: 446.50 Matches: 89  
 Percent Similarity: 79.84% Conservative: 10  
 Best Local Similarity: 71.77% Mismatches: 16  
 Query Match: 70.76% Indels: 9  
 DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q96K68\_HUMAN (1-494)

QY 1 GAGGTGCAATGTTGAGTCTGGAGGAGGATGGTGAACCTGGGGGTCAATGAGACTC 60  
 Db 20 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 39

QY 61 TCATGTGACGCTCTGGATTCTACTTTCAGTGTGCTACGCCATGAACCTGGGTCCGCCAGGCT 120  
 Db 40 SerCysAlaAlaSerGlyLeuSerPheSerThrTyrAlaMetAsnTrpValArgGlnAla 59

QY 121 CCAGGAAGGGTTTGAATGGTGGCCGCTAAGAACTAAATAATTAATTTATGCAACA 180  
 Db 60 ProGlyLysGlyLeuGluTrpValSerSerIleSerSerArgSerAsp-----TyrIle 77

QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACATCTCAGAGATGATTCAAAACACG 240  
 Db 78 TyrTyrArgAspSerValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 97

QY 241 CTCTATCTCAATGAACAGCTTGAAGTGGTGGCCGCTAAGAACTAAATAATTAATTTATGCT 294  
 Db 98 LeuTyrLeuGlnMetAsnSerLeuArgValAspThrAlaValTyrTyrCysAlaArg 117

QY 295 -----ACCACCTTTTACGTAACGGTGTCTGGGGCCAGGGACCTGGTGC 339

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Db 118 AppSerCysAenGlyAlaIleCysTyrGlyPheSerProTrpGlyGlnGlyThrLeuVal 137
QY 340 ACCGTCAGCTCA 351
Db 138 ThrValSerSer 141
RESULT 12
Q8WUK1_HUMAN
ID Q8WUK1_HUMAN PRELIMINARY; PRT; 613 AA.
AC Q8WUK1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skaleka U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2117273;
RA Schroeder H.W. Jr., Wang J.Y.;
RT "Preferential utilization of conserved immunoglobulin heavy chain
variable gene segments during human fetal life.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150 (1990).
[4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1393695; DOI=10.1016/0161-5890(92)90173-U;
RA Cuisinier A.M., Fumoux F., Fougereau M., Tonnelie C.;
RT "IGM kappa/lambda EBV human B cell clone: an early step of
differentiation of fetal B cells or a distinct B lineage?";
RL Mol. Immunol. 29:1363-1373 (1992).
[5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
complementarity-determining regions (CDR3) in human fetal B lymphocyte
immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251 (1992).
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RN [6]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1904154;
RA Neale G.A., Kitchingman G.R.;
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy
chain enhancer region contain a non-translatable exon and are
extremely heterogeneous at the 5' end.";
RL Nucleic Acids Res. 19:2427-2433 (1991).
[7]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2840480; DOI=10.1084/jem.168.1.229;
RA Bird J., Gallili N., Link M., Stites D., Sklar J.;
RT "Continuing rearrangement but absence of somatic hypermutation in
immunoglobulin genes of human B cell precursor leukemia.";
RL J. Exp. Med. 168:229-245 (1988).
[8]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RT "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal
B cell lines. Preferential utilization of the most JH-proximal D
segment (DQ52) and two unusual VH-related rearrangements.";
RL J. Exp. Med. 169:1391-1403 (1989).
[9]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germline-encoded VH3 immunoglobulin binding
to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336 (1993).
DR EMBL; BC020240; AAH20240.1; -; mRNA.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSSP; P01861; 1ADQ.
DR SMR; Q8WUK1; 20-242.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
Alignment Scores:
Pred. No.: 8 81e-42 Length: 613
Score: 446.50 Matches: 89
Percent Similarity: 81.15% Conservative: 10
Best Local Similarity: 72.95% Mismatches: 16
Query Match: 70.76% Indels: 7
DB: 2 Gaps: 2
US-10-733-563-108 (1-351) x Q8WUK1_HUMAN (1-613)
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QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATGGTGAAGCGCTGGGGGCTCATTTGAGACTC 60
Db 20 GlnValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 39
QY 61 TCATGTGCAGCCTCTGGATTTCATTTCAGTCCCTACGCCATCGAAGCTGGTCCGCCAGCT 120
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Db 40 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 59  
QY 121 CCAGGAAGGGTTTGGAAATGGGTTGGCCGCATAGAACTAAATAATAATATGCAACA 180  
Db 60 ProGlyLysGlyLeuGluTrpValAlaValIleSerTyrAspGlySerAsn-----Lys 77  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTACCAATCTCAGAGATGATTCAGAAACACG 240  
Db 78 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 97  
QY 241 CTCATCTCCTCAATGAACAGCTTGAAGAACTGAGGACACAGCGGTGATTACTGTACCACC 300  
Db 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 117  
QY 301 TTTTACGGTAAACGGTGTCT-----TGGGGCCAGGGGACCCCTGGTCCACCGTC 345  
Db 118 AspTrpSerGluGlyValGluThrPheAspIleTrpGlyGlnGlyThrMetValThrVal 137  
QY 346 AGCTCA 351  
Db 138 SerSer 139

## RESULT 13

Q9UL71\_HUMAN  
ID Q9UL71\_HUMAN PRELIMINARY; PRT; 121 AA.  
AC Q9UL71;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035043; AAD56279.1; -; mRNA.  
DR HSP; P01852; 1NPD.  
DR SMR; Q9UL71; 1-121.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFASD50736 CRC64;

Alignment Scores:  
Pred. No.: 7,85e-42 Length: 121  
Score: 446.00 Matches: 89  
Percent Similarity: 81.30% Conservative: 11  
Best Local Similarity: 72.36% Mismatches: 15  
Query Match: 70.68% Indels: 8  
DB: 2 Gaps: 3

US-10-733-563-108 (1-351) x Q9UL71\_HUMAN (1-121)

QY 1 GAGGTGCAATGTTGAGTCTGGAGGAGGATTGGAAGCCCTGGGGGTTCATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyValValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCACTTTCAGTGCCTAGGCCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 PheCysAlaAlaSerGlyPheThrPheAspGlyTyrAlaMetHisTrpValArgGlnAla 40

QY 121 CCAGGAAGGGTTTGGAAATGGGTTGGCCGCATAGAACTAAATAATAATATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValSerLeuIle-----SerGlyAspGlySerThr 58  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTACCAATCTCAGAGATGATTCAGAAACACG 240  
Db 59 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnSer 78  
QY 241 CTCATCTCCTCAATGAACAGCTTGAAGAACTGAGGACACAGCGGTGATTACTGT----- 294  
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrTyrCysAlaLys 98  
QY 295 -----ACCACCTTTTACGGTAAC---GGTGTCTGGGGCCAGGGGACCCCTGGTCCACC 342  
Db 99 GlyLysValThrThrIleTyrAspArgPheAspIleTrpGlyGlnGlyThrMetValThr 118  
QY 343 GTCAGCTCA 351  
Db 119 ValSerSer 121

## RESULT 14

HV28\_MOUSE  
ID HV28\_MOUSE STANDARD; PRT; 113 AA.  
AC P01797;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V-III region U61.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=78158406; PubMed=417344;  
RA Vrana M., Rudikoff S., Potter M.;  
RT "Sequence variation among heavy chains from inulin-binding myeloma  
proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).  
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
binds inulin.  
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC PIR; B93818; AVMS61.  
DR HSP; P01783; 1IGC.  
DR SMR; P01797; 1-113.  
DR Ensembl; ENSMUSG00000045097; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT DOMAIN 1 >113 Ig-like.  
FT DISULFID 22 98 By similarity.  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Alignment Scores:  
Pred. No.: 1.32e-41 Length: 113  
Score: 444.00 Matches: 83  
Percent Similarity: 85.22% Conservative: 15  
Best Local Similarity: 72.17% Mismatches: 15  
Query Match: 70.36% Indels: 2  
DB: 1 Gaps: 1

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US-10-733-563-108 (1-351) x HV28_MOUSE (1-113)
QY 1 GAGGTGCAATTGGTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGGTTCATTGAGACTC 60
Db 1 GluValLysLeuGluGluSerGlyGlyGlyLeuValGlnProGlyGlySerMetLysLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTCAGTGCCTACGCATGAATCGGTCGCCAGGCT 120
Db 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 40
QY 121 CCAGGAAAGGTTTGGATTTGGATTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGGTTCATTGAGACTC 180
Db 41 ProGluLysGlyLeuGluTyrValAlaGluLeuArgLysSerHisAsnTyrAlaThr 60
QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCACATCTCCAGAGATGATTCAAAAACACG 240
Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSer 80
QY 241 CTCTATCTGCAAAATGAACAGCTTGAATTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGGTTCATTGAGACTC 300
Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
QY 301 TTTTACGTAACGGTGTCTGGGGCCAGGACCGTGGTCCACGCTC 345
Db 101 -----GlyPheAlaTyrTrpGlyGlnGlyThrLeuValProVal 113

RESULT 15
Q80217_MOUSE
ID Q80217_MOUSE PRELIMINARY; PRT; 487 AA.
AC Q80217;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049143; AAH49143.1; -; mRNA.
DR HSSP; P01789; 1MCP.
DR SMR; Q80217; 20-242.
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DR MGI; 96486; Igh-VJ558.  
DR GO; 0003823; F:antigen binding; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

Alignment Scores:  
Pred. No.: 1,64e-41 Length: 487  
Score: 444.00 Matches: 85  
Percent Similarity: 82.93% Conservative: 17  
Best Local Similarity: 69.11% Mismatches: 15  
Query Match: 70.36% Indels: 6  
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q80217\_MOUSE (1-487)

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QY 61 TCATGTGCAGCCTCTGGATTCACTTTCAGTGCCTACGCATGAATCGGTCGCCAGGCT 120  
Db 40 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTyrValArgGlnSer 59  
QY 121 CCAGGAAAGGTTTGGATTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGGTTCATTGAGACTC 180  
Db 60 ProGluLysGlyLeuGluTyrValAlaGluLeuArgLysSerHisAsnTyrAlaThr 79  
QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCACATCTCCAGAGATGATTCAAAAACACG 240  
Db 80 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSer 99  
QY 241 CTCTATCTGCAAAATGAACAGCTTGAATTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGGTTCATTGAGACTC 297  
Db 100 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrArg 119  
QY 298 ACCTTTTACGGTAAC-----GGTGTCTGGGGCCAGGACCGTGGTTCACC 342  
Db 120 ArgGlyTyrGlyAspProAsnTyrPheAspValTyrGlyAlaGlyThrThrValThr 139  
QY 343 GTCAGCTCA 351  
Db 140 ValSerSer 142

Search completed: January 28, 2006, 08:43:56  
Job time : 56.8446 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:22:17 ; Search time 13.8784 Seconds  
(without alignments)  
4181.924 Million cell updates/sec

Title: US-10-733-563-108

Perfect score: 631

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	2	US-09-809-739-20
2	620	98.3	117	2	US-09-840-459-17
3	620	98.3	117	2	US-09-497-625A-17
4	620	98.3	119	2	US-09-840-459-104
5	620	98.3	119	2	US-09-497-625A-104
6	613	97.1	117	2	US-09-809-739-21
7	613	97.1	117	2	US-09-840-459-18
8	613	97.1	117	2	US-09-497-625A-18
9	604	95.7	117	2	US-09-809-739-22
10	604	95.7	117	2	US-09-840-459-19
11	604	95.7	117	2	US-09-497-625A-19
12	599	94.9	117	2	US-09-809-739-23

ALIGNMENTS

RESULT 1

US-09-809-739-20  
; Sequence 20, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-20

Alignment Scores:  
Pred. No.: 1,14e-68 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-809-739-20 (1-117)

QY 1 GAGGTGCAATTGTTGAGTCTCGAGGAGGATTGGTGAACGCTGGGGGGTCATTGAGACTC 60  
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Sequence 20, Appl  
Sequence 20, Appl  
Sequence 12, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 100, App  
Sequence 100, App  
Sequence 10, Appl  
Sequence 87, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 71, Appl  
Sequence 71, Appl  
Sequence 74, Appl  
Sequence 74, Appl  
Sequence 36, Appl  
Sequence 83, Appl  
Sequence 83, Appl  
Sequence 73, Appl  
Sequence 73, Appl  
Sequence 70, Appl  
Sequence 93, Appl  
Sequence 93, Appl  
Sequence 7, Appl  
Sequence 94, Appl  
Sequence 94, Appl  
Sequence 11, Appl  
Sequence 16, Appl  
Sequence 93, Appl

Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTGCTACGCCATGAACCTGGGCTCGCCAGGCT 120  
Db 21 SerCysAlaLaSerGlyPheThrPheSerAlaTyrAlaMetAsnTyrValArgGlnAla 40  
QY 121 CCAGAAAGGGTTTGGATTGGTGGCGCATAGAACCTAAATAATAATTATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTyrValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAAAATGAACAGCTTGAAGACTGAGACACAGCCGCTGATTCTGTATGACCA 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 2

US-09-840-459-17

; Sequence 17, Application US/09840459

; Patent No. 6696550

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; FILE REFERENCE: 1855.1052-012

; CURRENT APPLICATION NUMBER: US/09/840,459

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: PCT/US01/03537

; PRIOR FILING DATE: 2001-02-02

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Humanized sequence

US-09-840-459-17

Alignment Scores:

Pred. No.: 1.14e-68 Length: 117

Score: 620.00 Matches: 117

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.26% Indels: 0

DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-17 (1-117)

QY 1 GAGGTGCAATTTGGATTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTGCTACGCCATGAACCTGGGCTCGCCAGGCT 120  
Db 21 SerCysAlaLaSerGlyPheThrPheSerAlaTyrAlaMetAsnTyrValArgGlnAla 40



QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGGTGTATTACTGTACCACC 300  
|||||  
Db 81 LeuTyrLeuGlnMetAsnSerLeuTyrThrGluAspThrAlaValTyrTyrCysThrThr 100  
|||||  
QY 301 TTTTACGGTAACCGTCTCTGGGGCCAGGGACCGCTGTCACCGTCAGCTCA 351  
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Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117  
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## RESULT 4

US-09-840-459-104  
; Sequence 104, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-09-840-459-104

Alignment Scores:  
Pred. No.: 1.15e-68 Length: 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-104 (1-119)

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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuValArgLeu 20  
|||||  
QY 61 TCATGTGACGCTCTCGATTCTACTTTTCAGTGTCTAGCGCATCACTGAGTCCGCCAGGCT 120  
|||||  
Db 21 SerCysAlaAspSerValLysAspArgPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
|||||  
QY 121 CCAGAAAGGGTTTGAATGGTGTGGCCGCATAGAACTTAAATAATTAATTATGCAACA 180  
|||||  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgGlyLeuThrLysAsnAsnAsnTyrAlaThr 60  
|||||  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCAGAGATGATTCAAAAACACG 240  
|||||  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrLysSerArgAspSerLysAsnThr 80  
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QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGGTGTATTACTGTACCACC 300  
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Db 81 LeuTyrLeuGlnMetAsnSerLeuTyrThrGluAspThrAlaValTyrTyrCysThrThr 100  
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QY 301 TTTTACGGTAACCGTCTCTGGGGCCAGGGACCGCTGTCACCGTCAGCTCA 351  
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Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117  
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## RESULT 5

US-09-497-625A-104  
; Sequence 104, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-09-497-625A-104

Alignment Scores:  
Pred. No.: 1.15e-68 Length: 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-104 (1-119)

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QY 61 TCATGTGACGCTCTCGATTCTACTTTTCAGTGTCTAGCGCATCACTGAGTCCGCCAGGCT 120  
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Db 21 SerCysAlaAspSerValLysAspArgPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
|||||  
QY 121 CCAGAAAGGGTTTGAATGGTGTGGCCGCATAGAACTTAAATAATTAATTATGCAACA 180  
|||||  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgGlyLeuThrLysAsnAsnAsnTyrAlaThr 60  
|||||  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCAGAGATGATTCAAAAACACG 240  
|||||  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrLysSerArgAspSerLysAsnThr 80  
|||||  
QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGGTGTATTACTGTACCACC 300  
|||||  
Db 81 LeuTyrLeuGlnMetAsnSerLeuTyrThrGluAspThrAlaValTyrTyrCysThrThr 100  
|||||  
QY 301 TTTTACGGTAACCGTCTCTGGGGCCAGGGACCGCTGTCACCGTCAGCTCA 351  
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Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117  
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## RESULT 6

US-09-809-739-21  
; Sequence 21, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.

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; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-21
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Alignment Scores:
Pred. No.:      8,51e-68      Length:      117
Score:          613.00      Matches:      115
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.29%      Mismatches: 0
Query Match:     97.15%      Indels:      0
DB:              2          Gaps:      0

US-10-733-563-108 (1-351) x US-09-809-739-21 (1-117)

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DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTCTACGCCATGAACCTGGGTCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheSerPheAlaTyrAlaMetAsnTyrValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGAAATGGTTGGCGCGCATAGAATCAAAATAATAATTATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTyrValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCCGATTCAAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAACACG 240
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCGGTGATTACTGTACCAACC 300
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY 301 TTTTACGTAAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
DB 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117
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RESULT 7
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
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; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-18

Alignment Scores:
Pred. No.:      8,51e-68      Length:      117
Score:          613.00      Matches:      115
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.29%      Mismatches: 0
Query Match:     97.15%      Indels:      0
DB:              2          Gaps:      0

US-10-733-563-108 (1-351) x US-09-840-459-18 (1-117)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTCTACGCCATGAACCTGGGTCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheSerPheAlaTyrAlaMetAsnTyrValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGAAATGGTTGGCGCGCATAGAATCAAAATAATAATTATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTyrValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCCGATTCAAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAACACG 240
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCGGTGATTACTGTACCAACC 300
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY 301 TTTTACGTAAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
DB 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117
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RESULT 8
US-09-497-625A-18
; Sequence 18, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
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;
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-18

Alignment Scores:
Pred. No.: 8,51e-68 Length: 117
Score: 613.00 Matches: 115
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.29% Mismatches: 0
Query Match: 97.15% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-18 (1-117)
QY 1 GAGGTGCAATGTTGAGTCTCGAGGAGGATTCGTTGAAGCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCTCTCGATTCACTTTTCAGTGCCTACGCATCAAGTAACTAAATAATTAATTATGCAACA 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGAATGGGTTGCCCGCATAGAACTAAATAATTAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAAACAACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCATCTGCAATGAACAGCTTGAAACTTGAGGACACACAGCCGTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCTCGTCCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 10
US-09-840-459-19
; Sequence 19, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-19

Alignment Scores:
Pred. No.: 1.13e-66 Length: 117
Score: 604.00 Matches: 113
Percent Similarity: 99.15% Conservative: 3
Best Local Similarity: 96.58% Mismatches: 1
Query Match: 95.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-19 (1-117)
QY 1 GAGGTGCAATGTTGAGTCTCGAGGAGGATTCGTTGAAGCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCTCTCGATTCACTTTTCAGTGCCTACGCATCAAGTAACTAAATAATTAATTATGCAACA 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGAATGGGTTGCCCGCATAGAACTAAATAATTAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAAACAACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCATCTGCAATGAACAGCTTGAAACTTGAGGACACACAGCCGTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCTCGTCCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 9
US-09-809-739-22
; Sequence 22, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-22

Alignment Scores:
Pred. No.: 1.13e-66 Length: 117
Score: 604.00 Matches: 113
Percent Similarity: 99.15% Conservative: 3
Best Local Similarity: 96.58% Mismatches: 1
Query Match: 95.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-809-739-22 (1-117)
QY 1 GAGGTGCAATGTTGAGTCTCGAGGAGGATTCGTTGAAGCTGGGGGGTCAATTGAGACTC 60
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Db 21 SerCysAlaLaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGAAATGGGTTGGCCGATAGAACTAAATAATTAATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAACAGAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGTTATTACGTACACAC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 11
US-09-497-625A-19
; Sequence 19, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-19

Alignment Scores:
Pred. No.: 1,136-66 Length: 117
Score: 604.00 Matches: 113
Percent Similarity: 99.15% Conservative: 3
Best Local Similarity: 96.58% Mismatches: 1
Query Match: 95.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-19 (1-117)
QY 1 GAGGTGCAATTTGGTTCAGTCTGGAGAGGATTTGGTGAAGCCTGGGGGCTCATTTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyLysLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTCGCCCTACGCCATGAACCTGGGTCGCCAGGCT 120
Db 21 SerCysAlaLaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGAAATGGGTTGGCCGATAGAACTAAATAATTAATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAACAGAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGTTATTACGTACACAC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 13
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
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QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGTTATTACGTACACAC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 12
US-09-739-739-23
; Sequence 23, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia E.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-23

Alignment Scores:
Pred. No.: 4,736-66 Length: 117
Score: 599.00 Matches: 112
Percent Similarity: 98.29% Conservative: 3
Best Local Similarity: 95.73% Mismatches: 2
Query Match: 94.93% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-809-739-23 (1-117)
QY 1 GAGGTGCAATTTGGTTCAGTCTGGAGAGGATTTGGTGAAGCCTGGGGGCTCATTTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyLysLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTCGCCCTACGCCATGAACCTGGGTCGCCAGGCT 120
Db 21 SerCysAlaLaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGAAATGGGTTGGCCGATAGAACTAAATAATTAATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAACAGAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGTTATTACGTACACAC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 13
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
```

APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT FILING DATE: 2001-02-02  
CURRENT APPLICATION NUMBER: US/09/840,459  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR FILING DATE: 2000-02-03  
PRIOR FILING DATE: 1999-07-22  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 20  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Humanized sequence  
US-09-840-459-20

Alignment Scores:  
Pred. No.: 4,73e-66 Length: 117  
Score: 599.00 Matches: 112  
Percent Similarity: 98.29% Conservative: 3  
Best Local Similarity: 95.73% Mismatches: 2  
Query Match: 94.93% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-20 (1-117)

QY 1 GAGGTGCAATGGTGTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGTGATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCTCTGGATTCACTTTCAGTGCCTACGCCCATGAACCTGAGTGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGTTGGATGGTGGCCCATAGAACTAAATAATTAATTAATGCAACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAGTACACAGC 240  
DB 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGCAACAGCTTGAAGACTGAGGACACAGCCGCTGATTAATGCAACA 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysValThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCGAGGACCTGGTCCAGCTGACCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 14  
US-09-497-625A-20  
Sequence 20, Application US/09497625A  
Patent No. 6727349  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-004  
CURRENT APPLICATION NUMBER: US/09/497,625A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 20  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Humanized sequence  
US-09-497-625A-20

Alignment Scores:  
Pred. No.: 4,73e-66 Length: 117  
Score: 599.00 Matches: 112  
Percent Similarity: 98.29% Conservative: 3  
Best Local Similarity: 95.73% Mismatches: 2  
Query Match: 94.93% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-20 (1-117)

QY 1 GAGGTGCAATGGTGTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGTGATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCTCTGGATTCACTTTCAGTGCCTACGCCCATGAACCTGAGTGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGTTGGATGGTGGCCCATAGAACTAAATAATTAATTAATGCAACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAGTACACAGC 240  
DB 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGCAACAGCTTGAAGACTGAGGACACAGCCGCTGATTAATGCAACA 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysValThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCGAGGACCTGGTCCAGCTGACCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 15  
US-09-739-12  
Sequence 12, Application US/09809739  
Patent No. 6663863  
GENERAL INFORMATION:  
APPLICANT: Horvath, Christopher J.  
APPLICANT: Rao, Patricia E.  
TITLE OF INVENTION: Method of Inhibiting Stenosis and  
TITLE OF INVENTION: Restenosis  
FILE REFERENCE: 1855.1069-003  
CURRENT APPLICATION NUMBER: US/09/809,739  
CURRENT FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: US 09/528,267  
PRIOR FILING DATE: 2000-03-17  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Unknown

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
; NAME/KEY: SITE
; LOCATION: (31)...(35)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (50)...(68)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (101)...(106)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-12
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## Alignment Scores:

Pred. No.:	1,078-59	Length:	117
Score:	548.00	Matches:	101
Percent Similarity:	94.87%	Conservative:	10
Best Local Similarity:	86.32%	Mismatches:	6
Query Match:	86.85%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-108 (1-351) x US-09-809-739-12 (1-117)

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QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProLysGlySerLeuLysLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTCAGTCGCTACGCCATGAACCTGGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGTTTGGATGGTTCGCCGCATAGAACTAAATAATAATATATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAAGACACAGATTTCACCATCTCCAGAGATGATTCAAAAACACG 240
DB 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerGluSerMet 80
QY 241 CTCTATCTGCAATGAACAGCTTGAACAACTGAGGACACAGCGGTGTATTACTGTACCACC 300
DB 81 LeuPheLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
DB 101 PheTyrGlyAsnGlyValTrpGlyThrGlyThrThrValThrValSerSer 117
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Search completed: January 28, 2006, 08:48:44  
Job time : 14.8784 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: January 28, 2006, 08:44:22 ; Search time 42.8649 Seconds  
(without alignments)  
6842.811 Million cell updates/sec

Title: US-10-733-563-108  
Perfect score: 631  
Sequence: 1 gaggtgcaattggttgagtc.....ccttggtaccgcagctca 351

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPTO\_spool\_p/US10733563/runat\_27012006\_180007\_4900/app\_query.fasta\_1.2716  
-DB=Published Applications AA Main -OFMT=fasta -SUFFIX=n2p.rapbm  
-MINMATCH=0.1 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct  
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext  
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1.497 @runat\_27012006\_180007\_4900 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA Main:  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pcp.\*  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pcp.\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pcp.\*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	3	US-09-835-087-10 Sequence 10, Appl
2	620	98.3	117	3	US-09-809-739-20 Sequence 20, Appl
3	620	98.3	117	3	US-09-840-459-17 Sequence 17, Appl
4	620	98.3	117	4	US-10-766-773-17 Sequence 17, Appl
5	620	98.3	117	4	US-10-766-610-17 Sequence 17, Appl
6	620	98.3	117	4	US-10-733-563-17 Sequence 17, Appl
7	620	98.3	117	5	US-10-662-061-20 Sequence 20, Appl
8	620	98.3	119	3	US-09-840-459-104 Sequence 104, Appl
9	620	98.3	119	4	US-10-766-773-104 Sequence 104, Appl
10	620	98.3	119	4	US-10-766-610-104 Sequence 104, Appl
11	620	98.3	119	4	US-10-733-563-104 Sequence 104, Appl

12	613	97.1	117	3	US-09-835-087-11	Sequence 11, Appl
13	613	97.1	117	3	US-09-809-739-21	Sequence 21, Appl
14	613	97.1	117	3	US-09-840-459-18	Sequence 18, Appl
15	613	97.1	117	4	US-10-766-773-18	Sequence 18, Appl
16	613	97.1	117	4	US-10-766-610-18	Sequence 18, Appl
17	613	97.1	117	4	US-10-733-563-18	Sequence 18, Appl
18	613	97.1	117	5	US-10-662-061-21	Sequence 21, Appl
19	604	95.7	117	3	US-09-835-087-12	Sequence 12, Appl
20	604	95.7	117	3	US-09-809-739-22	Sequence 22, Appl
21	604	95.7	117	3	US-09-840-459-19	Sequence 19, Appl
22	604	95.7	117	4	US-10-766-773-19	Sequence 19, Appl
23	604	95.7	117	4	US-10-766-610-19	Sequence 19, Appl
24	604	95.7	117	4	US-10-733-563-19	Sequence 19, Appl
25	604	95.7	117	5	US-10-662-061-22	Sequence 22, Appl
26	599	94.9	117	3	US-09-835-087-13	Sequence 13, Appl
27	599	94.9	117	3	US-09-809-739-23	Sequence 23, Appl
28	599	94.9	117	3	US-09-840-459-20	Sequence 20, Appl
29	599	94.9	117	4	US-10-766-773-20	Sequence 20, Appl
30	599	94.9	117	4	US-10-766-610-20	Sequence 20, Appl
31	599	94.9	117	4	US-10-733-563-20	Sequence 20, Appl
32	599	94.9	117	5	US-10-662-061-23	Sequence 23, Appl
33	548	86.8	117	3	US-09-835-087-8	Sequence 8, Appl
34	548	86.8	117	3	US-09-809-739-12	Sequence 12, Appl
35	548	86.8	117	3	US-09-840-459-10	Sequence 10, Appl
36	548	86.8	117	4	US-10-766-773-10	Sequence 10, Appl
37	548	86.8	117	4	US-10-766-610-10	Sequence 10, Appl
38	548	86.8	117	4	US-10-733-563-10	Sequence 10, Appl
39	548	86.8	117	5	US-10-662-061-12	Sequence 12, Appl
40	548	86.8	125	4	US-10-272-899A-84	Sequence 84, Appl
41	548	86.8	148	3	US-09-840-459-100	Sequence 100, App
42	548	86.8	148	4	US-10-766-773-100	Sequence 100, App
43	548	86.8	148	4	US-10-766-610-100	Sequence 100, App
44	548	86.8	148	4	US-10-733-563-100	Sequence 100, App
45	499.5	79.2	120	5	US-10-920-899-1779	Sequence 1779, Ap

ALIGNMENTS

RESULT 1  
US-09-835-087-10  
; Sequence 10, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; TITLE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-10

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Pred. No.: 2,32e-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-108 (1-351) x US-09-835-087-10 (1-117)

QY 1 GAGGTGCAATTGGTGTGAGTCTCGAGGAGGATTGGTGAACCTGGGGGTCATTGAGACTTC 60  
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Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCTTTAGTGTGCTAGCCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGTTTGGATGGTTCGCCGCATAGAACATAAAATAATATATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTTCAGTGAACACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATCAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCACC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351  
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RESULT 2  
US-09-809-739-20  
; Sequence 20, Application US/09809739  
; Patent No. US20020106369A1  
; GENERAL INFORMATION:  
; APPLICANT: Rao, Patricia E.  
; APPLICANT: Horvath, Christopher J.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; TITLE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-20  
Alignment Scores:  
Pred. No.: 2,32e-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 3 Gaps: 0  
US-10-733-563-108 (1-351) x US-09-809-739-20 (1-117)  
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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCTTTAGTGTGCTAGCCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGTTTGGATGGTTCGCCGCATAGAACATAAAATAATATATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTTCAGTGAACACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 181 TATTATGCGGATTTCAGTGAACACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATCAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCACC 300

Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117  
RESULT 3  
US-09-840-459-17  
; Sequence 17, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-17  
Alignment Scores:  
Pred. No.: 2,32e-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 3 Gaps: 0  
US-10-733-563-108 (1-351) x US-09-840-459-17 (1-117)  
QY 1 GAGGTGCAATTTGGTGTAGTCTGGAGGAGGATGGTGAAGCCCTGGGGGTCTATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCTTTAGTGTGCTAGCCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGTTTGGATGGTTCGCCGCATAGAACATAAAATAATATATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTTCAGTGAACACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATCAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCACC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351



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Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 4
US-10-766-773-17
; Sequence 17, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-17
Alignment Scores:
Pred. No.: 2,32e-58 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGACGCTCTGGATTCACTTTTCAGTGCCTAGCCCATCACTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTTGGAAATGGTTCGCGCATAGAACTATAAATAATATATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCATCTCGCAATGAACAGCTTGAAGACTGAGGACACAGCCGCTGATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 5
US-10-766-610-17
; Sequence 17, Application US/10766610
; Publication No. US20040132960A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-610-17
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Pred. No.: 2,32e-58 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGACGCTCTGGATTCACTTTTCAGTGCCTAGCCCATCACTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTTGGAAATGGTTCGCGCATAGAACTATAAATAATATATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCATCTCGCAATGAACAGCTTGAAGACTGAGGACACAGCCGCTGATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 6
US-10-733-563-17
; Sequence 17, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
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; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIORITY FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-17

Alignment Scores:
Pred. No.: 2,32e-58 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

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QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATGAACTGAGTGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaIyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGAAAGGGTTTGGATTGGTGGCGGCATAGAAGCTAAAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTGAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACAGC 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTTACTGTACCAACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
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RESULT 7
US-10-662-061-20
; Sequence 20, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20

; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIORITY FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-17

Alignment Scores:
Pred. No.: 2,32e-58 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

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QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATGAACTGAGTGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaIyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGAAAGGGTTTGGATTGGTGGCGGCATAGAAGCTAAAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTGAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACAGC 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTTACTGTACCAACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
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RESULT 8
US-09-840-459-104
; Sequence 104, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
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US-09-840-459-104

## Alignment Scores:

Pred. No.: 2,33e-58 Length: 119  
 Score: 620.00 Matches: 117  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.26% Indels: 0  
 DB: 3 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-104 (1-119)

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 DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
 QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGGCTACGCCATCAACTGGGTCCGCCAGGCT 120  
 DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
 QY 121 CCAGGAAAGGGTTTGGAAATGGTGGCCGCATTAAGAACTAAATAATAATTATGCAACA 180  
 DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
 QY 181 TATTATGCCGATTCAGTGAAGACAGATTACCATCTCCAGAGATGATTCAAAAACACG 240  
 DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
 QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGTGTATTACTGTACCA 300  
 DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
 QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
 DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 9

US-10-766-773-104

; Sequence 104, Application US/10766773

; Publication No. US20040126851A1

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; FILE REFERENCE: 1855.1052-028

; CURRENT FILING DATE: 2004-01-27

; PRIOR APPLICATION NUMBER: US/10/766,773

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/497,625

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 104

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Humanized heavy chain

US-10-766-773-104

## Alignment Scores:

Pred. No.: 2,33e-58 Length: 119  
 Score: 620.00 Matches: 117  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

Query Match:

DB: 98.26%

US-10-733-563-108 (1-351) x US-10-766-773-104 (1-119)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAACCTGGGGGTCAATTGAGACTC 60  
 DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
 QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGGCTACGCCATCAACTGGGTCCGCCAGGCT 120  
 DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
 QY 121 CCAGGAAAGGGTTTGGAAATGGTGGCCGCATTAAGAACTAAATAATAATTATGCAACA 180  
 DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
 QY 181 TATTATGCCGATTCAGTGAAGACAGATTACCATCTCCAGAGATGATTCAAAAACACG 240  
 DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
 QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGTGTATTACTGTACCA 300  
 DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
 QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
 DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 10

US-10-766-610-104

; Sequence 104, Application US/10766610

; Publication No. US20040132980A1

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; FILE REFERENCE: 1855.1052-029

; CURRENT APPLICATION NUMBER: US/10/766,610

; CURRENT FILING DATE: 2004-01-27

; PRIOR APPLICATION NUMBER: 09/840,459

; PRIOR FILING DATE: 2001-04-23

; PRIOR APPLICATION NUMBER: PCT/US01/03537

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 104

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Humanized heavy chain

US-10-766-610-104

## Alignment Scores:

Pred. No.: 2,33e-58 Length: 119  
 Score: 620.00 Matches: 117  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.26% Indels: 0  
 DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x US-10-766-610-104 (1-119)

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QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATGAATCGGTCGCCGAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerAlaTyraAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGATTGGTGGCCGCGCATAGCACTTAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTAGTGAACACAGATTCCACATCTCCAGAGATGATTTCAAAAACACG 240
Db 61 TyrTyraIaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80
QY 241 CTCATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAAACGGTCTCGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
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## RESULT 11

```
US-10-733-563-104
; Sequence 104, Application US/10733563
; Publication No. US2004015121A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized heavy chain
```

## US-10-733-563-104

```
Alignment Scores:
Pred. No.: 2,33e-58 Length: 119
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0
```

US-10-733-563-108 (1-351) x US-10-733-563-104 (1-119)

```
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATGAATCGGTCGCCGAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerAlaTyraAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGATTGGTGGCCGCGCATAGCACTTAAATAATAATTATGCAACA 180
```

```
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTAGTGAACACAGATTCCACATCTCCAGAGATGATTTCAAAAACACG 240
Db 61 TyrTyraIaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80
QY 241 CTCATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAAACGGTCTCGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
```

## RESULT 12

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US-09-835-087-11
; Sequence 11, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
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## Alignment Scores:

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Pred. No.: 1.34e-57 Length: 117
Score: 613.00 Matches: 115
Percent Similarity: 100.00% Conservativeness: 2
Best Local Similarity: 98.29% Mismatches: 0
Query Match: 97.15% Indels: 0
DB: 3 Gaps: 0
```

US-10-733-563-108 (1-351) x US-09-835-087-11 (1-117)

```
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATGAATCGGTCGCCGAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerAlaTyraAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGATTGGTGGCCGCGCATAGCACTTAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTAGTGAACACAGATTCCACATCTCCAGAGATGATTTCAAAAACACG 240
Db 61 TyrTyraIaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80
QY 241 CTCATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAAACGGTCTCGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
```

## RESULT 13

RESULT 14  
US-09-840-459-18  
; Sequence 18, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: Larrosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran H.  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02

```
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-18
```

```
Alignment Scores:
Pred. No.:      1.34e-57      Length:      117
Score:          613.00      Matches:      115
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.29%      Mismatches: 0
Query Match:      97.15%      Indels:      0
DB:              4          Gaps:      0
```

US-10-733-563-108 (1-351) x US-10-766-773-18 (1-117)

```
Qy      1  GAGGTGCAATTGGTTGAGTCTGAGAGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db      1  GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

Qy     61  TCATGTGCAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATGAACCTGGGTCCGCCAGGCT 120
Db     21  SerCysAlaIaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40

Qy     121  CCAGGAAAGGTTTGGAAATGGTTGGCGGCATAGAACTAAAAATAAATAATTATGCAACA 180
Db     41  ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60

Qy     181  TATTATGCCGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240
Db     61  TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

Qy     241  CTCTATCTGCAAAATGAACAGCTTGAAAACTGAGGACACAGCCGCTGTTACTGTACCAACC 300
Db     81  LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

Qy     301  TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
Db    101  PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
```

Search completed: January 28, 2006, 09:31:10  
Job time : 44.8649 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:46:13 ; Search time 4.47973 Seconds  
(without alignments)  
1696.980 Million cell updates/sec

Title: US-10-733-563-108  
Perfect score: 631  
Sequence: 1 gaggtgcaattggttgagtc.....ccctggtcacgcgtcaca 351

Scoring table:

BLASUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-O=/cn2\_1/USPTO\_spool\_p/US10733563/runat\_27012006\_180008\_4917/app\_query\_fasta\_1.2716  
-DB=Published Applications\_AA\_New -QPM=fabcan -SUFFIX=n2p.rapbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USRR=US10733563 @CGN 1 1 @runat\_27012006\_180008\_4917  
-NCPUS=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*
- 2: /cn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*
- 3: /cn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*
- 4: /cn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pcp.\*
- 5: /cn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pcp.\*
- 6: /cn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*
- 7: /cn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pcp.\*
- 8: /cn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	7	US-11-075-184A-8
2	613	97.1	117	7	US-11-075-184A-9
3	604	95.7	117	7	US-11-075-184A-10
4	599	94.9	117	7	US-11-075-184A-11
5	548	86.8	117	7	US-11-075-184A-2
6	487	77.2	123	7	US-11-193-440-87
7	478.5	75.8	251	7	US-11-054-515-997
8	478.5	75.8	251	7	US-11-054-515-1346
9	476.5	75.5	139	7	US-11-125-837-24
10	475	75.3	257	7	US-11-054-515-958

11	474	75.1	244	7	US-11-054-515-1991	Sequence 1991, Ap
12	473.5	75.0	258	7	US-11-054-515-1841	Sequence 1841, Ap
13	471.5	74.7	120	6	US-10-834-397-38	Sequence 38, Appl
14	471.5	74.7	120	6	US-10-834-397-63	Sequence 63, Appl
15	471.5	74.7	256	7	US-11-054-515-1209	Sequence 1209, Ap
16	471.5	74.7	281	6	US-10-834-397-178	Sequence 178, App
17	471	74.6	250	7	US-11-054-515-1179	Sequence 1179, Ap
18	470	74.5	253	7	US-11-054-515-1650	Sequence 1650, Ap
19	469.5	74.4	256	7	US-11-054-515-843	Sequence 843, App
20	468	74.2	115	7	US-11-127-903-33	Sequence 33, Appl
21	468	74.2	470	7	US-11-144-248-46	Sequence 46, Appl
22	468	74.2	470	7	US-11-144-222-46	Sequence 46, Appl
23	467.5	74.1	116	6	US-10-925-366A-1	Sequence 1, Appl
24	467.5	74.1	240	6	US-10-925-366A-219	Sequence 219, App
25	467	74.0	117	7	US-11-127-903-32	Sequence 32, Appl
26	466.5	73.9	256	7	US-11-054-515-872	Sequence 872, App
27	466	73.9	125	7	US-11-144-248-16	Sequence 16, Appl
28	466	73.9	125	7	US-11-144-222-16	Sequence 16, Appl
29	465.5	73.8	120	6	US-10-925-366A-235	Sequence 235, App
30	465.5	73.8	250	7	US-11-054-515-1325	Sequence 1325, Ap
31	465	73.7	248	7	US-11-054-515-913	Sequence 913, App
32	465	73.7	248	7	US-11-054-515-2070	Sequence 2070, Ap
33	465	73.7	472	7	US-11-086-289-2	Sequence 2, Appl
34	464	73.5	117	6	US-10-834-397-24	Sequence 24, Appl
35	464	73.5	117	7	US-11-127-903-29	Sequence 29, Appl
36	464	73.5	117	7	US-11-127-903-30	Sequence 30, Appl
37	464	73.5	117	7	US-11-127-903-37	Sequence 37, Appl
38	463.5	73.5	254	7	US-11-054-515-1701	Sequence 1701, Ap
39	463.5	73.5	254	7	US-11-054-515-1735	Sequence 1735, Ap
40	463	73.4	119	7	US-11-127-903-36	Sequence 36, Appl
41	463	73.4	119	7	US-11-127-903-31	Sequence 31, Appl
42	462.5	73.3	248	7	US-11-054-515-921	Sequence 921, App
43	462.5	73.3	248	7	US-11-054-515-1456	Sequence 1456, Ap
44	462.5	73.3	248	7	US-11-054-515-1974	Sequence 1974, Ap
45	462	73.2	113	6	US-10-665-658-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-11-075-184A-8  
; Sequence 8, Application US/11075184A  
; Publication NO. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2 Receptor Antagonists  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE  
US-11-075-184A-8  
Alignment Scores:  
Pred. No.: 1.15e-61 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 7 Gaps: 0  
US-10-733-563-108 (1-351) x US-11-075-184A-8 (1-117)

QY	1	GAGGTGCAATTGGTTGAGTCTCGGAGGAGGANTTGGTGAAGCCTCGGGGGTCAATTGAGACTC	60
Db	1		
QY	61	TCATGTGCAGGCTCTCTGGATTCACTTTTCAGTGTGCTACGCCATGCAACTCGGTCCGCCAGGCT	120
Db	21	SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla	40
QY	121	CCAGGAAGGGTTTGGATTGGGTTCGCCGCATAGAACATAAAAAATAATATTGCAACA	180
Db	41	ProGlyLysGlyLeuGluTrpValGlyArgIleargThrLysAsnAsnTyrAlaThr	60
QY	181	TATTATGCCGATTCAGTGAACACAGATTCCACCATCTCCAGAGATGATTCAAAAAACAGC	240
Db	61	TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr	80
QY	241	CTCTATCTCAAAATGAACAGCTTGAAACTTCAGGACACAGCCGGTGTAATTACTGTACCACC	300
Db	81	LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr	100
QY	301	TTTTACGGTAACGGTGTCTCGGGGCCAGGGGACCTGTGTCACCGTCAGCTCA	351
Db	101	PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer	117

RESULT 2  
US-11-075-184A-9  
; Sequence 9, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2

```

; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody heavy chain variable region
US-11-075-184A-9

Alignment Scores:
Pred. No.:      6,898-61      Length:      117
Score:          613.00      Matches:     115
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.23%      Mismatches:  0
Query Match:     97.15%      Indels:      0
DB:              7          Gaps:        0

```

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Db      61  TyrTyrAlaAspSerValIysAspArgPheThrIleSerArgAspAspSerIysAsnThr 80
Qy      241  CTCATCTCGCAAAATGAACAGCTTGAAACCTGAGGCACACAGCCGCTGTATTACTGTACCACC 300
Db      81  LeuTyrLeuGlnMetAsnSerLeuIysThrGluAspThrAlaValTyrCysThrThr 100
Qy      301  TTTTACCGTTAAACGGTGTCTCGGGCCGAGGGAGCCCTCGTCCACCGTCACTCA 351
Db      101  PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 3
US-11-075-184A-10
; Sequence 10, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30

```

Alignment Scores:	
Pred. No.:	6,916-60
Score:	604.00
Percent Similarity:	99.15%
Best Local Similarity:	96.58%
Query Match:	95.72%
DB:	7
Length:	117
Matches:	113
Conservative:	3
Mismatches:	1
Indels:	0
Gaps:	0

QY	1	GAGGTGCAATTGGTTGAGTCTGGAGGAGGAGTTGGTGAAGCCTGGGGGGTTCATTGAGACTC	60
Db	1	GluValGlnLeuValGluSerGlyGlyGlyLeuValValysProGlyGlySerLeuArgLeu	20
QY	61	TCATGTGAGCGCTCTGGATTCACTTTCAGTGCCTACGCCATGAATGGGTGCGCCAGGCT	120
Db	21	SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla	40
QY	121	CCAGAAAGGGTTTGGAAATGGGTGGCCGCATAGAACAATAAAATAATATATGCAACA	180
Db	41	ProGlyIysGlyLeuGluTrpValAlaArgIleargThrIysAsnAsnAsnTyrAlaThr	60
QY	181	TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG	240
Db	61	TyrTyrAlaAspSerValIysAspArgTyrThrIleSerArgAspAspSerLysAsnThr	80
QY	241	CTCTATCTGCAAAATGAACAGCTTGAACCTGAGGACACACCCGTGTATTACTGTACCACC	300
Db	81	LeuTyrLeuGlnMetAsnSerLeuIysThrGluAspThrAlaValTyrTyrCysThrThr	100
QY	301	TTTTTACGTACGGTGTCTGGGGCCAGGGACCTGGTCACTCCGTCAAGCTCA	351
Db	101	PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer	117

RESULT 4  
US-11-075-184A-11  
; Sequence 11, Application US/11075184A  
; Publication NO. US20050260139A1  
; GENERAL INFORMATION:



```
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody heavy chain variable region, 1D9RH
US-11-075-184A-11

Alignment Scores:
Pred. No.:          2,49e-59          Length:          117
Score:              599.00           Matches:         112
Percent Similarity: 98.29%           Conservative:     3
Best Local Similarity: 95.73%         Mismatches:      2
Query Match:        94.93%           Indels:          0
DB:                  7               Gaps:            0

US-10-733-563-108 (1-351) x US-11-075-184A-11 (1-117)

QY 1 GAGGTGCAATTGGTTCAGTCTCGAGAGAGGATTGGTGAAGCCCTGGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCGAGCTCTGGATTCACTTTCACTGCTGCTAGTGCCTACGCCATCACTGGGTCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGAATGGTTCAGTGCCTAGCCATCAAGAACTTAAATAATTAATTCGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCACAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerGluSerMet 80
QY 241 CTCTATCTGCAATCAACAGCTTGAAGAACTGAGGACACAGCCGTGTATTACTGTACACACC 300
Db 81 LeuPheLeuGlnMetAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyThrGlyThrValThrValThrValSerSer 117

RESULT 5
US-11-075-184A-2
; Sequence 2, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
```

```
; FEATURE:
; OTHER INFORMATION: Murine antibody 1D9 heavy chain variable region; presumably Mus
; OTHER INFORMATION: musculus
US-11-075-184A-2

Alignment Scores:
Pred. No.:          1.18e-53          Length:          117
Score:              548.00           Matches:         101
Percent Similarity: 94.87%           Conservative:    10
Best Local Similarity: 86.32%         Mismatches:      6
Query Match:        86.85%           Indels:          0
DB:                  7               Gaps:            0

US-10-733-563-108 (1-351) x US-11-075-184A-2 (1-117)

QY 1 GAGGTGCAATTGGTTCAGTCTCGAGAGAGGATTGGTGAAGCCCTGGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProLysGlySerLeuLysLeu 20
QY 61 TCATGTGCGAGCTCTGGATTCACTTTCACTGCTGCTAGTGCCTACGCCATCACTGGGTCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGAATGGTTCAGTGCCTAGCCATCAAGAACTTAAATAATTAATTCGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCACAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerGluSerMet 80
QY 241 CTCTATCTGCAATCAACAGCTTGAAGAACTGAGGACACAGCCGTGTATTACTGTACACACC 300
Db 81 LeuPheLeuGlnMetAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyThrGlyThrValThrValThrValSerSer 117

RESULT 6
US-11-193-440-87
; Sequence 87, Application US/11193440
; Publication No. US20060002939A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Gerald W.
;              Schuman, Richard F.
;              Wong, Hing
;              Stinson, Jeffrey L.
; TITLE OF INVENTION: OPISONIC AND PROTECTIVE MONOCLONAL AND
;                   CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
;                   POSITIVE BACTERIA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
;              DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/193,440
; FILING DATE: 01-Aug-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/893,615
; FILING DATE: 29-Jun-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
```

```
;
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 04995.0041-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-11-193-440-87
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Alignment Scores:
Pred. No.: 7,21e-47 Length: 123
Score: 487.00 Matches: 93
Percent Similarity: 86.18% Conservative: 13
Best Local Similarity: 75.61% Mismatches: 11
Query Match: 77.18% Indels: 6
DB: 7 Gaps: 1
```

US-10-733-563-108 (1-351) x US-11-193-440-87 (1-123)

```
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
DB 1 GluValMetLeuValGluSerGlyGlyLeuValGlnProLysGlySerLeuLysLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTAGTGCCTAGCCATCACTGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheAsnAenrYrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGATTGGTTCGGCCGATAGAACTAAATAATATATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgSerLysSerAsnAsnTyrAlaThr 60

QY 181 TATTATGCGGATTAGTGAAGACAGATTCCATCTCAGAGATGATTCAAAAACACG 240
DB 61 PheTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerGlnSerMet 80

QY 241 CTCATCTGCAATCAACAGCTTGAAGACTGAGGACAGCCGCTATTACTGTACCACC 300
DB 81 LeuTyrLeuGlnMetCAsnLeuLysThrGluAspThrAlaMetCtyrTyrCysValArg 100

QY 301 TTTTACGGTAACGGTGC-----TGGGGCCAGGGGACCCCTGCTACC 342
DB 101 ArgGlyAlaSerGlyIleAspTyrAlaMetAspTyrTrpGlyGlnGlyThrSerLeuThr 120

QY 343 GTCAGCTCA 351
DB 121 ValSerSer 123
```

## RESULT 7

```
US-11-054-515-997
; Sequence 997, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
```

```
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 997
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-997

Alignment Scores:
Pred. No.: 6.53e-46 Length: 251
Score: 478.50 Matches: 94
Percent Similarity: 81.25% Conservative: 10
Best Local Similarity: 73.44% Mismatches: 13
Query Match: 75.83% Indels: 11
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-054-515-997 (1-251)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
DB 1 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTAGTGCCTAGCCATCACTGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAspHisTyrMetAspTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGATTGGTTCGGCCGATAGAACTAAATAATATATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgAlaArgAsnLysAlaAsnSerTyrThrIle 60

QY 181 TATTATGCGGATTAGTGAAGACAGACTTCACCATCTCAGAGATGATTCAAAAACACG 240
DB 61 GluTyrAlaAlaSerValLysGlyArgPheThrIleSerArgAspAspSerLysAsnSer 80

QY 241 CTCATCTGCAATCAACAGCTTGAAGACTGAGGACAGCCGCTATTACTGT----- 294
DB 81 LeuPheLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysAlaArg 100

QY 295 -----ACCACCTTTTACGGTAACGGTGTCTGGGGCCAG 327
DB 101 AlaProTyrAspIleLeuThrGlyTyrSerAspTyrTyrGlyMetAspValTrpGlyArg 120

QY 328 GGGACCCCTGGTCCACCGTCAGCTCA 351
DB 121 GlyThrLeuValThrValSerSer 128
```

## RESULT 8

```
US-11-054-515-1346
; Sequence 1346, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
```

```
; PRIORITY APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1346
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1346

Alignment Scores:
Pred. No.: 6,53e-46 Length: 251
Score: 478.50 Matches: 94
Percent Similarity: 81.25% Conservative: 10
Best Local Similarity: 73.44% Mismatches: 13
Query Match: 75.83% Indels: 11
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-054-515-1346 (1-251)

QY 1 GAGGTGCAATTGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCGACCTCTCGATTCACTTTCAGTGCCTACGCCATGACCTGAGTGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAspHisThrMetAspTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTGGAATGGGTGGCCGCATAGAAGCTAAATAATTAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgAlaArgAsnLysAlaAsnSerThrIle 60
QY 181 TATTATGCCGATTCACTGAAGACAGATTCCACCATCTCCAGAGATGATTCATAAAACACG 240
Db 61 GluTyrAlaAlaSerValLysGlyArgPheThrIleSerArgAspAspSerLysAsnSer 80
QY 241 CTCATCTCTCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGT----- 294
Db 81 LeuPheLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysAlaArg 100
QY 295 -----ACCACCTTTTACGGTAACCGTGTCTGGGGCCAG 327
Db 101 AlaProTyrAspIleLeuThrGlyTyrSerAspTyrTyrGlyMetAspValTrpGlyArg 120
QY 328 GGGACCTGTGTCACCTCAGCTCA 351
Db 121 GlyThrLeuValThrValSerSer 128

RESULT 9
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
```

```
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Alignment Scores:
Pred. No.: 1,07e-45 Length: 139
Score: 476.50 Matches: 90
Percent Similarity: 87.50% Conservative: 15
Best Local Similarity: 75.00% Mismatches: 12
Query Match: 75.52% Indels: 3
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-125-837-24 (1-139)

QY 1 GAGGTGCAATTGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCATTGAGACTC 60
Db 20 GluValGlnLeuValGluThrGlyGlyGlyLeuValGlnProLysGlySerLeuValLeu 39
QY 61 TCATGTGCGACCTCTCGATTCACTTTCAGTGCCTACGCCATGACCTGAGTGGTCCGCCAGGCT 120
Db 40 SerCysAlaAlaSerGlyPheThrPheAsnThrAsnAlaMetAsnTrpValArgGlnAla 59
QY 121 CCAGGAAGGGTTGGAATGGGTGGCCGCATAGAAGCTAAATAATTAATTATGCAACA 180
Db 60 ProGlyLysGlyLeuGluTrpValAlaArgIleArgSerLysSerAsnAsnTyrAlaThr 79
QY 181 TATTATGCCGATTCACTGAAGACAGATTCCACCATCTCCAGAGATGATTCATAAAACACG 240
Db 80 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspThrGlnSerMet 99
QY 241 CTCATCTCTCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTAC--- 297
Db 100 IleTyrLeuGlnMetAsnAsnLeuLysThrGluAspThrGlyMetTyrTyrCysValArg 119
QY 298 -----ACCTTTTACGGTAACCGTGTCTGGGGCCAGGACCTGTGTCACCGTCAGCTCA 351
Db 120 GlyGlySerTyrTrpTyrPheAspValTrpGlyAlaGlyThrValThrValSerSer 139

RESULT 10
US-11-054-515-958
; Sequence 958, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
```



```
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1841
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1841

Alignment Scores:
Pred. No.: 2,35e-45 Length: 258
Score: 473.50 Matches: 92
Percent Similarity: 78.46% Conservative: 10
Best Local Similarity: 70.77% Mismatches: 15
Query Match: 75.04% Indels: 13
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-054-515-1841 (1-258)

QY 1 GAGGTGCAATGTTGAGTCTGGAGGAGGATGTTGTAAGCTGGGGGTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluThrGlyGlyGlyLeuValValysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCGACCTCGATTCACATTCAGTGTGCTAGCCATGACCTGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerGlyTyrSerMetAsnTrpValArgLeuAla 40
QY 121 CCAGGAAGGGTTGGAATGGGTGGCGCATGAAGAACTAAATAATAATTATGCAACA 180
DB 41 ProGlyValGlyLeuGluTrpValAlaSerIleArgSerGlyGlyThrTyrIle 60
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
DB 61 TyrTyrAlaAspSerValysGlyArgPheThrIleSerArgAspAsnAlaValSer 80
QY 241 CTCATCTGCAATGCAAGCTGTTGAACTGAGGACACAGCCGCTGTATTACTGTACCAC 300
DB 81 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaArg 100
QY 301 TTTTACGGTAACGGT-----TTTTACGGTAACGGTGTCTG 321
DB 101 AppProGlyAsnTyrAspIleLeuThrGlyTyrTyrTyrTyrTyrGlyMetAspValTrp 120
QY 322 GCGCGGAGGACCTGCTGTCACCGTCAGCTCA 351
DB 121 GlyGlnGlyThrLeuValThrValSerSer 130

RESULT 13
US-10-834-397-38
; Sequence 38, Application US/10834397
; Publication No. US2006000334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Pluckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-834-397-38

Alignment Scores:
Pred. No.: 3,82e-45 Length: 120
Score: 471.50 Matches: 94
Percent Similarity: 84.43% Conservative: 9
Best Local Similarity: 77.05% Mismatches: 12
Query Match: 74.72% Indels: 7
DB: 6 Gaps: 2

US-10-733-563-108 (1-351) x US-10-834-397-38 (1-120)

QY 1 GAGGTGCAATGTTGAGTCTGGAGGAGGATGTTGTAAGCTGGGGGTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCTCTGGATTCATCTTCACTGCTAGCCATGAACTGGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTGGAATGGGTGGCGCATGAAGAACTAAATAATAATTATGCAACA 180
DB 41 ProGlyValysGlyLeuGluTrpValSerAlaIle-----SerGlySerGlySerThr 58
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
DB 59 TyrTyrAlaAspSerValysGlyArgPheThrIleSerArgAspAsnSerIleValThr 78
QY 241 CTCATCTGCAATGCAAGCTGTTGAACTGAGGACACAGCCGCTGTATTACTGTACCAC 300
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaArg 98
QY 301 TTTTACGGTAACGGT-----GTCCTGGGCGGCGGAGGACCTGTCTACCCGTC 345
DB 99 TrpGlyGlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrVal 118
QY 346 AGCTCA 351
DB 119 SerSer 120

RESULT 14
US-10-834-397-63
; Sequence 63, Application US/10834397
; Publication No. US2006000334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
```



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Db      81 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 100
QY      301 -----TTTACGGTAACGGTGTCTGG 321
Db      101 AspProGlyAsnTyrAspIleLeuThrGlyTyrTyrTyrTyrGlyMetAspValTrp 120
QY      322 GGCACGGGACCCCTGGTCACCGTCAGCTCA 351
Db      121 GlyGlnGlyThrMetValThrValSerSer 130
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Search completed: January 28, 2006, 09:32:13  
Job time : 6.47973 secs

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GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:12:21 ; Search time 52.4685 Seconds  
(without alignments)  
5627.428 Million cell updates/sec

Title: US-10-733-563-109  
Perfect score: 590  
Sequence: 1 gatgtagtgtgacccagtc.....ggaccgactggagatcaag 336

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cpn2\_1/USPTO spool\_p/US10733563/runat\_27012006\_180005\_4773/app\_query.fasta\_1.2716  
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CGN 1 1 624 @runat\_27012006\_180005\_4773 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq 21:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	112	4	Aae06949 Humanised
2	590	100.0	112	4	Aau09921 Humanised
3	590	100.0	112	5	Abg75530 Humanised
4	590	100.0	112	5	Aao14973 Humanised
5	590	100.0	112	5	Adf98233 Humanised
6	590	100.0	112	5	Adg98234 Humanised
7	590	100.0	112	9	Aeb09507 Humanised
8	584	99.0	114	4	Aae07035 Humanised
9	584	99.0	114	8	Adq99328 Humanised

10	594	99.0	114	9	AEB09601	Humanised
11	577	97.8	112	4	AAE06950	Humanised
12	577	97.8	112	4	AAU09922	Humanised
13	577	97.8	112	5	ABG75531	Humanised
14	577	97.8	112	5	ADF98234	Humanised
15	577	97.8	112	8	ADQ89235	Humanised
16	577	97.8	112	9	AEB09508	Humanised
17	572	96.9	112	4	AAE07036	Humanised
18	572	96.9	112	4	AAU09925	Humanised
19	572	96.9	112	5	ABG75534	Humanised
20	572	96.9	112	5	ADF98237	Humanised
21	572	96.9	112	8	ADQ89329	Humanised
22	572	96.9	112	9	AEB09602	Humanised
23	570	96.6	112	4	AAE06951	Humanised
24	570	96.6	112	4	AAU09923	Humanised
25	570	96.6	112	5	ABG75532	Humanised
26	570	96.6	112	5	ADF98235	Humanised
27	570	96.6	112	8	ADQ89236	Humanised
28	570	96.6	112	9	AEB09509	Humanised
29	569	96.4	112	8	ADQ31290	Humanised
30	566	95.9	112	8	ADQ31289	Humanised
31	565	95.8	112	4	AAE06952	Humanised
32	565	95.8	112	4	AAU09924	Humanised
33	565	95.8	112	5	ABG75533	Humanised
34	565	95.8	112	5	AAO14976	Humanised
35	565	95.8	112	5	ADF98236	Humanised
36	565	95.8	112	8	ADQ89237	Humanised
37	565	95.8	112	9	AEB09510	Humanised
38	559	94.7	113	6	ABP58270	Humanised
39	559	94.7	219	6	ABP58272	Humanised
40	559	94.7	239	6	ABP58274	Humanised
41	557.5	94.5	111	5	AAO14977	Humanised
42	554.5	94.0	111	5	AAO14975	Humanised
43	544	92.2	110	5	AAO14974	Humanised
44	542	91.9	132	5	ABG76931	Humanised
45	542	91.9	132	8	ADR88415	Humanised

ALIGNMENTS

RESULT 1	AAE06949	standard; protein; 112 AA.
ID	AAE06949	standard; protein; 112 AA.
XX	AAE06949;	
AC	AAE06949;	
XX		
DT	11-SEP-2003	(revised)
DT	16-OCT-2001	(first entry)
XX		
DE	Humanised murine 1D9 antibody kappa light chain variable region, 1D9RKA.	
XX		
KW	Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;	
KW	neointimal hyperplasia; VK; kappa light chain variable region; 1D9RKA.	
XX		
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
FF	Key	Location/Qualifiers
FF	Region	23..39
FT		/label= CDR1
FT		/note= "Complementarity determining region 1"
FT		55..61
FT	Region	/label= CDR2
FT		/note= "Complementarity determining region 2"
FT	Region	94..102

```
FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US003537.
XX 03-FEB-2000; 2000US-00497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX WPI; 2001-488888/53.
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
XX disorder in a patient, comprises a binding specificity for CCR2, and a
XX non-human antigen binding region and human immunoglobulin.
XX Claim 61; Fig 11; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
XX comprising an antigen binding region of non-human origin and at least a
XX portion of an immunoglobulin of human origin. The humanised antibodies
XX are useful for inhibiting the interaction of a cell expressing CCR2. They
XX are useful for inhibiting or treating HIV infection. The proteins of the
XX invention are useful for inhibiting leukocyte trafficking, for treating
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune
XX disorders such as rheumatoid arthritis and multiple sclerosis,
XX atherogenesis and atherosclerosis, and for inhibiting restenosis. They
XX are useful in therapy or diagnosis, and in the manufacture of a
XX medicament for treating CCR-2 mediated disease. They are also useful for
XX treating allergy, anaphylaxis, malignancy, chronic and acute
XX inflammation, histamine and IgE-mediated allergic reaction, shock,
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
XX associated with vascular intervention, including angioplasty and/or stent
XX placement in a mammal. Humanised antibodies are also useful for
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
XX neointimal hyperplasia of a vessel in a mammal, preferably associated
XX with vascular intervention. The present sequence is humanised murine 1D9
XX antibody kappa light chain variable (VK) region, 1D9RKA. (Updated on 11-
XX SEP-2003 to standardise OS field)
XX SQ Sequence 112 AA;

Alignment Scores:
Pred. No.: 3.74e-59 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x AA06949 (1-112)
QY 1 GATGTAGTGATGACCCAGCTCTCCACTCTCTGCGCCGTTACCTTGGACAGCCAGCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTAGATAGTGATGGAACACACATTTTGAATTGG 120
Db 21 lIeSerCyLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTCAGCAGAGCCAGCCAGCTCTCAAGCGCCCTAATCTATCTGGTCTCTAAATCGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgLeuLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTGACGGCGAGTCAGGATCAGGACAGATTTTACACTGAATTC 240
Db 181 TCTGGAGTCCCTGACAGGTTGACGGCGAGTCAGGATCAGGACAGATTTTACACTGAATTC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTTATTATTGCTGCAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACACGTTCCGACCAAGGACCCGACTCGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 2
AAU09921
ID AAU09921 standard; protein; 112 AA.
XX AC AAU09921;
XX 18-JUN-2002 (first entry)
XX Humanised 1D9 light chain variable region, 1D9RKA protein sequence.
DE Human; mouse; 1D9 light chain variable region; vasotropic;
XX antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;
KW insulin-dependent diabetes mellitus; inflammatory bowel disease;
KW ulcerative colitis; HF-21/28; graft rejection; allergic disease;
KW antipsoriatic; 1D9RKA; antiarthritic; nephrotropic; antithyroid;
KW restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;
KW vascular injury; autoimmune disease; immunoglobulin;
KW complementarity determining region; CDR; CD18; CCR2; atherosclerosis;
KW mutant; mutein.
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FH Region 24..39
FT /note= "Complementarity determining region 1 (CDR1),
FT grafted from mouse mAb 1D9 light chain sequence
FT (AAU09918)"
FT Region 55..61
FT /note= "Complementarity determining region 2 (CDR2),
FT grafted from mouse mAb 1D9 light chain sequence
FT (AAU09918)"
FT Region 94..102
FT /note= "Complementarity determining region 3 (CDR3),
FT grafted from mouse mAb 1D9 light chain sequence
FT (AAU09918)"
FT Misc-difference 112
FT /note= "Addition of Lys residue normally present in mouse
FT mAb 1D9 sequence and absent in human antibody HF-21/28
FT sequence (AAU09920)"
XX WO200170266-A2.
XX 27-SEP-2001.
XX 15-MAR-2001; 2001WO-US008266.
XX 17-MAR-2000; 2000US-00528267.
XX (MILL-) MILLENNIUM PHARM INC.
XX Horvath CJ, Rao PE;
XX WPI; 2001-607511/69.
XX Inhibiting stenosis or restenosis of a blood vessel following vascular
XX injury or angioplasty in a subject by administering agent which inhibits
XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.
XX Claim 32; Fig 17; 108pp; English.
```

alveolar, smooth muscle, inflammatory or allergic diseases (such as

1

KW rec:

KW Mouse; stenosis

neutrophil; antagonist; CCR2; mononuclear

r cell; angioplasty;

CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
 CC chain variable region (VK), 1D9RKAVK, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human HF-21/28  
 CC mAb VK regions with a mouse derived lys at position 112  
 XX  
 SQ Sequence 112 AA;

Alignment Scores:  
 Pred. No.: 3.74e-59 Length: 112  
 Score: 590.00 Matches: 112  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x ABG75530 (1-112)

QY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCGCTCC 60  
 DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
 QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTAGATAGTGTGAAAGACATTTTGAATTGG 120  
 DB 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
 QY 121 TTTGACGAGAGCCAGCCAGCTCTCAAGGCGCTTAATCTATCTGCTCTAAACTGGAC 180  
 DB 41 PheGlnGlnArgProGlyGlnSerProArgGlnLeuLeuValSerLysLeuAsp 60  
 QY 181 TCTGGAGTCCCTGACAGGTTGACGGCAGTGTGATCAGGACAGATTTCACTGAAATC 240  
 DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys 80  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACACATTTCCG 300  
 DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
 QY 301 TACAGTTTCGACAGGACCCGACTGGAGATCAAG 336  
 DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluLeuLys 112

#### RESULT 4

AAO14973  
 ID AAO14973 standard; protein; 112 AA.

AC AAO14973;

XX 05-SEP-2002 (first entry)

DE Humanised murine light chain variable region (1D9Rka Vk).

XX Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
 KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
 KW bowel transplant; heart transplant; graft versus host disease;  
 KW chronic graft rejection; antibody light chain variable region; 1D9Rka Vk.

XX Mus musculus.

OS Synthetic.

XX US2002042370-A1.

XX 11-APR-2002.

XX 13-APR-2001; 2001US-00835087.

PR 14-APR-2000; 2000US-00549448.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Hancock WW;  
 PI WPI; 2002-351265/38.  
 XX  
 DR Inhibiting graft rejection, graft versus host disease or chronic  
 XX rejection of a transplanted graft, involves administering a CCR2  
 PT antagonist.  
 PT  
 XX Claim 26; Fig 1; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
 CC versus host disease or chronic rejection of a transplanted graft. The  
 CC method involves administering an antagonist of CC chemokine receptor 2  
 CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
 CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
 CC complementarity determining regions from various non-human origins). CCR2  
 CC is known to be involved in the rejection of transplanted grafts. The  
 CC method of the invention is useful for inhibiting graft rejection -  
 CC particularly allografts such as kidney, liver, lung, heart-lung,  
 CC pancreas, bowel and heart. The method of the invention is also useful for  
 CC inhibiting graft versus host disease and for inhibiting chronic rejection  
 CC of a transplanted graft. The present amino acid sequence represents a  
 CC humanised murine antibody light chain variable region (1D9Rka Vk)

SQ Sequence 112 AA;

#### Alignment Scores:

Pred. No.: 3.74e-59 Length: 112  
 Score: 590.00 Matches: 112  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x AAO14973 (1-112)

QY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCGCTCC 60

DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20

QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTAGATAGTGTGAAAGACATTTTGAATTGG 120

DB 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTGACGAGAGCCAGCCAGCTCTCAAGGCGCTTAATCTATCTGCTGGCAGGTACACATTTCCG 180

DB 41 PheGlnGlnArgProGlyGlnSerProArgGlnLeuLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTGACGGCAGTGTGATCAGGACAGATTTCACTGAAATC 240

DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACACATTTCCG 300

DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTTCGACAGGACCCGACTGGAGATCAAG 336

DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluLeuLys 112

#### RESULT 5

ADP98233  
 ID ADP98233 standard; protein; 112 AA.

XX AC ADP98233;

XX 26-FEB-2004 (first entry)

XX Humanised 1D9 light chain variable region, 1D9Rka V kappa, SEQ ID 3.

XX Immunosuppressive; CCR2 function inhibitor; graft rejection;  
KW graft versus host disease; CC chemokine receptor 2; CCR2;  
KW anti-CCR2 antibody.  
XX Synthetic.  
OS Mus musculus.  
OS Homo sapiens.  
XX WO200178653-A2.  
XX 25-OCT-2001.  
XX 13-APR-2001; 2001WO-US012139.  
XX 14-APR-2000; 2000US-00549448.  
XX (WILL-) MILLENNIUM PHARM INC.  
XX Hancock WW;  
XX WPI; 2002-017543/02.  
XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
PT involves use of CC chemokine receptor 2 inhibitor.  
XX Claim 26; Fig 1; 44pp; English.  
XX The present invention relates to a method for inhibiting graft rejection  
CC or graft versus host diseases. The method comprises administration of a  
CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
CC recipient of a transplanted graft. The CCR2 function antagonist is an  
CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
CC ADF98240-ADP98249). The method is useful for inhibiting rejection,  
CC particularly chronic rejection of a graft, particularly an allograft of  
CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
CC inhibiting graft versus host disease for a bone marrow graft.  
XX Sequence 112 AA;  
SQ  
Alignment Scores:  
Pred. No.: 3,748-59 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0  
US-10-733-563-109 (1-336) x ADF98233 (1-112)  
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DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTGCAGTCAAGTCCAGAGCTCTTAGATGATGATGGAAGACATTTTGAATTGG 120  
DB 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTTCAGCAGAGCCAGCCAGTCTCAAGCGCTTAATCTATCTGGTGTCTAACTGGAC 180  
DB 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCTGATCAGGACAGATTTTCACTGAAATC 240  
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 ACCAGAGTGGAGCTGAGGATGTGGAGTTATTATTGCTGGCAGGATACACATTTTCG 300  
DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTyrGlnGlyThrHisPhePro 100  
QY 301 TACACGTTGGACAGGACCCGACCTGGAGATCAAG 336  
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 6  
ADQ89234  
ID ADQ89234 standard; protein; 112 AA.  
XX AC ADQ89234;  
XX DT 21-OCT-2004 (first entry)  
XX Humanised immunoglobulin protein #1.  
XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX OS Synthetic.  
XX US2004151721-A1.  
XX 05-AUG-2004.  
XX 10-DEC-2003; 2003US-00733563.  
XX 19-OCT-2001; 2001US-0350166P.  
PR 26-JUN-2002; 2002US-0392364P.  
PR 17-OCT-2002; 2002US-00272899.  
XX (OKEE/) O'KEEFE T.  
PA (PONA/) PONATH P.  
XX O'keefe T, Ponath P;  
XX WPI; 2004-580175/56.  
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX Claim 5; SEQ ID NO 12; 128pp; English.  
XX The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.  
XX SQ Sequence 112 AA;

Alignment Scores:  
Pred. No.: 3,748-59 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0  
US-10-733-563-109 (1-336) x ADQ89234 (1-112)  
QY 1 GATGTAGTGTGATGACCCAGTCTCCACTCTCTGCGGTTACCTTGGACAGCCAGCTCC 60  
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTGCAGTCAAGTCCAGGCTCTTAGATGATGATGGAAGACATTTTGAATTGG 120  
DB 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCTAATCTATCTGCTGTCTAACTGGAC 180  
 Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyLeuValSerIysLeuAseP 60  
 QY 181 TCTGAGTCCCTGACACAGTTTCAGCGGCAGTGGATCAGGACAGATTTTCACACTGAAATC 240  
 Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuIysIle 80  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCAAGGTACACATTTCCG 300  
 Db 81 SerArgValGluAlaGluAsePValGlyValTyTyTyCysTrpGlnGlyThrHisPhePro 100  
 QY 301 TACAGTTTCGACAGAGGACCGGACTGGAGATCAAG 336  
 Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleIys 112

## RESULT 7

AEBO9507  
 ID AEBO9507 standard; protein; 112 AA.

XX AC  
 XX AEBO9507;

XX DT  
 XX 08-SEP-2005 (first entry)

XX DE  
 XX Humanized ID9 kappa light chain variable region SEQ ID NO 12.

XX KW  
 KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW light chain variable region.

XX OS  
 OS Homo sapiens.

XX OS  
 OS Mus musculus.

XX OS  
 OS Synthetic.

XX XX  
 XX WO2005060368-A2.

XX XX  
 XX 07-JUL-2005.

XX XX  
 XX 10-DEC-2003; 2003WO-US039599.

XX XX  
 XX 10-DEC-2003; 2003WO-US039599.

XX XX  
 XX (MILL-) MILLENNIUM PHARM INC.

XX XX  
 XX Okeefe T, Ponath P;

XX XX  
 XX WPI; 2005-488561/49.

XX XX  
 XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.

XX PS  
 XX Claim 1; SEQ ID NO 12; 192pp; English.

XX XX  
 XX The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for  
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
 CC construct comprising nucleic acid molecule encoding (I); and host cell

CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocytic-mediated disorders such as atherosclerosis. (I) Is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of a humanized ID9  
 CC kappa light chain variable region used in the creation of a humanized  
 CC anti-CCR2-antibody.

XX SQ  
 XX Sequence 112 AA;

## Alignment Scores:

Pred. No.: 3,74e-59 Length: 112  
 Score: 590.00 Matches: 112  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-733-563-109 (1-336) x AEBO9507 (1-112)

QY 1 GATGTAGTGTATGATGACCCAGTCTCCACTCTCTCTGCGCGTACCTTGGACAGCCCTCC 60  
 Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
 QY 61 ATCTCTTGAAGTCAAGTCAGAGGCTCTTAGATAGTGTATGATGAGAAAGACATTTTGAATTGG 120  
 Db 21 IleSerCysIysSerSerGlnSerLeuLeuAsePArgGlyIysThrPheLeuAsePTrp 40  
 QY 121 TTTCAGCAGAGCCAGGCGGCTCTCCAGGCGCCTAATCTATCTGCTGTCTAACTGGAC 180  
 Db 41 PheGlnGlnArgProGlyGlnSerProArgGlyLeuIleTyLeuValSerIysLeuAseP 60  
 QY 181 TCTGAGTCCCTGACAGGTTTCAGGCGGCTGATGATGAGGACAGATTTTCACACTGAAATC 240  
 Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuIysIle 80  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCAAGGTACACATTTCCG 300  
 Db 81 SerArgValGluAlaGluAsePValGlyValTyTyTyCysTrpGlnGlyThrHisPhePro 100  
 QY 301 TACAGTTTCGACAGAGGACCGGACTGGAGATCAAG 336  
 Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleIys 112

## RESULT 8

AAE07035

ID AAE07035 standard; protein; 114 AA.

XX AC  
 XX AAE07035;

XX XX  
 XX 11-SEP-2003 (revised)

XX DT  
 XX 16-OCT-2001 (first entry)

XX XX  
 XX Humanised murine antibody light chain ID9RKA protein.

XX XX  
 XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; atherosclerosis; atherosclerosis; atherosclerosis;  
 KW anaphylaxis; malignancy; inflammation; stenosis; acquired immune deficiency syndrome; AIDS;  
 KW fibrotic disease; angiolysis; acquired immune deficiency syndrome; AIDS;  
 KW neointimal hyperplasia; antibody ID9 light chain; ID9RKA.

XX OS  
 XX Mus sp.

XX OS  
 XX Homo sapiens.

XX OS  
 XX Chimeric.

XX WO200157226-A1.  
XX 09-AUG-2001.  
XX 02-FEB-2001; 2001WO-US003537.  
XX 03-FEB-2000; 2000US-00497625.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
XX WPI; 2001-488888/53.  
XX N-PSDB; AAD13180.  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
XX disorder in a patient, comprises a binding specificity for CCR2, and a  
XX non-human antigen binding region and human immunoglobulin.  
XX Disclosure; Fig 24; 183pp; English.  
XX The patent discloses a humanised antibody or its antigen-binding  
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
XX comprising an antigen binding region of non-human origin and at least a  
XX portion of an immunoglobulin of human origin. The humanised antibodies  
XX are useful for inhibiting the interaction of a cell expressing CCR2. They  
XX are useful for inhibiting or treating HIV infection. The proteins of the  
XX invention are useful for inhibiting leukocyte trafficking, for treating  
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune  
XX disorders such as rheumatoid arthritis and multiple sclerosis,  
XX atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
XX are useful in therapy or diagnosis, and in the manufacture of a  
XX medicament for treating CCR-2 mediated disease. They are also useful for  
XX treating allergy, anaphylaxis, malignancy, chronic and acute  
XX inflammation, histamine and IgE-mediated allergic reaction, shock,  
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
XX associated with vascular intervention, including angioplasty and/or stent  
XX placement in a mammal. Humanised antibodies are also useful for  
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
XX neointimal hyperplasia of a vessel in a mammal, preferably associated  
XX with vascular intervention. The present sequence is humanised murine  
XX antibody light chain region, LD9RKA. (Updated on 11-SEP-2003 to  
XX standardise OS field)  
XX Sequence 114 AA;  
XX  
XX Alignment Scores:  
XX Pred. No.: 1.86e-58 Length: 114  
XX Score: 584.00 Matches: 111  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 98.98% Indels: 0  
XX DB: 4 Gaps: 0  
XX  
XX US-10-733-563-109 (1-336) x AAE07035 (1-114)  
XX  
XX 4 GTAGTGATGACCGAGTCTCCATCTCTCTGCGGTACCTTGGACAGCCAGCTCCATC 63  
XX  
XX 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
XX  
XX 64 TCTTCGCAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAACACATCTTTGAATTGGTTT 123  
XX  
XX 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
XX  
XX 124 CAGCAGAGCCAGCGGAGTCTCCAGGCGCCCTAAATCTATCTGGTGTCTAAACTGGACTCT 183  
XX  
XX 42 GlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAspSer 61  
XX  
XX 184 GSAGTCCCTCAGCAGGTTCCGCGGAGTGGATCAGGACAGATTCACACTGAAATCAGC 243  
XX  
XX 62 GlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIleSer 81  
XX  
XX QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTATTATTCTGCTGCAAGGTACACATTTCCGTAC 303  
XX  
XX Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
XX  
XX QY 304 ACGTTCGACACAGGAGCCCGACTGGAGATCAAG 336  
XX  
XX Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
XX  
XX RESULT 9  
XX ADQ89328  
XX ID ADQ89328 standard; protein; 114 AA.  
XX XX  
XX AC ADQ89328;  
XX XX  
XX DT 21-OCT-2004 (first entry)  
XX XX  
XX DE Humanised immunoglobulin protein #10.  
XX XX  
XX KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
XX inflammatory disease; autoimmune disorder; graft rejection;  
XX HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
XX anti-HIV; virucide; antiarteriosclerotic.  
XX OS Synthetic.  
XX XX  
XX PN US2004151721-A1.  
XX XX  
XX XX 05-AUG-2004.  
XX PD  
XX XX 10-DEC-2003; 2003US-00733563.  
XX PF  
XX XX 19-OCT-2001; 2001US-0350166P.  
XX PR 26-JUN-2002; 2002US-0392364P.  
XX PR 17-OCT-2002; 2002US-0027289P.  
XX XX  
XX PA (OKEE/) O'KEEFE T.  
XX PA (PONA/) PONATH P.  
XX XX  
XX PI O'keefe T, Ponath P;  
XX XX  
XX DR WPI; 2004-580175/56.  
XX DR N-PSDB; ADQ89320.  
XX XX  
XX PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
XX PT useful for diagnosing and/or treating inflammatory or autoimmune  
XX PT diseases, and HIV infection.  
XX XX  
XX PS Disclosure; SEQ ID NO 106; 128pp; English.  
XX XX  
XX CC The invention relates to humanised immunoglobulin heavy and light chains  
XX CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
XX CC immunoglobulin or its antigen binding fragment comprising the chains. The  
XX CC humanised immunoglobulin or its antigen binding fragment preferably  
XX CC comprises two heavy chains and two light chains. The humanised  
XX CC immunoglobulin and its heavy and light chains are useful for the  
XX CC diagnosis, prevention and/or treatment of diseases or conditions  
XX CC associated with aberrant expression or activity of the CCR2 polypeptide,  
XX CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
XX CC infection and atherosclerosis. This sequence represents a humanised  
XX CC immunoglobulin protein of the invention.  
XX XX  
XX SQ Sequence 114 AA;  
XX  
XX Alignment Scores:  
XX Pred. No.: 1.86e-58 Length: 114  
XX Score: 584.00 Matches: 111  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 98.98% Indels: 0  
XX DB: 8 Gaps: 0  
XX  
XX US-10-733-563-109 (1-336) x ADQ89328 (1-114)

QY 4 GTAGTGTGACCCAGCTCTCCACTCTCTTGCCCGTTACCTTGGACAGCCAGCTCCATC 63  
 DB 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerile 21  
 QY 64 TCTTGCAGTCAAGTCAGAGCTCTTAGATAGTAGGAAAGACATTTTGAATTGGTTT 123  
 DB 22 SerCysIysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
 QY 124 CAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTAACTCTATCTGGTCTCTAAACTGACACT 183  
 DB 42 GlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAspSer 61  
 QY 184 GGAGTCCCTGACAGCTTCCAGGCGCAGTGGATCAGGACAGATTTTCCACTGAAATCAGC 243  
 DB 62 GlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIleSer 81  
 QY 244 AGAGTGGAGGCTGAGGATTTGGAGTTTATTTATCTGCTGCAAGGTACACATTTCCGTAC 303  
 DB 82 ArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPheProTyr 101  
 QY 304 ACGTTCCGACAGGACCGACTCGAGATCAAG 336  
 DB 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
 RESULT 10  
 AEB09601  
 ID AEB09601 standard; protein; 114 AA.  
 XX  
 AC AEB09601;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE Humanized light chain 1D9RKA.  
 XX  
 KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW light chain variable region.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2005060368-A2.  
 XX  
 PD 07-JUL-2005.  
 XX  
 PP 10-DEC-2003; 2003WO-US039599.  
 XX  
 PR 10-DEC-2003; 2003WO-US039599.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Okeefe T, Ponath P;  
 XX  
 DR WPI; 2005-488561/49.  
 XX  
 DR N-PSDB; AEB09593.  
 XX  
 XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.  
 XX  
 PS Disclosure; SEQ ID NO 106; 192pp; English.  
 XX

CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (1); a  
 CC construct comprising nucleic acid molecule encoding (1); and host cell  
 CC comprising the nucleic acid molecule. (1) is useful as a therapeutic  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocyte-mediated disorders such as atherosclerosis. (1) is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of humanized light  
 CC chain 1D9RKA.  
 XX  
 SQ Sequence 114 AA;  
 Alignment Scores:  
 Pred. No.: 1.86e-58 Length: 114  
 Score: 584.00 Matches: 111  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.98% Indels: 0  
 DB: Gaps: 0  
 US-10-733-563-109 (1-336) x AEB09601 (1-114)  
 QY 4 GTAGTGTGACCCAGCTCTCCACTCTCTTGCCCGTTACCTTGGACAGCCAGCTCCATC 63  
 DB 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerile 21  
 QY 64 TCTTGCAGTCAAGTCAGAGCTCTTAGATAGTAGGAAAGACATTTTGAATTGGTTT 123  
 DB 22 SerCysIysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
 QY 124 CAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTAACTCTATCTGGTCTCTAAACTGACACT 183  
 DB 42 GlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAspSer 61  
 QY 184 GGAGTCCCTGACAGCTTCCAGGCGCAGTGGATCAGGACAGATTTTCCACTGAAATCAGC 243  
 DB 62 GlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIleSer 81  
 QY 244 AGAGTGGAGGCTGAGGATTTGGAGTTTATTTATCTGCTGCAAGGTACACATTTCCGTAC 303  
 DB 82 ArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPheProTyr 101  
 QY 304 ACGTTCCGACAGGACCGACTCGAGATCAAG 336  
 DB 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
 RESULT 11  
 AAE06950  
 ID AAE06950 standard; protein; 112 AA.  
 XX  
 AC AAE06950;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Humanised murine 1D9 antibody kappa light chain variable region, 1D9RKB.  
 XX  
 KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;



KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention; ID9 antibody;  
 KW neointimal hyperplasia; VK; kappa light chain variable region; ID9RKB.

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX Key Location/Qualifiers

FT Region 23..39

FT /label= CDR1

FT /note= "Complementarity determining region 1"

FT Region 55..61

FT /label= CDR2

FT /note= "Complementarity determining region 2"

FT Region 94..102

FT /label= CDR3

FT /note= "Complementarity determining region 3"

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003537.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;

XX WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.

XX Claim 61; Fig 11; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IGF-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is humanised murine ID9 antibody kappa light chain variable (VK) region, ID9RKB. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 112 AA;

Alignment Scores:

Pred. No.: 1.19e-57 Length: 112  
 Score: 577.00 Matches: 110  
 Percent Similarity: 98.21% Conservative: 0  
 Best Local Similarity: 98.21% Mismatches: 2  
 Query Match: 97.80% Indels: 0  
 DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x AA06950 (1-112)

QY 1 GATGTAGTAGTACACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20

QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGTAGTAGTGGAAAGACATTTTGAATTGG 120

Db 21 IleSerCysValSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTCAGCAGAGCCAGCCAGTCTCCAGGCCCTAACTATCTGCTGTCTAACTGGAC 180

Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60

QY 181 TCTGAGTCCCTCAGCAGTTTCAGCGCAGTCAGGACAGATTCACACTGAAATC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTATTATTGCTGCAAGGTACACATTTTCG 300

Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100

QY 301 TACACGTTCCGACCAAGGGACCGACTCGAGATCAAG 336

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 12

AAU09922

ID AAU09922 standard; protein; 112 AA.

XX AC AAU09922;

XX 18-JUN-2002 (first entry)

XX DE Humanised ID9 light chain variable region, ID9RKB protein sequence.

KW Human; mouse; ID9 light chain variable region; vasotropic;  
 KW antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;  
 KW insulin-dependent diabetes mellitus; inflammatory bowel disease;  
 KW ulcerative colitis; HP-21/28; graft rejection; allergic disease;  
 KW atipsoiratic; ID9RKB; antiarthritic; nephrotropic; antithyroid;  
 KW restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;  
 KW vascular injury; autoimmune disease; immunoglobulin;  
 KW complementarity determining region; CDR; CD18; CCR2; atherosclerosis;  
 KW mutant; mutein.

OS Homo sapiens.

OS Mus sp.

OS Synthetic.

OS Chimeric.

Key Location/Qualifiers

FT Region 24..39

FT /note= "Complementarity determining region 1 (CDR1), grafted from mouse mAb ID9 light chain sequence (AAU09918)"

FT Misc-difference 41

FT /note= "Substitution of Phe residue normally present in human HF-21/28 sequence (AAU09920) by Leu residue normally present in mouse mAb ID9 light chain sequence (AAU09918)"

FT Misc-difference 42

FT /note= "Substitution of Gln residue normally present in human HF-21/28 sequence (AAU09920) by Leu residue normally present in mouse mAb ID9 light chain sequence (AAU09918)"

FT Region 55..61

FT /note= "Complementarity determining region 2 (CDR2), grafted from mouse mAb ID9 light chain sequence (AAU09918)"

FT Region 94..102

FT /note= "Complementarity determining region 3 (CDR3), grafted from mouse mAb ID9 light chain sequence (AAU09918)"

FT Misc-difference 112 (AAU09918) "  
FT /note= "Addition of Lys residue normally present in mouse  
FT mAb 1D9 sequence and absent in human antibody HF-21/28  
FT sequence (AAU09920) "  
XX  
XX WO200170266-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-US008266.  
XX  
XX 17-MAR-2000; 2000US-00528267.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Horvath CJ, Rao PE;  
XX  
XX WPI; 2001-607511/69.  
XX  
XX Inhibiting stenosis or restenosis of a blood vessel following vascular  
XX injury or angioplasty in a subject by administering agent which inhibits  
XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.  
XX  
XX Claim 32; Fig 17; 108pp; English.  
XX  
XX The present invention relates to a new method of inhibiting stenosis or  
XX restenosis of a blood vessel following vascular injury in a subject. The  
XX new method comprises administering to the subject agents which inhibit  
XX the adhesion and/or recruitment of neutrophils and mononuclear cells to a  
XX site of vascular injury by binding CCR2 or CCR2. The method of the  
XX invention inhibits stenosis or restenosis of a blood vessel following  
XX vascular injury arising from a vascular intervention procedure such as  
XX vascular by-pass or transplantation surgery. The method is also useful  
XX for treating a subject having an inflammatory disease or condition  
XX mediated by neutrophil and mononuclear cell activity e.g. asthma and  
XX graft versus host disease. Chronic inflammatory diseases of the lung,  
XX collagen diseases, and insulin-dependent diabetes mellitus can also be  
XX treated. The method is further useful for treating inflammatory bowel  
XX diseases, such as ulcerative colitis. Additional diseases or conditions  
XX include inflammatory or allergic diseases and conditions, including  
XX systemic anaphylaxis of hypersensitivity responses, drug allergies,  
XX psoriasis and inflammatory dermatoses, autoimmune diseases such as  
XX arthritis, graft rejection and other diseases including atherosclerosis.  
XX The present sequence represents the variable region of one of several  
XX humanised 1D9 light chains (AAU09921-AAU09925). These light chains were  
XX used in the invention for the production of anti-CCR2 antibody or antigen  
XX -binding fragment  
XX  
XX Alignment Scores:  
XX  
XX Pred. No.: 1.19e-57 Length: 112  
XX Score: 577.00 Matches: 110  
XX Percent Similarity: 98.21% Conservative: 0  
XX Best Local Similarity: 98.21% Mismatches: 2  
XX Query Match: 97.80% Indels: 0  
XX DB: 4 Gaps: 0  
XX  
XX US-10-733-563-109 (1-336) x AAU09922 (1-112)  
XX  
XX 1 GATGTAGTGTGACCCAGTCTCCATCTCTTGGCCGTTACCTTGGACAGCCAGCCCTCC 60  
XX  
XX 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
XX  
XX 61 ATCTCTTCAGTCAAGTCAGAGCCCTCTAGTACTGTAGTGGAAAGACATTTTGAATTGG 120  
XX  
XX 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
XX  
XX 121 TTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
XX  
XX 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTCCAGCGGCGAGTCAGGACAGATTCACACTGAAATC 240  
Db |||||||  
61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCGCAGGTACACATTTCCG 300  
Db |||||||  
81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACACGTTCCGACCAAGGAGCCCGACTGGAGATCAAG 336  
Db |||||||  
101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
RESULT 13  
ID AEG75531  
XX AEG75531 standard; protein; 112 AA.  
XX  
XX AEG75531;  
XX  
XX 16-APR-2003 (first entry)  
XX  
XX Humanised mouse mAb 1D9 light chain variable region, 1D9RKBVK.  
XX  
XX Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
XX antigen binding fragment; cellular adhesion molecule; adhesion;  
XX recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
XX percutaneous transluminal coronary angioplasty; PTCA; stent;  
XX vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
XX endovascular stenting; prosthetic valve; transplantation;  
XX inflammatory disease; mastitis; vaginitis; cholecystitis;  
XX chronic bronchitis; asthma; graft-versus-host disease;  
XX chronic inflammatory disease; hypersensitivity pneumonitis;  
XX collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;  
XX insulin dependent; diabetes mellitus; inflammatory bowel disease;  
XX Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
XX allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
XX graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RKBVK;  
XX light chain variable region; VK; complementarity determining region; CDR;  
XX mutant; mutein.  
XX  
XX Mus sp.  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Region 24..39  
XX /note= "Mouse complementarity determining region 1  
XX (CDR1) "  
XX Misc-difference 41..42  
XX /note= "Leu's derived from the mouse 1D9 mAb sequence"  
XX Region 55..61  
XX /note= "Mouse complementarity determining region 2  
XX (CDR2) "  
XX Region 94..102  
XX /note= "Mouse complementarity determining region 3  
XX (CDR3) "  
XX Misc-difference 112  
XX /note= "Lys derived from the mouse 1D9 mAb sequence"  
XX  
XX US2002106369-A1.  
XX  
XX 08-AUG-2002.  
XX  
XX 15-MAR-2001; 2001US-00809739.  
XX  
XX 17-MAR-2000; 2000US-00528267.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Horvath CJ, Rao PE;  
XX  
XX WPI; 2002-697861/75.  
XX  
XX Inhibiting (re)stenosis of blood vessel following vascular injury, by

PT administering first and second agents that inhibit adhesion and/or  
PT recruitment of neutrophils and mononuclear cells, respectively to site of  
PT vascular injury.  
XX  
PS  
PS Claim 32; Fig 17; 59pp; English.

XX The invention discloses a method for inhibiting stenosis or restenosis of  
CC a blood vessel following vascular injury in a subject. The method  
CC involves administering to the subject a first therapeutic agent, which  
CC comprises an antibody or its antigen binding fragment which binds a  
CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
CC of neutrophils to a site of vascular injury and a second therapeutic  
CC agent, which comprises an antagonist of CCR2 function, that inhibits  
CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
CC injury. The vascular injury arises from a vascular intervention procedure  
CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
CC stenting, insertion of a prosthetic valve and transplantation of organs,  
CC tissues or cells. The method is also useful for treating inflammatory  
CC diseases or conditions mediated by early neutrophil activity and later  
CC mononuclear cell activity. Preferably, the method is useful for treating  
CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
CC asthma and graft-versus-host disease, chronic inflammatory disease of  
CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
CC mellitus. The method is also useful for treating inflammatory bowel  
CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
CC (such as arthritis and multiple sclerosis), graft rejection,  
CC atherosclerosis and myositis. The method enables simultaneous inhibition  
CC of neutrophil and mononuclear cell participation in response to vascular  
CC injury or inhibition of neutrophil participation followed by inhibition  
CC of mononuclear cell participation, and thus provides superior therapy for  
CC inhibiting stenosis or restenosis following vascular injury. The sequence  
CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
CC chain variable region (VK), 1D9K8VK, which is comprised of the mouse 1D9  
CC mAb complementarity determining regions (CDR's) linked by human HF-21/28  
CC MAB VK regions with a mouse derived Lys at position 112 and Leu's at  
XX positions 41 and 42

SQ Sequence 112 AA;

Alignment Scores:  
Pred. No.: 1.19e-57 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x ABG75531 (1-112)

QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120  
Db 21 IleSerCysLysSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180  
Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuLeuTyLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGTTACGCGCACTGGATGATGATGATGATGATGATGATGATGATGATG 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 ACAGAGTGGAGCTGAGATCTGGAGTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyTyTyCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTTCGACAGAGGACCCGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 14

ADP98234  
ID ADP98234 standard; protein; 112 AA.

XX AC ADP98234;

XX DT 26-FEB-2004 (first entry)

DE Humanised 1D9 light chain variable region, 1D9RKB V kappa, SEQ ID 4.

KW Immunosuppressive; CCR2 function inhibitor; graft rejection;  
KW graft verses host disease; CC chemokine receptor 2; CCR2;  
KW anti-CCR2 antibody.

XX Synthetic.

OS Mus musculus.

OS Homo sapiens.

XX WO200178653-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US012139.

XX 14-APR-2000; 2000US-00549448.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hancock WW;

XX WPI; 2002-017543/02.

XX Inhibition of rejection of graft e.g. heart or graft verses host disease  
XX involves use of CC chemokine receptor 2 inhibitor.

XX Claim 26; Fig 1; 44pp; English.

XX The present invention relates to a method for inhibiting graft rejection  
XX or graft verses host diseases. The method comprises administration of a  
XX CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
XX recipient of a transplanted graft. The CCR2 function antagonist is an  
XX anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
XX ADP98240-ADP98249). The method is useful for inhibiting rejection,  
XX particularly chronic rejection of a graft, particularly an allograft of  
XX kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
XX inhibiting graft verses host disease for a bone marrow graft.

SQ Sequence 112 AA;

Alignment Scores:  
Pred. No.: 1.19e-57 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x ADP98234 (1-112)

QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20

QY 61 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120

Db 21 IleSerCysLysSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180

Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerIysLeuAsp 60  
 QY 181 TCTGAGTCCCTGACAGGTTTCAGCGCAGTGGATCAGGACAGATTTTCACACTGAAATC 240  
 Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuIysIle 80  
 QY 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATTCCTGGCAAGGTACACATTTTCG 300  
 Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100  
 QY 301 TACAGTTCGACCAAGGACCGACTGGAGATCAAG 336  
 Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleIys 112

## RESULT 15

ADQ89235  
 ID ADQ89235 standard; protein; 112 AA.  
 XX  
 AC ADQ89235;  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Humanised immunoglobulin protein #2.  
 XX  
 KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
 KW inflammatory disease; autoimmune disorder; graft rejection;  
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 KW anti-HIV; virucide; antiarteriosclerotic.  
 XX  
 OS Synthetic.

XX US2004151721-A1.  
 XX  
 XX  
 XX 05-AUG-2004.  
 XX  
 XX 10-DEC-2003; 2003US-00733563.  
 XX  
 XX 19-OCT-2001; 2001US-0350166P.  
 PR 26-JUN-2002; 2002US-0392364P.  
 PR 17-OCT-2002; 2002US-00272899.  
 XX  
 XX (OKEE/) O'KEEFE T.  
 PA (PONA/) PONA P.  
 PA  
 PI O'keefe T, Ponath P;  
 XX  
 XX WPI; 2004-580175/56.  
 DR  
 XX  
 XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
 PT useful for diagnosing and/or treating inflammatory or autoimmune  
 PT diseases, and HIV infection.  
 XX  
 XX Example 2; SEQ ID NO 13; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a humanised  
 CC immunoglobulin protein of the invention.

XX Sequence 112 AA;

## Alignment Scores:

Pred. No.: 1.19e-57 Length: 112  
 Score: 577.00 Matches: 110  
 Percent Similarity: 98.21% Conservative: 0  
 Best Local Similarity: 98.21% Mismatches: 2

Query Match: 97.80% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-733-563-109 (1-336) x ADQ89235 (1-112)  
 QY 1 GATCTAGTATGATGACCCAGTCTCCACTCTCTTGGCCGTTACCCCTTGGACAGCCAGCTCC 60  
 Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
 QY 61 ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
 Db 21 ILeSerCysIysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnIrp 40  
 QY 121 TTTTCAGCAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTTAAACTGGAC 180  
 Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60  
 QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGAGTGGATCAGGACAGATTTTCACACTGAAATC 240  
 Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
 QY 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCG 300  
 Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100  
 QY 301 TACAGTTCGACCAAGGACCGACTGGAGATCAAG 336  
 Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleIys 112

Search completed: January 28, 2006, 08:33:32  
 Job time : 53.4685 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:20:11 ; Search time 9.16516 Seconds  
(without alignments)  
7054.719 Million cell updates/sec

Title: US-10-733-563-109

Perfect score: 590

Sequence: 1 gatgtagtgtgaccagtc.....ggaccgcgactggagatcaag 336

Scoring table: BLOSUMP62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-Q=/csm2\_1/USPTO\_spool\_p/US10733563/runat\_27012006.180006.4797/app\_query.fasta\_1.2716  
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1.83 @runat\_27012006.180006.4797 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:\*\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	531	90.0	113	2 F30560	Ig kappa chain V r
2	530	89.8	132	2 C32513	Ig kappa chain pre
3	526	89.2	133	2 S23230	Ig kappa chain pre
4	526	89.2	142	2 S22902	Ig kappa chain V r
5	517	87.6	112	2 A36259	Ig kappa chain V r
6	514	87.1	133	1 K2HURP	Ig kappa chain pre
7	513.5	87.0	114	2 S49572	Ig kappa chain pre
8	512	86.8	111	2 S20709	Ig kappa chain V r
9	512	86.8	112	2 A55491	Ig kappa chain V r
10	506	85.8	133	1 A24452	proteolytic antibo
11	505.5	85.7	140	2 S22658	Ig kappa chain pre
12	505	85.6	133	2 S40324	Ig kappa chain pre
13	503	85.3	131	2 S31577	Ig kappa chain V r
14	501	84.9	112	2 PL0273	Ig kappa chain V r

15	501	84.9	133	2	S42611	HUNVK protein prec
16	499	84.6	118	2	S40374	Ig kappa chain - h
17	499	84.6	122	2	S40338	Ig kappa chain - h
18	496.5	84.2	114	2	B49002	Ig kappa chain V r
19	491	83.2	132	2	S40322	Ig kappa chain - h
20	488	82.7	101	2	A37330	Ig kappa chain V r
21	477	80.8	126	2	S40312	Ig kappa chain - h
22	470	79.7	120	2	S42268	Ig kappa chain V r
23	470	79.7	120	2	S42267	Ig kappa chain V r
24	461.5	78.2	134	2	S40376	Ig kappa chain - h
25	457	77.5	103	2	PH1056	Ig light chain V r
26	457	77.5	112	2	A31807	Ig kappa chain V r
27	456	77.3	103	2	PH1055	Ig light chain V r
28	456	77.3	219	2	S16112	Ig kappa chain V r
29	454	76.9	115	2	S38715	Ig kappa chain V r
30	452	76.6	131	2	B39276	Ig kappa chain V r
31	450	76.3	113	1	K2HUTW	Ig light chain pre
32	449	76.1	113	1	K2HUTR	Ig kappa chain V-I
33	448.5	76.0	130	2	S40321	Ig kappa chain V-I
34	448	75.9	113	2	PL0203	Ig kappa chain - h
35	447	75.8	114	2	A32967	anti-DNA autoantib
36	446	75.6	112	2	E27887	Ig kappa chain V-I
37	445	75.4	91	2	S42186	Ig kappa chain V r
38	445	75.4	131	2	B32513	Ig kappa chain pre
39	444	75.3	219	2	S52028	Ig kappa chain - m
40	443	75.1	111	2	PL0257	Ig kappa chain V r
41	443	75.1	112	2	S58207	Ig light chain V r
42	443	75.1	131	2	B30577	Ig kappa chain pre
43	443	75.1	136	2	S40357	Ig kappa chain V-J
44	442.5	75.0	115	1	K2HUCM	Ig kappa chain V-I
45	442	74.9	115	2	S60066	Ig kappa chain V r

ALIGNMENTS

RESULT 1

F30560  
Ig kappa chain V region (28.4.10A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C:Accession: F30560  
R:Matseuda, T.; Kabat, E.A.  
J. Immunol. 142, 863-870, 1989  
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclon

A:Reference number: A30560; MUID:89110062; PMID:2464028

A:Accession: F30560

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAT>

A:Cross-references: UNIPARC:UPI0000114E24; GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:				
Pred. No.:	7.63e-48	Length:	113	
Score:	531.00	Matches:	99	
Percent Similarity:	95.54%	Conservative:	8	
Best Local Similarity:	88.39%	Mismatches:	5	
Query Match:	90.00%	Indels:	0	
DB:	2	Gaps:	0	

US-10-733-563-109 (1-336) x F30560 (1-113)

Qy	1	GATGTAGTATGACCCAGTCTCCCTGCGCTTACCTTGACGACGACCTCC	60
Db	1	AspValValMetThrGlnIleProLeuSerValThrIleGlyGlnProAlaSer	20
Qy	61	ATCTCTTCAGTCAAGTCAGAGCTCTTAGATAGTGAAGACATTTTGAATGG	120
Db	21	IleSerCysLysSerSerGlnSerLeuAspSerAspGlyLysThrTyrLeuAsnTrp	40

QY 121 TTTCCAGCAGCGCCAGCCAGTCTCCAGAGCGCCTAATCTATCTGCTCTAARACTGCAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 60  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 TCTGGAGTCCCTGCACAGGTTTCAGCGGCAGTGGATCAGGCAGACAGATTTTCACACTGAAAATC 240  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 AGCAGAGTGAGGCTGAGAGTGTGGAGTTTATTTATTTGCTGGCAAGGTACACATTTTCCG 300  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 TACACGTTCCGACAAAGGACCCGACTCGAGATCAAG 336  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 101 HisThrPheGlyGlyThrLysLeuGluIleLys 112  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
RESULT 2  
C32513  
Ig kappa chain precursor V region (BXW14) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C:Accession: C32513  
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
J. Clin. Invest. 82, 852-860, 1988  
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A:Reference number: A94689; MUID: 88331394; PMID:3138286  
A:Accession: C32513  
A:Molecule type: DNA  
A:Residues: 1-132 <KOF>  
A:Cross-references: UNIPARC:UPI0000114D99; GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 9.75e-48 Length: 132  
Score: 530.00 Matches: 99  
Percent Similarity: 95.54% Conservative: 8  
Best Local Similarity: 88.39% Mismatches: 5  
Query Match: 89.83% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-109 (1-336) x C32513 (1-132)  
QY 1 GATGTAGTAGACCCAGTCTCCAGGCGCCTAATCTATCTGCTCTAARACTGCAC 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
21 AspValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 40  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 ATCTCTTGCAGTCAAGTCAAGGCTCTTAGATAGTAGTATGGAAGACATTTTGAATGG 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 41 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrTyrLeuAsnTrp 60  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 TTTCCAGCAGCGCCAGCCAGTCTCCAGGCGCCTAATCTATCTGCTCTAARACTGCAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 80  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 TCTGGAGTCCCTGCACAGGTTTCAGCGGCAGTGGATCAGGCAGACAGATTTTCACACTGAAAATC 240  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 81 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 100  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 AGCAGAGTGAGGCTGAGAGTGTGGAGTTTATTTATTTGCTGGCAAGGTACACATTTTCCG 300  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 101 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 TACACGTTCCGACAAAGGACCCGACTCGAGATCAAG 336  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 ArgThrPheGlyGlyThrLysLeuGluIleLys 132  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
RESULT 3  
S23230  
Ig kappa chain precursor V-J region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S23230  
R:Kennedy, M.A.  
J. Exp. Med. 173, 1033-1036, 1991  
A:Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and lig  
A:Reference number: S23230; MUID:91178438; PMID:1840606  
A:Accession: S23230  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <KEN>  
A:Cross-references: UNIPARC:UPI0000115EA9; EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:  
C:Genetics:  
A:Introns: 17/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 2.57e-47 Length: 133  
Score: 526.00 Matches: 101  
Percent Similarity: 93.75% Conservative: 4  
Best Local Similarity: 90.18% Mismatches: 7  
Query Match: 89.15% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-109 (1-336) x S23230 (1-133)  
QY 1 GATGTAGTAGACCCAGTCTCCAGGCGCCTAATCTATCTGCTCTAARACTGCAC 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 ATCTCTTGCAGTCAAGTCAAGGCTCTTAGATAGTAGTATGGAAGACATTTTGAATGG 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 41 IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrHisLeuAsnTrp 60  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 TTTCCAGCAGCGCCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGCTCTAARACTGCAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 PheGlnGlnArgProGlyGlnSerProArgGluIleTyrLysValSerAsnArgasp 80  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 TCTGGAGTCCCTGCACAGGTTTCAGCGGCAGTGGATCAGGCAGACAGATTTTCACACTGAAAATC 240  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 AGCAGAGTGAGGCTGAGAGTGTGGAGTTTATTTATTTGCTGGCAAGGTACACATTTTCCG 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 TACACGTTCCGACAAAGGACCCGACTCGAGATCAAG 336  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 TyrThrPheGlyGlnGlyThrLysLeuGluIleLys 132  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
RESULT 4  
S22902  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S22902  
R:Chastagner, P.; Theze, J.; Zouali, M.  
Gene 101, 305-306, 1991  
A:Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region usi  
A:Reference number: S22902; MUID:91276289; PMID:1905262  
A:Accession: S22902  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-142 <CHA>  
A:Cross-references: UNIPARC:UPI0000176CAB; EMBL:X56510  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-126/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 2.58e-47 Length: 142  
Score: 526.00 Matches: 100  
Percent Similarity: 94.59% Conservative: 5

Best Local Similarity: 90.09% Mismatches: 6  
Query Match: 89.15% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x S22902 (1-142)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGGTTACCTTGGACAGCCAGCTCC 60  
DB 32 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 51  
QY 61 ATCTCTTCAAGTCAAGTCAAGTCTCTAGATAGTGTGAAAGACATTTTGAATGG 120  
DB 52 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 71  
QY 121 TTTTACAGAGCCAGGCCAGTCTCAAGGCCCTTAATCTATCTGGTGTCTAAACTGGAC 180  
DB 72 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 91  
QY 181 TCTGGAGTCCCTGACAGGTTTCAAGCGGAGTGTGATCAGGACAGATTCACACTGAAATC 240  
DB 92 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 111  
QY 241 AGCAGAGTGGAGCTGAGATCTTGGAGTTTATTATTGCTGCAAGGTACACATTTTCG 300  
DB 112 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 131  
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATC 333  
DB 132 PheThrPheGlyGlnGlyThrArgLeuGluile 142

## RESULT 5

A36259  
Ig kappa chain V region (TE34) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 21-Jan-2000  
C:Accession: A36259  
R:Zilber, B.; Scherff, T.; Levitt, M.; Anglistter, J.  
Biochemistry 29, 10032-10041, 1990  
A:Title: NMR-derived model for a peptide-antibody complex.  
A:Reference number: A36259; MUID:91104915; PMID:2271636  
A:Accession: A36259  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <ZIL>  
A:Cross-references: UNIPARC:UPI000176AFD; GB:M30459; GB:M30480; GB:M30481; G  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2,286-46 Length: 112  
Score: 517.00 Matches: 97  
Percent Similarity: 93.75% Conservative: 8  
Best Local Similarity: 86.61% Mismatches: 7  
Query Match: 87.63% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x A36259 (1-112)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTTGGCGGTTACCTTGGACAGCCAGCTCC 60  
DB 1 AspValValMetIleGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAAGTCTCTAGATAGTGTGAAAGACATTTTGAATGG 120  
DB 21 IleSerCysLysSerSerGlnSerLeuAspSerAspGlyLysThrTyrLeuAsnTrp 40  
QY 121 TTTTACAGAGCCAGGCCAGTCTCAAGGCCCTTAATCTATCTGGTGTCTAAACTGGAC 180  
DB 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGGAGTCCCTGACAGGTTTCAAGCGGAGTGTGATCAGGACAGATTCACACTGAAATC 240

DB 61 SerGlyValProThrArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysile 80  
QY 241 AGCAGAGTGGAGCTGAGATGTTGAGTATTTATTGTCGCAAGGTACACATTTTCG 300  
DB 81 SerArgValGluAlaGluAspGlyGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336  
DB 101 TrpThrPheGlyGlyGlyThrLysLeuGluileLys 112  
RESULT 6  
K2HURP  
Ig kappa chain precursor V-II region (RPMI) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C:Accession: A01890  
R:Klobeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zachau, H.G.  
Nucleic Acids Res. 13, 6499-6513, 1985  
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.  
A:Reference number: A93588; MUID:86041852; PMID:2997711  
A:Accession: A01890  
A:Molecule type: DNA  
A:Residues: 1-133 <KLO>  
A:Cross-references: UNIPROT:P06310; UNIPARC:UPI000012E159  
A:Note: the sequence was determined from the differentiated gene  
C:Genetics:  
A:Gene: GDB:IGKV2  
A:Cross-references: GDB:136265  
A:Map position: 2p12-2p12  
A:Introns: 17/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a;

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MNT>  
F:21-43/Region: framework 1  
F:36-115/Domain: immunoglobulin homology <IMM>  
F:44-59/Region: complementarity-determining 1  
F:60-74/Region: framework 2  
F:75-81/Region: complementarity-determining 2  
F:82-113/Region: framework 3  
F:114-122/Region: complementarity-determining 3  
F:123-133/Region: framework 4  
F:43-113/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 4,74e-46 Length: 133  
Score: 514.00 Matches: 98  
Percent Similarity: 93.75% Conservative: 7  
Best Local Similarity: 87.50% Mismatches: 7  
Query Match: 87.12% Indels: 0  
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x K2HURP (1-133)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTTGGCGGTTACCTTGGACAGCCAGCTCC 60  
DB 21 AspValValMetThrGlnSerProLeuSerLeuValThrLeuGlyGlnProAlaSer 40  
QY 61 ATCTCTTCAAGTCAAGTCAAGTCTCTAGATAGTGTGAAAGACATTTTGAATGG 120  
DB 41 IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60  
QY 121 TTTTACAGAGCCAGGCCAGTCTCCAGGCCCTTAATCTATCTGGTGTCTAAACTGGAC 180  
DB 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80  
QY 181 TCTGGAGTCCCTGACAGGTTTCAAGCGGAGTGTGATCAGGACAGATTCACACTGAAATC 240  
DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
QY 241 AGCAGAGTGGAGCTGAGATGTTGAGTATTTATTGTCGCAAGGTACACATTTTCG 300

Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpSer 120  
:::|||||  
Qy 301 TACAGTTCGACCAAGGACCCGACTGGAGATCAAG 336  
:::|||||  
Db 121 TrpThrPheGlyGlnGlyThrLysValGluLeuLys 132  
:::|||||  
RESULT 7  
S49572  
Ig kappa chain precursor - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1995 #sequence\_revision 14-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S49572  
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.  
submitted to the EMBL Data Library, November 1994  
A;Description: K+1 dual receptor B cells are present in the human peripheral repertoire  
A;Reference number: S49571  
A;Accession: S49572  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-114 <GTA>  
A;Cross-references: UNIPARC:UPI0000116709; EMBL:Z46626; NID:9575261; PIDN:CAA96596.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-95/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 5.34e-46 Length: 114  
Score: 513.50 Matches: 99  
Percent Similarity: 93.81% Conservative: 7  
Best Local Similarity: 87.61% Mismatches: 6  
Query Match: 87.03% Indels: 1  
DB: 2 Gaps: 1  
US-10-733-563-109 (1-336) x S49572 (1-114)  
Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGCGTACCCCTTGACAGCCAGCTCC 60  
Db 1 AspValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCCTTTAGATAGTATGATGATGAAAGACATTTTGAATGG 120  
Db 21 IleSerCysArgSerSerGlnSerLeuValTyrThrAspGlyAenThrTyrLeuAsnTrp 40  
Qy 121 TTTCCAGCAGAGGCCAGCCAGTCTCCAGGCGCTATCTATCTGCTGCTTAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgLeuLeuIleTyrLysValSerAsnArgAsp 60  
Qy 181 TCTGGAGTCCCTCAGACGTTCCAGCGCAGTGGATCAGGACAGATTTTACACTGAAAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTATATTATTTGCTGGCAGGTACACATTTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyIleTyrCysIleGlnGlyThrHisTrpPro 100  
Qy 301 ---TACAGTTCGACCAAGGACCCGACTGGAGATCAAG 336  
Db 101 GlnTyrThrPheGlyGlnGlyThrLysLeuGluLeuLys 113  
RESULT 8  
S20709  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S20709  
R;Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osh  
submitted to the EMBL Data Library, April 1992  
A;Description: Binding specificity and variable region sequences of two monoclonal anti  
A;Reference number: S20706  
A;Accession: S20709  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-111 <BRE>

A;Cross-references: UNIPARC:UPI00001163E1; EMBL:Z11917; NID:952655; PIDN:CAA77975.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 7.68e-46 Length: 111  
Score: 512.00 Matches: 95  
Percent Similarity: 93.69% Conservative: 9  
Best Local Similarity: 85.59% Mismatches: 7  
Query Match: 86.78% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-109 (1-336) x S20709 (1-111)  
Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGCGTACCCCTTGACAGCCAGCTCC 60  
Db 1 AspIleGlnLeuThrGlnSerProLeuThrLeuSerValThrIleGlyGlnProAlaSer 20  
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCCTTTAGATAGTATGATGATGAAAGACATTTTGAATGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuHisSerAspGlyLysThrTyrLeuAsnTrp 40  
Qy 121 TTTCCAGCAGAGGCCAGCCAGTCTCCAGGCGCTATCTATCTGCTGCTTAACTGGAC 180  
Db 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuLeuIleTyrLeuValSerLysLeuAsp 60  
Qy 181 TCTGGAGTCCCTCAGACGTTCCAGCGCAGTGGATCAGGACAGATTTTACACTGAAAAATC 240  
Db 61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTATATTATTTGCTGGCAGGTACACATTTTCCG 300  
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
Qy 301 TACAGTTCGACCAAGGACCCGACTGGAGATC 333  
Db 101 GlnThrPheGlyGlyThrLysLeuGluLeu 111  
RESULT 9  
A55491  
proteolytic antibody light chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A55491  
R;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.;  
J. Biol. Chem. 269, 32389-32393, 1994  
A;Title: Molecular cloning of a proteolytic antibody light chain.  
A;Reference number: A55491; MUID:95096089; PMID:7798238  
A;Accession: A55491  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <GAO>  
A;Cross-references: UNIPROT:Q8K0P8; UNIPARC:UPI0000176CCE; GB:L34775  
A;Note: authors translated the codon TAT for residue 37 as Thr  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-95/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 7.69e-46 Length: 112  
Score: 512.00 Matches: 96  
Percent Similarity: 93.75% Conservative: 9  
Best Local Similarity: 85.71% Mismatches: 7  
Query Match: 86.78% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-109 (1-336) x A55491 (1-112)  
Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGCGTACCCCTTGACAGCCAGCTCC 60  
Db 1 AspValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 20  
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCCTTTAGATAGTATGATGATGAAAGACATTTTGAATGG 120



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Db 21 ILeSerCysLysSerSerGlnSerLeuLeuHisThrAspGlyLysThrTyrLeuIleTrp 40
Qy 121 TTTGACGACAGCCAGGCGCAGTCTCCAGGCGCCCTAAATCTATCTGCTGCTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 60
Qy 181 TCTGGAGTCCCTGACAGTTCTCAGCGGCGAGTGGATCAGGACAGAGATTTCCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATCTGCTGCGCAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAGGACCCGACTCGGAGATCAAG 336
Db 101 GlnThrPheGlyGlyGlyThrLysLeuGluLys 112
RESULT 10
Ig kappa chain precursor V-II region (RPMI 6410) - human
A:Species: Homo sapiens (man)
C:Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: A24452
R:Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A:Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A:Reference number: A24452; MUID:86232631; PMID:3086847
A:Accession: A24452
A:Molecule type: DNA
A:Residues: 1-133 <WEI>
A:Cross-references: UNIPARC:UPI0000113B46; GB:M36859; NID:G185932; PID:AAA58920.1; PID:
A:Note: this sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted
Alignment Scores:
Pred. NO.: 3.3e-45 Length: 133
Score: 506.00 Matches: 97
Percent Similarity: 92.86% Conservative: 7
Best Local Similarity: 86.61% Mismatches: 8
Query Match: 85.76% Indels: 0
DB: 1 Gaps: 0
US-10-733-563-109 (1-336) x A24452 (1-133)
Qy 1 GATCTAGTGTGACCCAGTCTCCACTCTCCTTGGCCGTTACCTTGGACAGCCGCTCC 60
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
Qy 61 ATCTCTTGCAGTCAAGTCCAGTCTCTAGATAGTGTGATGAAAGACATTTTGAATGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 60
Qy 121 TTTGACGAGGCGCAGGCTCTCCAGGCGCTCTCTATCTATCTGCTGCTTAAACTGGAC 180
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrArgValSerAsnArgAsp 80
Qy 181 TCTGGAGTCCCTGACAGTTCAGGCGGAGTGGATCAGGACAGATTTCCACACTGAAATC 240
Db 81 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 100
Alignment Scores:
Pred. NO.: 3.3e-45 Length: 133
Score: 506.00 Matches: 97
Percent Similarity: 92.86% Conservative: 7
Best Local Similarity: 86.61% Mismatches: 8
Query Match: 85.76% Indels: 0
DB: 1 Gaps: 0
US-10-733-563-109 (1-336) x A24452 (1-133)
Qy 1 GATCTAGTGTGACCCAGTCTCCACTCTCCTTGGCCGTTACCTTGGACAGCCGCTCC 60
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
Qy 61 ATCTCTTGCAGTCAAGTCCAGTCTCTAGATAGTGTGATGAAAGACATTTTGAATGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 60
Qy 121 TTTGACGAGGCGCAGGCTCTCCAGGCGCTCTCTATCTATCTGCTGCTTAAACTGGAC 180
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80
Qy 181 TCTGGAGTCCCTGACAGTTCAGGCGGAGTGGATCAGGACAGATTTCCACACTGAAATC 240
Db 81 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 100
```

```
Qy 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATCTGCTGCGCAAGGTACACATTTCCG 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpSer 120
Qy 301 TACAGTTCGGACAGGACCCGACTCGGAGATCAAG 336
Db 121 TrpThrPheGlyGlnGlyThrLysValGluIleLys 132
RESULT 11
S22658
Ig kappa chain precursor V region (0-81VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 31-Dec-2004
C:Accession: S22658
R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as
A:Reference number: S22657; MUID:92285150; PMID:1598223
A:Accession: S22658
A:Molecule type: mRNA
A:Residues: 1-140 <HIR>
A:Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI00001769CF; EMBL:X59135
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. NO.: 3.73e-45 Length: 140
Score: 505.50 Matches: 99
Percent Similarity: 92.04% Conservative: 5
Best Local Similarity: 87.61% Mismatches: 8
Query Match: 85.68% Indels: 1
DB: 2 Gaps: 1
US-10-733-563-109 (1-336) x S22658 (1-140)
Qy 1 GATCTAGTGTGACCCAGTCTCCACTCTCCTTGGCCGTTACCTTGGACAGCCGCTCC 60
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
Qy 61 ATCTCTTGCAGTCAAGTCCAGTCTCTAGATAGTGTGATGAAAGACATTTTGAATGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 60
Qy 121 TTTGACGAGGCGCAGGCTCTCCAGGCGCTCTCTATCTATCTGCTGCTTAAACTGGAC 180
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrArgValSerAsnArgAsp 80
Qy 181 TCTGGAGTCCCTGACAGTTCAGGCGGAGTGGATCAGGACAGATTTCCACACTGAAATC 240
Db 81 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 100
Qy 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATCTGCTGCGCAAGGTACACATTTT 297
Db 101 SerArgValGluAlaGluAspValGlyLeuTyrCysMetGlnHisThrHisTrpSer 120
Qy 298 CCGTACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
Db 121 ProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 133
RESULT 12
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
```



QY 241 AGCAGAGTGGAGGCTGAGAGTTCAGATTATTTGCTGCAAGGTACACATTTTCG 300  
|||||  
Db 81 SerArgValGluAlaGluAsePLeuGlyValTyrCysValGlnGlyThrHisPhePro 100  
|||||  
QY 301 TACAGGTTCCGACACAGGACCCGACTGAGATCAAG 336  
|||||  
Db 101 TrpThrPheGlyGlyThrLysLeuGluIleLys 112  
|||||

## RESULT 15

S42611  
HUNVK protein precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42611  
R:Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.  
J. Neuroimmunol. 36, 29-39, 1992  
A:Title: DNA sequence analysis and comparison of the variable heavy and light chain regi  
A:Reference number: S42610; MUID:92138794; PMID:1370957  
A:Accession: S42611  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <SPA>  
A:Cross-references: UNIPARC:UPI000011378B; EMBL:X54137; NID:G433889; PIDN:CNA38072.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:36-115/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1..11e-44	Length:	133
Scores:	501.00	Matches:	95
Percent Similarity:	91.89%	Conservative:	7
Best Local Similarity:	85.59%	Mismatches:	9
Query Match:	84.92%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-109 (1-336) x S42611 (1-133)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTTGGCCGTTACCCCTTGGACAGCCGCTCC 60  
|||||  
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40  
|||||  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTATGAGAAAGACATTTTGAATTGG 120  
|||||  
Db 41 IleSerCysArgSerSerGlnSerLeuValPheSerAspGlyAsnThrTyrLeuAsnTrp 60  
|||||  
QY 121 TTTCAGACAGGCCAGGCCAGTCTCAAGGCCCTAATCTATCTGCTGTCTAAACTGGAC 180  
|||||  
Db 61 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 80  
|||||  
QY 181 TCTGGAGTCCCTGACAGGTTCAAGCGGCGAGTGATCAGGGACAGATTTCACACTGAAATC 240  
|||||  
Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100  
|||||  
QY 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTGCTGCAAGGTACACATTTTCG 300  
|||||  
Db 101 SerArgValGluAlaGluAsePLeuGlyIleTyrCysMetGlnGlyAlaHisTrpPro 120  
|||||  
QY 301 TACAGGTTCCGACACAGGACCCGACTGAGATC 333  
|||||  
Db 121 LeuThrPheGlyGlyThrLysValGluIle 131  
|||||

Search completed: January 28, 2006, 08:45:57  
Job time : 11.1652 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 ; Search time 51.5435 Seconds  
(without alignments)  
9198.340 Million cell updates/sec

Title: US-10-733-563-109

Perfect score: 590

Sequence: 1 gatgtagtgtaccagtc.....ggaccgactggagatcaag 336

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DEV=xlp  
-Q=/cgn2.1/USPTO\_spool\_p/US10733563/runat\_27012006\_180005\_4782/app query.fasta.1.2716  
-DB=UniProt -QMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563\_QCGN.1.1.632 @runat\_27012006\_180005\_4782 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	87.1	133	1 KV2P_HUMAN	P06310 homo sapien
2	511	86.6	239	2 QTCDO_HUMAN	Q8CDD0 homo sapien
3	496.5	84.2	114	2 Q9UL80_HUMAN	Q9UL80 homo sapien
4	491	83.2	239	2 Q58E08_MOUSE	Q58E08 mus musculus
5	459	77.8	239	2 Q6P491_HUMAN	Q6P491 homo sapien
6	450	76.3	113	1 KV2D_HUMAN	P01617 homo sapien
7	449	76.1	113	1 KV2B_HUMAN	P01615 homo sapien
8	447	75.8	239	2 Q9NEK0_HUMAN	Q9NEK0 homo sapien
9	445	75.4	248	2 Q65ZQ7_9MURI	Q65ZQ7 mus sp. b3(
10	442.5	75.0	115	1 KV2A_HUMAN	P01614 homo sapien
11	438	74.2	117	1 KV2E_HUMAN	P06309 homo sapien
12	430.5	73.0	115	2 Q5F2I0_MOUSE	Q5F2I0 mus musculus
13	430	72.9	113	1 KV2G_MOUSE	P01631 mus musculus
14	428	72.5	112	2 Q53VP8_MOUSE	Q53VP8 mus musculus
15	418	70.8	219	2 Q65ZC0_MOUSE	Q65ZC0 mus musculus
16	417.5	70.8	240	2 Q6PIH6_HUMAN	Q6PIH6 homo sapien

17	411	69.7	234	2 Q5XKG4_MOUSE	Q5XKG4 mus musculus
18	405.5	68.7	112	1 KV2C_HUMAN	P01616 homo sapien
19	402	68.1	113	1 KV2E_MOUSE	P03976 mus musculus
20	397	67.3	113	1 KV2C_MOUSE	P01628 mus musculus
21	396	67.1	112	1 KV2D_MOUSE	P01629 mus musculus
22	396	67.1	113	1 KV2F_MOUSE	P01630 mus musculus
23	390	66.1	112	1 KV2A_MOUSE	P01626 mus musculus
24	390	66.1	112	2 Q6LEM8_MOUSE	Q6LEM8 mus musculus
25	386.5	65.5	134	1 KV4C_HUMAN	P06314 homo sapien
26	385.5	65.3	108	1 KV1CANFA	P01618 canis fami
27	380.5	64.5	114	1 KV4A_HUMAN	P01625 homo sapien
28	378.5	64.2	111	1 KV3L_MOUSE	P01664 mus musculus
29	378.5	64.2	111	1 KV3M_MOUSE	P01665 mus musculus
30	377.5	64.0	111	1 KV3O_MOUSE	P01667 mus musculus
31	372.5	63.0	111	1 KV3Q_MOUSE	P01669 mus musculus
32	371.5	63.0	111	1 KV3N_MOUSE	P01665 mus musculus
33	370	62.7	86	2 Q723Y5_HUMAN	Q723Y5 homo sapien
34	368.5	62.5	111	1 KV3H_MOUSE	P01660 mus musculus
35	366	62.0	110	1 KV3P_MOUSE	P01668 mus musculus
36	365.5	61.9	111	1 KV3J_MOUSE	P01662 mus musculus
37	364.5	61.8	111	2 Q811U6_MOUSE	Q811U6 mus musculus
38	363	61.5	120	1 KV2B_MOUSE	P01627 mus musculus
39	361.5	61.3	111	2 Q920E9_MOUSE	Q920E9 mus musculus
40	360.5	61.1	131	1 KV3I_MOUSE	P01661 mus musculus
41	360.5	61.1	255	2 Q6KB05_MOUSE	Q6KB05 mus musculus
42	359	60.8	133	1 KV4B_HUMAN	P06313 homo sapien
43	356.5	60.4	111	1 KV3K_MOUSE	P01663 mus musculus
44	356.5	60.4	111	1 KV3U_MOUSE	P01673 mus musculus
45	355.5	60.3	240	2 Q52L64_MOUSE	Q52L64 mus musculus

ALIGNMENTS

RESULT 1  
KV2P\_HUMAN  
ID KV2P\_HUMAN STANDARD; PRT; 133 AA.  
AC P06310;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-II region RPMI 6410 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86041852; PubMed=2997711;  
RA Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;  
RT "Human immunoglobulin kappa light chain genes of subgroups II and  
RT III.";  
RL Nucleic Acids Res. 13:6499-6513(1985).

-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
-----  
CC EMBL; Z00020; CAA77315.1; -; Genomic\_DNA.  
CC PIR; A01890; K2HURP.  
CC HSSP; Q99M37; 1191.  
CC SMR; P06310; 21-133.  
CC Ensembl; ENSG00000173758; Homo sapiens.  
CC GO; GO:0005576; C:extracellular region; NAS.  
CC GO; GO:0003823; P:antigen binding; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003596; Ig\_v.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS00835; IG LIKE; 1.  
CC Immunoglobulin domain; Immunoglobulin V region; Signal.

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FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
FT REGION 21 43 Framework-1.
FT REGION 44 59 Complementarity-determining-1.
FT REGION 60 74 Framework-2.
FT REGION 75 81 Complementarity-determining-2.
FT REGION 82 113 Framework-3.
FT REGION 114 122 Complementarity-determining-3.
FT REGION 123 132 Framework-4.
FT DISULFID 43 113 By similarity.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009BE CRC64;

Alignment Scores:
Pred. No.: 2,37e-53 Length: 133
Score: 514.00 Matches: 98
Percent Similarity: 93.75% Conservativeness: 7
Best Local Similarity: 87.50% Mismatches: 7
Query Match: 87.12% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x KV2P_HUMAN (1-133)
QY 1 GATGTAGTGTGACCCAGTCTCCACTCTCTGTGCGGTACCTTGGACAGCCAGCTCC 60
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProLaser 40
QY 61 ATCTCTTGAAGTCAAGTCAAGCTCTTAGATAGTATGATGAAAGACATTTTGAATGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60
QY 121 TTTTCAGCAGAGGCCAGCCAGTCTCCAGGCGCTTATCTATCTGCTGTTAACTCGAC 180
Db 61 PheGlnGlnArgProGlyGlnSerProArgGluLeuIleTyrLysValSerAsnArgAsp 80
QY 181 TCTGTAGTCTCCGTGACAGGTTTCAGCGGCGATGATCAGGACAGATTTTCACACTCAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100
QY 241 AGCAGATGAGGCTGAGAGTGTGGAGTTTATATTATTTGCTGGCAAGTACACATTTCCG 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpSer 120
QY 301 TACAGTTCGACAGAGGACCCGACTCGAGATCAAG 336
Db 121 TrpThrPheGlnGlyThrLysValGluIleLys 132
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## RESULT 2

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Q8TCD0_HUMAN
ID Q8TCD0_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Narasina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
```

```
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus
RT nephritis-associated idiotype."
RL Nucleic Acids Res. 20:2601-0(1992).
[4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1551402;
RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
RA Thiebe R., Zocher I., Zachau H.G.;
RT "The human immunoglobulin kappa locus. Characterization of the
RT duplicated A regions."
RL Eur. J. Immunol. 22:1023-1029(1992).
[5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation."
RL Eur. J. Immunol. 23:3248-3262(1993).
[6]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; BC022362; AAH22362.1; -, mRNA.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; I17Z.
DR SMR; Q8TCD0; 21-237.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 239 AA; 26235 MW; FACEDC3A3B03871D CRC64;
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## Alignment Scores:

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Pred. No.: 6,12e-53 Length: 239
Score: 511.00 Matches: 97
Percent Similarity: 93.75% Conservativeness: 8
Best Local Similarity: 86.61% Mismatches: 7
Query Match: 86.61% Indels: 0
DB: 2 Gaps: 0
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US-10-733-563-109 (1-336) x Q8TCD0\_HUMAN (1-239)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGCCGTTACCTTGGACAGCCAGCTCC 60  
 DB |||||  
 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40  
 QY 61 ATCTCTTCAAGTCAAGTCAGAGCCCTTCTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
 DB |||||  
 41 IleSerCysArgSerThrGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60  
 QY 121 TTTTACAGCAGAGCCAGGCGAGTCTCAAGGCGCTTAATCTATCTGCTGCTCAAACTGCAC 180  
 DB |||||  
 61 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 80  
 QY 181 TCTGGAGTCCCTGACAGGTCAGCGCGAGTCAGTGCAGGAGCAGATTTTCACTGAAATC 240  
 DB |||||  
 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100  
 QY 241 AGCAGAGTGGAGGCTGAGATGTTGGAGTTTATTTCTGCTGCGAAGGTACACATTTCCG 300  
 DB |||||  
 101 ThrArgValGluAlaGluAspValGlyValTyrPheCysMetGlnGlyThrHisTrpPro 120  
 QY 301 TACAGCTTTCGACAGAGGACCGAGCTGCGAGATCAAG 336  
 DB |||||  
 121 SerThrPheGlyGlnGlyThrLysLeuGluLysile 132

RESULT 3

Q9UL80\_HUMAN  
 ID Q9UL80\_HUMAN PRELIMINARY; PRT; 114 AA.  
 AC Q9UL80;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1322670;  
 RA Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,  
 RA Gaskin F., Fu S.M.;  
 RT "A rheumatoid factor from a normal individual encoded by VH2 and V  
 RT kappa II gene segments";  
 RL Arthritis Rheum. 35:900-904(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8436174;  
 RA Wagner S.D., Iuzzatto L.;  
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
 RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1601042;  
 RA Huber C., Klobeck H.G., Zachau H.G.;  
 RT "Ongoing V kappa-J kappa recombination after formation of a productive  
 RT V kappa-J kappa coding joint";  
 RL Eur. J. Immunol. 22:1561-1565(1992).  
 DR EMBL; AF035034; AAD56270.1; -; mRNA.  
 DR PIR; B49002; B49002.

DR PIR; S23638; S23638.  
 DR PIR; S34094; S34094.  
 DR PIR; S34095; S34095.  
 DR HSSP; P01625; 1LVB.  
 DR SMR; Q9UL80; 1-114.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1 114  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Alignment Scores:  
 Pred. No.: 3,16e-51 Length: 114  
 Score: 496.50 Matches: 97  
 Percent Similarity: 92.04% Conservative: 7  
 Best Local Similarity: 85.84% Mismatches: 8  
 Query Match: 84.15% Indels: 1  
 DB: 2 Gaps: 1

US-10-733-563-109 (1-336) x Q9UL80\_HUMAN (1-114)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGCCGTTACCTTGGACAGCCAGCTCC 60  
 DB |||||  
 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuArgGlnProAlaSer 20  
 QY 61 ATCTCTTCAAGTCAAGTCAGAGCCCTTCTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
 DB |||||  
 21 IleSerCysArgSerGlnSerProValTyrSerAspGlyAsnThrTyrLeuAsnTrp 40  
 QY 121 TTTTACAGCAGAGCCAGGCGAGTCTCAAGGCGCTTAATCTATCTGCTGCTCAAACTGCAC 180  
 DB |||||  
 41 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 60  
 QY 181 TCTGGAGTCCCTGACAGGTCAGCGCGAGTCAGTGCAGGAGCAGATTTTCACTGAAATC 240  
 DB |||||  
 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 80  
 QY 241 AGCAGAGTGGAGGCTGAGATGTTGGAGTTTATTTCTGCTGCGAAGGTACACATTTT 297  
 DB |||||  
 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 100  
 QY 298 CCGTACACGTTTCGACAGAGGACCGAGCTGAGATCAAG 336  
 DB |||||  
 101 ProThrPheGlyGlnGlyThrLysValGluLysile 113

RESULT 4

Q58EU8\_MOUSE  
 ID Q58EU8\_MOUSE PRELIMINARY; PRT; 239 AA.  
 AC Q58EU8;  
 DT 10-MAY-2005 (TRENBLrel. 30, Created)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
 DE Igk-C protein.  
 GN Name=Igk-C;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,





Db 41 lIeSerCysArgSerSerGluSerLeuLeuHisSerAsnGlyAsnThrTyrLeuSerTrp 60  
QY 121 TTTCAGCAGAGCCAGGCGCAGCTCCAGAGCGCCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
Db 61 LeuHisGlnArgProGlyGlnProArgLeuLeuLeuTyrLysLeuSerAsnArgPhe 80  
QY 181 TCTGAGTCCCTGACAGGTTTCAGGCGCAGTGTGATCAGGACAGATTCACACTGAAATC 240  
Db 81 SerGlyValProAspArgPheSerGlySerGlyAlaGlyThrAspPheThrLeuLysIle 100  
QY 241 AGCAGAGTGGAGCGTGGAGTCTGAGTCTTATTTATTTGCTGGCAAGGTACACATTTCCG 300  
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnValSerHisPhePro 120  
QY 301 TACACGTTGGCAAGAGGACCGCAGCTGGAGATCAAG 336  
Db 121 ArgThrPheGlyGlnGlyThrArgValGluIleLys 132

## RESULT 6

KV2D\_HUMAN STANDARD; PRT; 113 AA.  
ID KV2D\_HUMAN  
AC P01617;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-II region TEW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE (BENCE-JONES PROTEIN TEW).  
RX MEDLINE=74148480; PubMed=4596149;  
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
RT "Amino acid sequence of a kappa Bence Jones protein from a case of  
primary amyloidosis.";  
RL Biochemistry 12:3763-3780(1973).  
RN [2]  
RP PROTEIN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
RX MEDLINE=7316638; PubMed=4700495;  
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,  
RA Glenner G.G.;  
RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
patient with plasma cell dyscrasia and amyloidosis.";  
RL J. Clin. Invest. 52:1276-1281(1973).  
CC -1- MISCELLANEOUS: The major amyloid protein appears to be identical  
with the Bence Jones protein isolated from the same patient.  
CC -1- MISCELLANEOUS: This protein was isolated from the urine of a  
patient with plasma cell dyscrasia and amyloidosis.  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
marker.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC PIR; A90370; K2HUTW.  
DR HSSP; Q99M37; 1191.  
DR SMR; P01617; 1-113.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Amyloid; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin domain; Immunoglobulin V region.  
FT REGION 1 23  
FT Complementarity-determining-1.  
PIR; A01886; K2HUPR.

FT REGION 40 54  
FT REGION 55 61  
FT REGION 62 93  
FT REGION 94 102  
FT REGION 103 112  
FT DISULFID 23 93  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;  
Alignment Scores:  
Pred. No.: 1.51e-45 Length: 113  
Score: 450.00 Matches: 87  
Percent Similarity: 84.82% Conservative: 8  
Best Local Similarity: 77.68% Mismatches: 17  
Query Match: 76.27% Indels: 0  
DB: 1 Gaps: 0  
US-10-733-563-109 (1-336) x KV2D\_HUMAN (1-113)  
QY 1 GATGTAGTGATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60  
Db 1 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20  
QY 61 ATCTCTTCCAAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
Db 21 lIeSerCysArgSerSerGlnSerLeuLeuHisSerAspGlyPheAspTyrLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGGCGCAGCTCCAGAGCGCCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 TyrLeuGlnLysProGlyGlnSerPro\*\*\*LeuLeuIleTyrAlaLeuSerAsnArgAla 60  
QY 181 TCTGAGTCCCTGACAGGTTTCAGGCGCAGTGTGATCAGGACAGATTTTCACACTGAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGCGTGGAGTGTGGAGTTTATTTATTTCTGCGCAGGTACACATTTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysMet\*\*\*AlaLeuGlnAlaPro 100  
QY 301 TACACGTTGGCAAGAGGACCGCAGCTGGAGATCAAG 336  
Db 101 lIeThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 7

KV2B\_HUMAN STANDARD; PRT; 113 AA.  
ID KV2B\_HUMAN  
AC P01615;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-II region FR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=76253627; PubMed=821524;  
RA Riesen W.F., Jaton J.-C.;  
RT "Variable region sequence of the light chain from a Waldenstroms IGM  
with specificity for phosphorylcholine.";  
RL Biochemistry 15:3829-3833(1976).  
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's  
macroglobulin that binds phosphorylcholine.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC PIR; A01886; K2HUPR.

DR HSSP; Q99M37; 1191.  
DR SMR; P01615; 1-109.  
DR GO; GO:0005578; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin v region.  
FT REGION 1 23  
FT REGION 24 39  
FT REGION 40 54  
FT REGION 55 61  
FT REGION 62 93  
FT REGION 94 102  
FT REGION 103 112  
FT REGION 113 113  
FT DISULFID 23 93  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Alignment Scores:  
Pred. No.: 1.99e-45 Length: 113  
Score: 449.00 Matches: 84  
Percent Similarity: 85.71% Conservative: 12  
Best Local Similarity: 75.00% Mismatches: 16  
Query Match: 76.10% Indels: 0  
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x KV2B\_HUMAN (1-113)

Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCTGTGCGGTACCTTGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyGluProAlaSer 20  
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGAAGAGATTTTGAATTGG 120  
Db 21 IleGlnCysArgSerGlnSerLeuValTyrArg\*\*\*Gly\*\*\*ThrTyrLeu\*\*\*Tyr 40  
Qy 121 TTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCTAATCTATCTGTGTCTAACTGGAC 180  
Db 41 TyrLeuGlnLysProGlyGlnSerProGluLeuLeuIleTyrLeuSerSerTyrArgAsp 60  
Qy 181 TCTGGAGTCCCTGACAGGTTTCAGCGGAGTGGATCAGGACAGATTTTCACACTGAAATC 240  
Db 61 SerGlyValProAspArgPheSerAspSerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCG 300  
Db 81 ThrArgValGlnAlaGluAspValGlyValTyrTyrCysMetGlnAlaThr\*\*\*SerPro 100  
Qy 301 TACACGTTCCGACAAAGGACCCGACTCGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrLysLeu\*\*\*IleLys 112

## RESULT 8

Q8NEKO\_HUMAN  
ID Q8NEKO\_HUMAN PRELIMINARY; PRT; 239 AA.  
AC Q8NEKO;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGKV1-5 protein.  
GN Name=IGKV1-5;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Prostate;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Prostate;  
RA Director MGC Project;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1601042;  
RA Huber C., Klobbeck H.G., Zachau H.G.;  
RT "Ongoing V kappa-J kappa recombination after formation of a productive  
V kappa-J kappa coding joint.";  
RL Eur. J. Immunol. 22:1561-1565(1992).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
distributed over a large portion of the V kappa locus and do not show  
somatic mutation.";  
RL Eur. J. Immunol. 23:391-397(1993).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8258341;  
RA Klein R., Jaenichen R., Zachau H.G.;  
RT "Expressed human immunoglobulin kappa genes and their hypermutation.";  
RL Eur. J. Immunol. 23:3248-3262(1993).  
DR EMBL; BC030814; AAH30814.1; -; mRNA.  
DR PIR; S23638; S23638.  
DR PIR; S34091; S34091.  
DR PIR; S40342; S40342.  
DR PIR; S40357; S40357.  
DR HSSP; P01834; 117Z.  
DR SMR; Q8NEKO; 21-237.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

Alignment Scores:  
Pred. No.: 4e-45 Length: 239  
Score: 447.00 Matches: 85  
Percent Similarity: 86.61% Conservative: 12  
Best Local Similarity: 75.89% Mismatches: 15  
Query Match: 75.76% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x Q8NEKO\_HUMAN (1-239)

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Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCTCCCTGGCCGTTACCTTGGACAGCCAGCTCC 60
Db 21 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
Qy 61 ATCTCTTCAAGTCAAGTCAAGTCAAGTCTTAGATGATGATGAAGACATTTTGAATGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuLeuHisSerAspGlyTyrAsnTyrLeuAspTrp 60
Qy 121 TTTCAGACAGCCAGCCAGTCTCCAGGCGCTTAATCTATCTCTGGTGTCTAACTGGAC 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 80
Qy 181 TCTGAGTCCCTGACAGGTTTCCAGGCGCAGTGGATCAGGACAGATTTTCCACTGAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACATTTCCG 300
Db 101 SerLysValGluAlaGluAspValGlyIleTyrTyrCysMetGlnGlyLeuGlnThrPro 120
Qy 301 TACAGTTCGACAGGAGGACCCGACTGGAGATCAAG 336
Db 121 GlnThrPheGlyGlnGlyThrLysValGluLys 132
```

## RESULT 9

```
Q65ZQ7_9MURI
ID Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B3 (Fv)-PB40 (Fragment).
GN Name=B3 (Fv)-PB40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3 (Fv)-PB38DEL, a single-chain immunotoxin that causes complete
RL regression of a human carcinoma in mice."
Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).
DR EMBL; S57990; AAB19971.2; -; mRNA.
DR SMR; Q65ZQ7; 4-247.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;
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## Alignment Scores:

Pred. No.:	7,07e-45	Length:	248
Score:	445.00	Matches:	83
Percent Similarity:	87.50%	Conservative:	15
Best Local Similarity:	74.11%	Mismatches:	14
Query Match:	75.42%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-109 (1-336) x Q65ZQ7\_9MURI (1-248)

```
Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCTCCCTGGCCGTTACCTTGGACAGCCAGCTCC 60
Db 136 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 155
Qy 61 ATCTCTTCAAGTCAAGTCAAGTCTTAGATGATGATGAAGACATTTTGAATGG 120
```

```
Db 156 IleSerCysArgSerSerGlnIleValHisSerAsnGlyAsnThrTyrLeuGluTrp 175
Qy 121 TTTCAGACAGCCAGCCAGTCTCCAGGCGCTTAATCTATCTCTGGTGTCTAACTGGAC 180
Db 176 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuIleTyrLysValSerAsnArgPhe 195
Qy 181 TCTGAGTCCCTGACAGGTTTCCAGGCGCAGTGGATCAGGACAGATTTTCCACTGAAAATC 240
Db 196 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 215
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACATTTCCG 300
Db 216 SerArgValGluAlaGluAspLeuGlyValTyrTyrCysPheGlnGlySerHisValPro 235
Qy 301 TACAGTTCGACAGGAGGACCCGACTGGAGATCAAG 336
Db 236 PheThrPheGlySerGlyThrLysLeuGluLys 247
```

## RESULT 10

```
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region CUM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RL type)."
HL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722 (1967).
RN [2]
RP SEQUENCE REVISION TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation."
RA Naturwissenschaften 56:195-205 (1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
```

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PIR; B91639; K2HUCM.
HSSP; P01751; 1NOB.
DR SMR; P01614; 2-115.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 24 95
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;
```

## Alignment Scores:

Pred. No.:	1.24e-44	Length:	115
Score:	442.50	Matches:	86

```

Percent Similarity: 86.73% Conservative: 12
Best Local Similarity: 76.11% Mismatches: 14
Query Match: 75.00% Indels: 1
DB: 1 Gaps: 1

US-10-733-563-109 (1-336) x KV2A_HUMAN (1-115)
Qy 1 GATCTAGTGTAGTACCCAGTCTCCACTCTCCCTGCGCGTTCACCTTGGACAGCCAGCTCC 60
Db 2 AspIleValMetThrGlnProLeuSerLeuProValThrProGlyGluProAlaSer 21
Qy 61 ATCTCTTGCAGTCAAGTCAAGTCAAGTCTCTAGTAGT---GATGAAAGACATTTTGAAT 117
Db 22 IleSerCysArgSerSerGlnSerLeuLeuAspSerGlyAspGlyAsnThrTyrLeuAsn 41
Qy 118 TGGTTTCAGCAGAGCCAGCCAGTCTCCAGGCGCTTAATCTATCTGTGTCCTAAACTG 177
Db 42 TrpTyrLeuGlnLysAlaGlyGlnSerProGlnLeuLeuIleTyrThrLeuSerTyrArg 61
Qy 178 GACTCTGGAGTCCCTGACAGCTTCAGCGGCGAGTGCAGGACGAGTTCACACTGAAA 237
Db 62 AlaSerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys 81
Qy 238 ATCAGCAGAGTGGAGGTGAGGATGTTGGAGTCTTATTATTCTGCTGGCAAGGTACACATTT 297
Db 82 IleSerArgValGlnAlaGluAspValGlyValTyrTyrCysMetGlnArgLeuGluIle 101
Qy 298 CCGTACAGTTCGGACAGAGGACCCGACTGAGATCAAG 336
Db 102 ProTyrThrPheGlyGlnGlyThrLysLeuGluIleArg 114

RESULT 11
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC PV6309;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC ENBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA.
CC PIR; A01889; K2HUGM.
CC HSPP; Q99M37; 1191.
CC SMR; P06309; 5-117.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1_
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin domain; Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN <1 4
FT REGION 5 117 Ig kappa chain V-II region GM607.
FT REGION 5 27 Framework-1.

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FT REGION 28 43 Complementarity-determining-1.
FT REGION 44 58 Framework-2.
FT REGION 59 65 Complementarity-determining-2.
FT REGION 66 97 Framework-3.
FT REGION 98 106 Complementarity-determining-3.
FT REGION 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719B558B1 CRC64;

Alignment Scores:
Pred. No.: 4,42e-44 Length: 117
Score: 438.00 Matches: 85
Percent Similarity: 85.71% Conservative: 11
Best Local Similarity: 75.89% Mismatches: 16
Query Match: 74.24% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x KV2E_HUMAN (1-117)
Qy 1 GATCTAGTGTAGTACCCAGTCTCCACTCTCCCTGCGCGTTCACCTTGGACAGCCAGCTCC 60
Db 5 AspIleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 24
Qy 61 ATCTCTTGCAGTCAAGTCAAGTCAAGTCTCTAGTAGTGTGATGATGATGATGATGATGATG 120
Db 25 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 44
Qy 121 TTCAGCAGAGGCGCAGGCGCTCCAGGCGCTAATCTATCTGCTGCTAAACTGGAC 180
Db 45 TyrLeuGlnLysProGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 64
Qy 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCGAGTGCAGGACGAGATTCACACTGAAAATC 240
Db 65 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 84
Qy 241 AGCAGAGTGCAGGCTGAGGATGTTGGAGTTTATTTATTTATTTATTTATTTATTTATTT 300
Db 85 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGlyLeuGlnThrPro 104
Qy 301 TACAGTTCGGACAGAGGCGCAGGCGCTGAGTGCAGTCAAG 336
Db 105 GlnThrPheGlyGlnGlyThrLysValGluIleLys 116

RESULT 12
Q5F210_MOUSE
ID Q5F210_MOUSE PRELIMINARY; PRT; 115 AA.
AC Q5F210;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Kappa light chain variable region (Fragment).
GN Name=IgG1 anti-TS1 VL;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
RT "Studies of the interactions between the anticytokerin 8 monoclonal
antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";
J. Mol. Recognit. 16:157-163(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Erlandsson A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ884575; CAI56337.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

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DR Pfam: PF07686; V-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;

Alignment Scores:
Pred. No.: 3,63e-43 Length: 115
Score: 430.50 Matches: 84
Percent Similarity: 86.73% Conservative: 14
Best Local Similarity: 74.34% Mismatches: 14
Query Match: 72.97% Indels: 1
DB: 2 Gaps: 1

US-10-733-563-109 (1-336) x Q5P210_MOUSE (1-115)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60
DB 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20

QY 61 ATCTCTTCAAGTCAAGTCAAGCTCTTAGATAGTATGATGATGATGATGATGATGATG 120
DB 21 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrThrLeuHisTrp 40

QY 121 TTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCCTAATCTATCTGGTGTCTAAACTGGAC 180
DB 41 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuLeuLeuLeuValSerAsnArgPhe 60

QY 181 TCTGGAGTCCCTGACAGGTTTCCAGGCGCAGTGGATCAGGACAGATTTTCACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTTATCTGCTGGCAGGTACACATTTT 297
DB 81 SerArgValGluAlaGluAspLeuGlyValTyrPheCysSerGlnThrThrHisValPro 100

QY 298 CCGTACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
DB 101 ProTyrThrPheGlyGlyThrLysLeuGluMetLys 113

RESULT 13
KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=81178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
protein that binds digoxin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A01914; KVM526.
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DR HSSP: Q9NM37; 1191.
DR Ensembl: ENSMUSG0000055315; Mus musculus.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23 Framework-1.
FT REGION 24 39 Complementarity-determining-1.
FT REGION 40 54 Framework-2.
FT REGION 55 61 Complementarity-determining-2.
FT REGION 62 93 Framework-3.
FT REGION 94 102 Complementarity-determining-3.
FT REGION 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Alignment Scores:
Pred. No.: 4.17e-43 Length: 113
Score: 430.00 Matches: 83
Percent Similarity: 85.71% Conservative: 13
Best Local Similarity: 74.11% Mismatches: 16
Query Match: 72.88% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x KV2G_MOUSE (1-113)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60
DB 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20

QY 61 ATCTCTTCAAGTCAAGTCAAGCTCTTAGATAGTATGATGATGATGATGATGATGATG 120
DB 21 IleSerCysArgSerSerGlnSerLeuValHisSerAsnGlyAsnThrThrLeuAsnTrp 40

QY 121 TTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCCTAATCTATCTGGTGTCTAAACTGGAC 180
DB 41 TyrLeuGlnLysAlaGlyGlnSerProLysLeuLeuLeuLeuLeuValSerAsnArgPhe 60

QY 181 TCTGGAGTCCCTGACAGGTTTCCAGGCGCAGTGGATCAGGACAGATTTTCACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysile 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTTATCTGCTGGCAGGTACACATTTTCCG 300
DB 81 SerArgValGluAlaGluAspLeuGlyValTyrPheCysSerGlnThrThrHisValPro 100

QY 301 TACACGTTCCGACAGGACCCGACTGGAGATCAAG 336
DB 101 ProThrPheGlyGlyThrLysLeuGluLeuLys 112

RESULT 14
Q53VP8_MOUSE PRELIMINARY; PRT; 112 AA.
AC Q53VP8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Kappa chain (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigen encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
```

RL EMBL J. 4:3681-3688 (1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 108-109.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03386; CAA27113.1; -, mRNA.  
FT NON\_TER 1 112  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12266 MW; C844B7881A89C18A CRC64;

Alignment Scores:  
Pred. No.: 7.3e-43 Length: 112  
Score: 428.00 Matches: 81  
Percent Similarity: 84.92% Conservative: 14  
Best Local Similarity: 72.32% Mismatches: 17  
Query Match: 72.54% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x Q53VP8\_MOUSE (1-112)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCCTTGCCGTTACCTTGGACAGCCAGCTCC 60  
Db 1 AspIleValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20  
QY 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
Db 21 ILeSerCysArgSerGlnSerIleValIleSerAenGlyPheThrTyrLeuGluTrp 40  
QY 121 TTTCCAGCAGAGCCAGGCGCAGTCTCCAGGCGCTTAATCTATCTGCTGTTAACTGGAC 180  
Db 41 TyrLeuGlnLysProGly\*\*\*\*\*LysLeuLeuIleTyrGlyIleSerAsnArgPhe 60  
QY 181 TCTGGAGTCCCTGACAGTTTCAGGCGCAGTGGATGATGAGGACAGATTTTCACACTGAAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATCTGCTGGCAGGTACACATTTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyIleTyrCysPheGlnGlyIleHisValPro 100  
QY 301 TACACGTTCCGACAAAGGACCCGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112

#### RESULT 15

Q65ZC0\_MOUSE  
ID Q65ZC0\_MOUSE PRELIMINARY; PRT; 219 AA.  
AC Q65ZC0;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Kappa light chain C region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Spleen;  
RX MEDLINE=96319505; PubMed=8768802;  
RA Kipp B., Schlaak M., Becker W.M.;  
RT "cloning and expression of a recombinant mouse Fab-fragment  
recognizing a defined linear epitope of Chironomus thummi major  
allergen Chi t I.";  
RL Int. Arch. Allergy Immunol. 110:348-353 (1996).  
DR EMBL; Z37499; CAA85724.1; -, mRNA.  
DR SMR; Q65ZC0; 1-219  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER 1 219  
FT NON\_TER 219 219  
SQ SEQUENCE 219 AA; 23944 MW; 7B1B82A14EAF8445 CRC64;

Alignment Scores:  
Pred. No.: 1.37e-41 Length: 219  
Score: 418.00 Matches: 80  
Percent Similarity: 85.71% Conservative: 16  
Best Local Similarity: 71.43% Mismatches: 16  
Query Match: 70.85% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x Q65ZC0\_MOUSE (1-219)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCCTTGCCGTTACCTTGGACAGCCAGCTCC 60  
Db 1 GluLeuValMetThrGlnSerProLeuSerLeuSerValSerLeuGlyAspGlnAlaSer 20  
QY 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
Db 21 ILeSerCysArgSerGlnSerLeuValIleThrAenGlyAenThrTyrLeuHisValPro 40  
QY 121 TTTCCAGCAGAGCCAGGCGCAGTCTCCAGGCGCTTAATCTATCTGCTGTTAACTGGAC 180  
Db 41 TyrLeuGlnLysProGlyLeuSerProLysLeuLeuIleTyrIleValSerAsnArgPhe 60  
QY 181 TCTGGAGTCCCTGACAGTTTCAGGCGCAGTGGATGATGAGGACAGATTTTCACACTGAAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATCTGCTGGCAGGTACACATTTTCCG 300  
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrPheCysSerGlnSerThrHisValPro 100  
QY 301 TACACGTTCCGACAAAGGACCCGACTGGAGATCAAG 336  
Db 101 GlyThrPheGlyGlyThrLysLeuGluIleLys 112

Search completed: January 28, 2006, 08:43:57  
Job time : 52.5435 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:22:17 ; Search time 13.2853 Seconds  
(without alignments)  
4181.924 Million cell updates/sec

Title: US-10-733-563-109  
Perfect score: 590  
Sequence: 1 gatgtagtgtgacccagtc.....ggaccgactggagatcaag 336

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool.p/US10733563/runat.27012006.180006.4815/app.query.fasta\_1.2716  
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human4.0.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CNC 1.1.141 @runat.27012006.180006.4815 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5 COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	112	2	US-09-809-739-14
2	590	100.0	112	2	US-09-840-459-12
3	590	100.0	112	2	US-09-497-625A-12
4	584	99.0	114	2	US-09-840-459-106
5	584	99.0	114	2	US-09-497-625A-106
6	577	97.8	112	2	US-09-809-739-15
7	577	97.8	112	2	US-09-840-459-13
8	577	97.8	112	2	US-09-497-625A-13
9	572	96.9	112	2	US-09-809-739-18
10	572	96.9	112	2	US-09-840-459-107
11	570	96.6	112	2	US-09-809-739-16
12	570	96.6	112	2	US-09-840-459-14

13	570	96.6	112	2	US-09-497-625A-14	Sequence 14, Appl
14	565	95.8	112	2	US-09-809-739-17	Sequence 17, Appl
15	565	95.8	112	2	US-09-840-459-15	Sequence 15, Appl
16	565	95.8	112	2	US-09-497-625A-15	Sequence 15, Appl
17	536	90.8	112	2	US-09-809-739-11	Sequence 11, Appl
18	536	90.8	112	2	US-09-840-459-9	Sequence 9, Appl
19	536	90.8	112	2	US-09-497-625A-9	Sequence 9, Appl
20	536	90.8	112	2	US-09-840-459-102	Sequence 102, App
21	536	90.8	142	2	US-09-497-625A-102	Sequence 102, App
22	527	89.3	257	2	US-09-419-788-113	Sequence 113, App
23	526	89.2	111	2	US-09-809-739-13	Sequence 13, Appl
24	526	89.2	111	2	US-09-840-459-59	Sequence 59, Appl
25	526	89.2	111	2	US-09-497-625A-11	Sequence 11, Appl
26	526	89.2	111	2	US-09-497-625A-59	Sequence 59, Appl
27	526	89.2	112	1	US-08-477-877B-89	Sequence 89, Appl
28	526	89.2	112	1	US-08-472-281A-89	Sequence 89, Appl
29	526	89.2	112	1	US-08-477-989B-89	Sequence 89, Appl
30	526	89.2	112	2	US-09-462-140D-97	Sequence 97, Appl
31	524	88.8	113	2	US-09-698-705-7	Sequence 7, Appl
32	524	88.8	218	2	US-09-698-705-12	Sequence 12, Appl
33	521	88.3	112	2	US-09-840-459-54	Sequence 54, Appl
34	521	88.3	112	2	US-09-497-625A-54	Sequence 54, Appl
35	521	88.3	112	2	US-09-254-180C-8	Sequence 8, Appl
36	521	88.3	353	2	US-09-203-958A-4	Sequence 4, Appl
37	520	88.1	111	2	US-09-840-459-11	Sequence 11, Appl
38	520	88.1	112	2	US-09-840-459-58	Sequence 58, Appl
39	520	88.1	112	2	US-09-497-625A-58	Sequence 58, Appl
40	518	87.8	112	2	US-09-647-468-149	Sequence 149, App
41	518	87.8	112	2	US-09-647-468-150	Sequence 150, App
42	518	87.8	131	2	US-09-647-468-163	Sequence 163, App
43	518	87.8	131	2	US-09-647-468-164	Sequence 164, App
44	518	87.8	243	2	US-09-297-181-2	Sequence 2, Appl
45	516	87.5	535	2	US-08-983-035A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-09-809-739-14  
; Sequence 14, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-14

Alignment Scores:  
Pred. No.: 5,84e-70 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-14 (1-112)

QY 1 GATGTAGTGTGACCCAGTCCTCCACTCTCTCTGCGCTTACCCCTTGACAGCCGCTCC 60  
|||||

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyClnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGGAAGACACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGGCGAGTCTCAAGGCGCCTAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGCTTCAAGCGCAGTGTGATCAGGACAGATTTTACACTGGAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTATTCCTGCAAGGTACACATTTTCGG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyTyCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTGGACAAGGACCGGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 2

US-09-840-459-12  
; Sequence 12, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-12

Alignment Scores:  
Pred. No.: 5.84e-70 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-12 (1-112)

QY 1 GATGTAGTAGTACCCAGCTCTCCACTCTCTTGGCCCGTTACCTTGGACAGCAGCCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyClnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGGAAGACACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTCAGCAGAGCCAGGCGAGTCTCAAGGCGCCTAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGCTTCAAGCGCAGTGTGATCAGGACAGATTTTACACTGGAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTATTCCTGCAAGGTACACATTTTCGG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyTyCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTGGACAAGGACCGGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 3

US-09-497-625A-12  
; Sequence 12, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-497-625A-12

Alignment Scores:  
Pred. No.: 5.84e-70 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-497-625A-12 (1-112)

QY 1 GATGTAGTAGTACCCAGCTCTCCACTCTCTTGGCCCGTTACCTTGGACAGCAGCCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyClnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGGAAGACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGGCGAGTCTCAAGGCGCCTAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGCTTCAAGCGCAGTGTGATCAGGACAGATTTTACACTGGAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80



QY 241 ACCAGTGGAGGCTGAGATGTTGGAGTTATTATTGCTGGCAAGGTACACATTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACACGTTTCGGACAAGGACCGGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 4  
US-09-840-459-106  
; Sequence 106, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-09-840-459-106

Alignment Scores:  
Pred. No.: 3,728-69 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-106 (1-114)  
QY 4 GTAGTGATGACCCAGCTCCACTCTCCCTGCGCGTACCTTGGACAGCCAGCTCCATC 63  
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTCCAAGTCAAGTCAGAGCTCTTAGATAGTGTGATGAAAGACATTTTGAATTGGTTT 123  
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerArgGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGGCGGACGCTCCAAAGCGCCCTAATCTATCTGGTGTCTAAACTGGACTCT 183  
Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGCTTCAGCGGCGAGTCAGGACAGATTTACACTGAAATCAGC 243  
Db 62 GlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTATTATTCTGCTGCAAGGTACACATTTCCGTAC 303  
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACGTTCCGACAAGGACCGGACTGGAGATCAAG 336

Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
RESULT 5  
US-09-497-625A-106  
; Sequence 106, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-09-497-625A-106  
Alignment Scores:  
Pred. No.: 3,728-69 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-109 (1-336) x US-09-497-625A-106 (1-114)  
QY 4 GTAGTGATGACCCAGCTCCACTCTCCCTGCGCGTACCTTGGACAGCCAGCTCCATC 63  
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTCCAAGTCAAGTCAGAGCTCTTAGATAGTGTGATGAAAGACATTTTGAATTGGTTT 123  
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerArgGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGGCGGACGCTCCAAAGCGCCCTAATCTATCTGGTGTCTAAACTGGACTCT 183  
Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGCTTCAGCGGCGAGTCAGGACAGATTTACACTGAAATCAGC 243  
Db 62 GlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTATTATTCTGCTGCAAGGTACACATTTCCGTAC 303  
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACGTTCCGACAAGGACCGGACTGGAGATCAAG 336  
Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
RESULT 6  
US-09-739-15  
; Sequence 15, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.

; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-15

Alignment Scores:  
Pred. No.: 3.18e-68 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-15 (1-112)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCTTGGCCGCTTACCTTGGACGCCAGCCCTCC 60  
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTATGATGGAAGACATTTTGAATTGG 120  
DB 21 IleSerCysIysSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40  
QY 121 TTTCCAGCAGAGCCAGCCAGCTCTCCAGGCGCTTATCTATCTGGTGTCTAAACTGGAC 180  
DB 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGCGATCGATCAGGACAGATTTCCACTGAAATC 240  
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTCTGGCAGGATACACATTTTCCG 300  
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACACGTTCCGACAGGACCCGACTGGAGATCAAG 336  
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 7  
US-09-840-459-13  
; Sequence 13, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Theresa  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-13

Alignment Scores:  
Pred. No.: 3.18e-68 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-13 (1-112)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCTTGGCCGCTTACCTTGGACGCCAGCCCTCC 60  
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTATGATGGAAGACATTTTGAATTGG 120  
DB 21 IleSerCysIysSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40  
QY 121 TTTCCAGCAGAGCCAGCCAGCTCTCCAGGCGCTTATCTATCTGGTGTCTAAACTGGAC 180  
DB 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGCGATCGATCAGGACAGATTTCCACTGAAATC 240  
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTCTGGCAGGATACACATTTTCCG 300  
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACACGTTCCGACAGGACCCGACTGGAGATCAAG 336  
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 8  
US-09-497-625A-13  
; Sequence 13, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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;
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-13

Alignment Scores:
Pred. No.: 3,18e-68 Length: 112
Score: 577.00 Matches: 110
Percent Similarity: 98.21% Conservative: 0
Best Local Similarity: 98.21% Mismatches: 2
Query Match: 97.80% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-497-625A-13 (1-112)
QY 1 GATGTAGTGAATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyHisProAlaSer 20
QY 61 ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTAGTGGAAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 121 TTTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCTAAATCTATCTGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgGluLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGGCGCAGTGCATCAGGACAGATTTTCACATGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 ACAGAGTGGAGCTGAGGATCTTGAGTTTATTATTGCTGCGCAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 9
US-09-809-739-18
; Sequence 18, Application US/09809739
; Patent No. 663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-18

Alignment Scores:
Pred. No.: 1,48e-67 Length: 112
Score: 572.00 Matches: 109
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.95% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-18 (1-112)
QY 1 GATGTAGTGAATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyHisProAlaSer 20
QY 61 ATCTCTTGAAGTCAAGTCAAGTCAGAGCTCTTAGATAGTAGTGGAAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 121 TTTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCTAAATCTATCTGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgGluLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGGCGCAGTGCATCAGGACAGATTTTCACATGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 ACAGAGTGGAGCTGAGGATCTTGAGTTTATTATTGCTGCGCAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 5
US-09-809-739-18
; Sequence 18, Application US/09809739
; Patent No. 663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-107

Alignment Scores:
Pred. No.: 1,48e-67 Length: 112
Score: 572.00 Matches: 109
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.95% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-107 (1-112)
QY 1 GATGTAGTGAATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCCTCC 60
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QY 61 ATCTCTTGAAGTCAAGTCAAGTCAGAGCTCTTAGATAGTAGTGGAAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 121 TTTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCTAAATCTATCTGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgGluLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGGCGCAGTGCATCAGGACAGATTTTCACATGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 ACAGAGTGGAGCTGAGGATCTTGAGTTTATTATTGCTGCGCAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112
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Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
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Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuValSerLysLeuAsp 60  
Qy 181 TCTGAGTCCCTGACAGGTTCCAGCGGAGTGGATCAGGACAGATTCACACTGAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGGCTGAGAGTTCGGAGTTTATTATTCTGCGCAGGTACACATTTTCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
Qy 301 TACAGTTCGACAGGACCGGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
RESULT 11  
US-09-809-739-16  
; Sequence 16, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-16  
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Pred. No.: 2.73e-67 Length: 112  
Score: 570.00 Matches: 109  
Percent Similarity: 97.32% Conservative: 0  
Best Local Similarity: 97.32% Mismatches: 3  
Query Match: 96.61% Indels: 0  
DB: 2 Gaps: 0  
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Qy 61 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
Qy 121 TTTCAGCAGAGCCAGCCAGTCTCCAAAGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuValSerLysLeuAsp 60  
Qy 181 TCTGAGTCCCTGACAGGTTCCAGCGGAGTGGATCAGGACAGATTCACACTGAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGGCTGAGAGTTCGGAGTTTATTATTCTGCGCAGGTACACATTTTCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
Qy 301 TACAGTTCGACAGGACCGGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112  
RESULT 12  
US-09-840-459-14  
; Sequence 14, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-14  
Alignment Scores:  
Pred. No.: 2.73e-67 Length: 112  
Score: 570.00 Matches: 109  
Percent Similarity: 97.32% Conservative: 0  
Best Local Similarity: 97.32% Mismatches: 3  
Query Match: 96.61% Indels: 0  
DB: 2 Gaps: 0  
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Qy 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTGCGGCTTACCTTGGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
Qy 61 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
Qy 121 TTTCAGCAGAGCCAGCCAGTCTCCAAAGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuValSerLysLeuAsp 60  
Qy 181 TCTGAGTCCCTGACAGGTTCCAGCGGAGTGGATCAGGACAGATTCACACTGAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGGCTGAGAGTTCGGAGTTTATTATTCTGCGCAGGTACACATTTTCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
Qy 301 TACAGTTCGACAGGACCGGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112  
RESULT 13  
US-09-497-625A-14

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; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIORITY FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

Alignment Scores:
Pred. No.:      2,73e-67      Length:      112
Score:          570.00        Matches:    109
Percent Similarity: 97.32%     Conservative: 0
Best Local Similarity: 97.32%   Mismatches: 3
Query Match:    96.61%         Indels:     0
DB:              2            Gaps:       0

US-10-733-563-109 (1-336) x US-09-497-625A-14 (1-112)

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Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20

QY 61 ATCTTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGATGATGAAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProArgArgLeuIleTyrlLeuValSerLysLeuAsnTrp 40

QY 121 TTTCAGCAGAGGCCAGGCTCCTCAAGCGCGCTTAATCTATCTGCTGCTAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrlLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTTCAGGCGGAGTGGATCAGGAGACAGATTTCACACTGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGAGGTTTATTATGCTGCGAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrlCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTCCGACAAGGCCCGAGCTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112

RESULT 14
US-09-809-739-17
; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739

; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIORITY FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

Alignment Scores:
Pred. No.:      2,73e-67      Length:      112
Score:          570.00        Matches:    109
Percent Similarity: 97.32%     Conservative: 0
Best Local Similarity: 97.32%   Mismatches: 3
Query Match:    96.61%         Indels:     0
DB:              2            Gaps:       0

US-10-733-563-109 (1-336) x US-09-497-625A-14 (1-112)

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QY 61 ATCTTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGATGATGAAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProArgArgLeuIleTyrlLeuValSerLysLeuAsnTrp 40

QY 121 TTTCAGCAGAGGCCAGGCTCCTCAAGCGCGCTTAATCTATCTGCTGCTAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrlLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTTCAGGCGGAGTGGATCAGGAGACAGATTTCACACTGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGAGGTTTATTATGCTGCGAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrlCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTCCGACAAGGCCCGAGCTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112

RESULT 14
US-09-809-739-17
; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739

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; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIORITY FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

Alignment Scores:
Pred. No.: 2,73e-67 Length: 112
Score: 570.00 Matches: 109
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.61% Indels: 0
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Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20

QY 61 ATCTTTGCAAGTCAAGTCAGAGCCCTTATAGATAGTAGTGGAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProArgArgLeuLeuValSerLysLeuAsnTrp 40

QY 121 TTTTCAGCAGAGCCAGCCAGCTCTCCAGCGCGCTTAATCTATCTGCTGCTAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCGAGTCAGGAGGATCAGGACAGATTCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysLeu 80

QY 241 AGCAGAGTGAGGCTGAGGATGTTGAGGTTTATTATGCTGCGCAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTCCGACAGGACCCGAGCTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlyThrArgLeuGluLeuLys 112

RESULT 14
US-09-809-739-17
; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739

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; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-15
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Alignment Scores:
Pred. No.:      1.27e-66      Length:      112
Score:          565.00        Matches:    108
Percent Similarity: 96.43%    Conservative: 0
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Db	21	IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp	40
QY	121	TTTCAGCAGAGCCAGGCCAGTCTCCAAGGGCCCTTAATCTATCTGGTGTCTAAACTGGAC	180
Db	41	LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp	60
QY	181	TCTGGAGTCCCTGACAGGTTCAAGCGGCAAGTGGATCAGGGACAGATTTCACACTGAAATC	240
Db	61	SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle	80
QY	241	AGCAGAGTGGAGGCTTGAGATCTTGGAGTTTATTATTCTGTCAGAGGTACACATTTTCGG	300
Db	81	SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro	100
QY	301	TACAGTTTCGACACAGGAGCCGACTGGAGATCAAG	336
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Job time : 15.2853 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

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(without alignments)  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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4	590	100.0	112	4	US-10-766-773-12
5	590	100.0	112	4	US-10-766-610-12
6	590	100.0	112	4	US-10-733-563-12
7	590	100.0	112	5	US-10-662-061-14
8	584	99.0	114	3	US-09-840-459-106
9	584	99.0	114	4	US-10-766-773-106
10	584	99.0	114	4	US-10-766-610-106
11	584	99.0	114	4	US-10-733-563-106

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13	577	97.8	112	3	US-09-809-739-15	Sequence 15, Appl
14	577	97.8	112	3	US-09-840-459-13	Sequence 13, Appl
15	577	97.8	112	4	US-10-766-773-13	Sequence 13, Appl
16	577	97.8	112	4	US-10-766-610-13	Sequence 13, Appl
17	577	97.8	112	4	US-10-733-563-13	Sequence 13, Appl
18	577	97.8	112	5	US-10-662-061-15	Sequence 15, Appl
19	572	96.9	112	3	US-09-835-087-7	Sequence 7, Appl
20	572	96.9	112	3	US-09-809-739-18	Sequence 18, Appl
21	572	96.9	112	3	US-09-840-459-107	Sequence 107, App
22	572	96.9	112	4	US-10-766-610-107	Sequence 107, App
23	572	96.9	112	4	US-10-733-563-107	Sequence 107, App
24	572	96.9	112	5	US-10-662-061-18	Sequence 18, Appl
25	570	96.6	112	3	US-09-835-087-5	Sequence 5, Appl
26	570	96.6	112	3	US-09-809-739-16	Sequence 16, Appl
27	570	96.6	112	3	US-09-840-459-14	Sequence 14, Appl
28	570	96.6	112	4	US-10-766-773-14	Sequence 14, Appl
29	570	96.6	112	4	US-10-766-610-14	Sequence 14, Appl
30	570	96.6	112	4	US-10-733-563-14	Sequence 14, Appl
31	570	96.6	112	5	US-10-662-061-16	Sequence 16, Appl
32	565	95.8	112	3	US-09-835-087-6	Sequence 6, Appl
33	565	95.8	112	3	US-09-809-739-17	Sequence 17, Appl
34	565	95.8	112	3	US-09-840-459-15	Sequence 15, Appl
35	565	95.8	112	4	US-10-766-773-15	Sequence 15, Appl
36	565	95.8	112	4	US-10-766-610-15	Sequence 15, Appl
37	565	95.8	112	4	US-10-733-563-15	Sequence 15, Appl
38	565	95.8	112	5	US-10-662-061-17	Sequence 17, Appl
39	559	94.7	113	5	US-10-476-265-9	Sequence 9, Appl
40	559	94.7	219	5	US-10-476-265-11	Sequence 11, Appl
41	559	94.7	239	5	US-10-476-265-19	Sequence 19, Appl
42	542	91.9	132	4	US-10-010-9428-11	Sequence 11, Appl
43	542	91.9	132	4	US-10-388-389-11	Sequence 11, Appl
44	542	91.9	132	4	US-10-703-713-11	Sequence 11, Appl
45	542	91.9	132	4	US-10-704-070-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-835-087-3  
; Sequence 3, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; TITLE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-3

Alignment Scores:			
Pred. No.:	1,76e-55	Length:	112
Score:	590.00	Matches:	112
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-733-563-109 (1-336) x US-09-835-087-3 (1-112)

QY 1 GATGTAGTGTGACCCAGTCTCCACTCTCTTGCCGGTTACCTTGGACGAGCCTCC 60  
|||||

```
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
Qy 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGAAGAACACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
Qy 121 TTTGAGCAGAGCCAGGCCAGTCTCAAGGCCCTAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60
Qy 181 TCTGAGTCCCTGACAGGTCAGAGTCTCAAGGCCCTAATCTATCTGGTGTCTAAACTGGAC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTGCTGGCAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAGGACCGAGCTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 2
US-09-809-739-14
; Sequence 14, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-14
Alignment Scores:
Pred. No.: 1.76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-14 (1-112)
Qy 1 GATGTAGTAGTACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
Qy 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGAAGAACACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
Qy 121 TTTGAGCAGAGCCAGGCCAGTCTCAAGGCCCTAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60
Qy 181 TCTGAGTCCCTGACAGGTCAGAGTCTCAAGGCCCTAATCTATCTGGTGTCTAAACTGGAC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTGCTGGCAAGGTACACATTTTCCG 300
Db 81 SerArgValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTGCTGGCAAGGTACACATTTTCCG 300
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```
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAGGACCGAGCTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 3
US-09-840-459-12
; Sequence 12, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-12
Alignment Scores:
Pred. No.: 1.76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-12 (1-112)
Qy 1 GATGTAGTAGTACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
Qy 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGAAGAACACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
Qy 121 TTTGAGCAGAGCCAGGCCAGTCTCAAGGCCCTAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60
Qy 181 TCTGAGTCCCTGACAGGTCAGAGTCTCAAGGCCCTAATCTATCTGGTGTCTAAACTGGAC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTGCTGGCAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAGGACCGAGCTGGAGATCAAG 336
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Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 4

US-10-766-773-12

Sequence 12, Application US/10766773

Publication No. US20040126851A1

GENERAL INFORMATION:

APPLICANT: LaRosa, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: Jones, S. Tarran

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

FILE REFERENCE: 1855.1052-028

CURRENT APPLICATION NUMBER: US/10/766,773

CURRENT FILING DATE: 2004-01-27

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1998-07-23

PRIOR APPLICATION NUMBER: 09/121,781

NUMBER OF SEQ ID NOS: 106

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 112

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanized sequence

US-10-766-773-12

Alignment Scores:

Pred. No.:	1-76e-55	Length:	112
Score:	590.00	Matches:	112
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-733-563-109 (1-336) x US-10-766-773-12 (1-112)

QY 1 GATGTAGTGTATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProIleSer 20

QY 61 ATCTCTTGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120

Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTTACGACAGCCAGCCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180

Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTTCAAGCGCAGTGTGATGATGATGATGATGATGATGATGATGAT 240

Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGTCGCAAGGTACACATTTTCGG 300

Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTCCGACAGGACCCGACTGGAGATCAAG 336

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 5

US-10-766-610-12

Sequence 12, Application US/10766610

Publication No. US20040132980A1

GENERAL INFORMATION:

APPLICANT: LaRosa, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: Jones, S. Tarran

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

FILE REFERENCE: 1855.1052-029

CURRENT APPLICATION NUMBER: US/10/766,610

CURRENT FILING DATE: 2004-01-27

PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: PCT/US01/03537

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 112

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanized sequence

US-10-766-610-12

Alignment Scores:

Pred. No.:	1-76e-55	Length:	112
Score:	590.00	Matches:	112
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-733-563-109 (1-336) x US-10-766-610-12 (1-112)

QY 1 GATGTAGTGTATGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProIleSer 20

QY 61 ATCTCTTGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120

Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTTACGACAGCCAGCCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180

Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTTCAAGCGCAGTGTGATGATGATGATGATGATGATGATGATGAT 240

Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGTCGCAAGGTACACATTTTCGG 300

Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTCCGACAGGACCCGACTGGAGATCAAG 336

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 6

US-10-733-563-12

Sequence 12, Application US/10733563

Publication No. US20040151721A1

GENERAL INFORMATION:

APPLICANT: O'Keefe, Theresa

APPLICANT: Ponath, Paul

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

```
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-12
Alignment Scores:
Pred. No.: 1,76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-109 (1-336) x US-10-733-563-12 (1-112)
QY 1 GATGTAGTGTGACCCAGTCTCCACTCTCTCTGTCGCCGTTACCCCTGGGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTGCAAGTCAAGTCAGAGCTCTTAGATAGTGTGGAAGACATTTTGAATTGG 120
Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTGACGAGAGCCAGGCGCAGTCTCCAAAGGCGCCTAATCTATCTGCTGCTAAACTGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGAGTCCCTGACAGGTTGAGCGGCGATGCGGATGCGGACAGATTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCGTCGCAAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACACGTTTCGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112
RESULT 7
US-10-662-061-14
; Sequence 14, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-12
Alignment Scores:
Pred. No.: 1,76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-109 (1-336) x US-10-733-563-12 (1-112)
QY 1 GATGTAGTGTGACCCAGTCTCCACTCTCTCTGTCGCCGTTACCCCTGGGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTGCAAGTCAAGTCAGAGCTCTTAGATAGTGTGGAAGACATTTTGAATTGG 120
Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTGACGAGAGCCAGGCGCAGTCTCCAAAGGCGCCTAATCTATCTGCTGCTAAACTGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGAGTCCCTGACAGGTTGAGCGGCGATGCGGATGCGGACAGATTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCGTCGCAAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACACGTTTCGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112
RESULT 7
US-10-662-061-14
; Sequence 14, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
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US-09-840-459-106

Alignment Scores:

Pred. No.: 7,98e-55 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-106 (1-114)

QY 4 GTAGTGTATGACCCAGTCTCCACTCTCTTCCCGGTTACCTTGGAGCAGCCTCCATC 63  
DB 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGAGAAAGACATTTTGAATGGTTT 123  
DB 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGCCAGTCTCCAGCGCCTTAATCTATCTGGTGTCTAAACTGGACTCT 183  
DB 42 GlnGlnArgProGlyGlnSerProArgAGLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGTTGACGGCAGTGTGATCAGGACAGATTTACACTGAAATCAGC 243  
DB 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGCGCTGAGGATGTTGGAGTTTATTATTCGTCGCAAGGTACACATTTCCGTAC 303  
DB 82 ArgValGluAlaGlnAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACCTTGGACAAAGGACCCGACTGGAGATCAAG 336  
DB 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 9

US-10-766-773-106  
; Sequence 106, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-028  
; CURRENT APPLICATION NUMBER: US/10/766,773  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-10-766-773-106

Alignment Scores:  
Pred. No.: 7,98e-55 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.98% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x US-10-766-773-106 (1-114)

QY 4 GTAGTGTATGACCCAGTCTCCACTCTCTTCCCGGTTACCTTGGAGCAGCCTCCATC 63  
DB 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGAGAAAGACATTTTGAATGGTTT 123  
DB 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGCCAGTCTCCAGCGCCTTAATCTATCTGGTGTCTAAACTGGACTCT 183  
DB 42 GlnGlnArgProGlyGlnSerProArgAGLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGTTGACGGCAGTGTGATCAGGACAGATTTACACTGAAATCAGC 243  
DB 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGCGCTGAGGATGTTGGAGTTTATTATTCGTCGCAAGGTACACATTTCCGTAC 303  
DB 82 ArgValGluAlaGlnAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACCTTGGACAAAGGACCCGACTGGAGATCAAG 336  
DB 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 10

US-10-766-610-106  
; Sequence 106, Application US/10766610  
; Publication No. US20040132980A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-029  
; CURRENT APPLICATION NUMBER: US/10/766,610  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/840,459  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-10-766-610-106

Alignment Scores:  
Pred. No.: 7,98e-55 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x US-10-766-610-106 (1-114)

QY 4 GTAGTGATGACCCAGCTCTCCACTCTCTTCCCGTTACCCCTGGACAGCCAGCTCCATC 63  
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerile 21  
QY 64 TCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATTTTGAATTGGTTT 123  
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCGCAGGCGAGTCTCCAGGCGCCTAATCTATCTGGTCTCTAAACTGACACT 183  
Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGACAGAGATTTCCACACTGAAAATCAGC 243  
Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCGCAAGGTACACATTTCCGTAC 303  
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACGTTCGACAGGACCGAGCTCGAGATCAAG 336  
Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 11

; Sequence 106, Application US/10733563  
; Publication No. US20040151721A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Paul  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 10448-213001  
; CURRENT APPLICATION NUMBER: US/10/733,563  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: US 10/272,899  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized light chain

## US-10-733-563-106

Alignment Scores:  
Pred. No.: 7,98e-55 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x US-10-733-563-106 (1-114)

QY 4 GTAGTGATGACCCAGCTCTCCACTCTCTTCCCGTTACCCCTGGACAGCCAGCTCCATC 63  
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerile 21  
QY 64 TCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATTTTGAATTGGTTT 123  
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCGCAGGCGAGTCTCCAGGCGCCTAATCTATCTGGTCTCTAAACTGACACT 183

Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGACAGAGATTTCCACACTGAAAATCAGC 243  
Db 62 GlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCGCAAGGTACACATTTCCGTAC 303  
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACGTTCGACAGGACCGAGCTCGAGATCAAG 336  
Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 12

US-09-835-087-4  
; Sequence 4, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; FILE REFERENCE: 1855-2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence

## Alignment Scores:

Pred. No.: 4.62e-54 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-109 (1-336) x US-09-835-087-4 (1-112)

QY 1 GATGTAGTGATGACCCAGCTCTCCACTCTCTTCCCGTTACCCCTGGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTGACAGAGCGCAGGCGAGTCTCCAGGCGCCTAATCTATCTGGTCTCTAAACTGAC 180  
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCTCTGACAGGTTCCAGCGCAGTGGATCAGGACAGATTTCCACACTGAAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCGCAAGGTACACATTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGACAGGACCGAGCTCGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 13

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US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia E.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Alignment Scores:
Pred. No.: 4,62e-54 Length: 112
Score: 577.00 Matches: 110
Percent Similarity: 98.21% Conservative: 0
Best Local Similarity: 98.21% Mismatches: 2
Query Match: 97.80% Indels: 0
DB: 3 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-15 (1-112)
QY 1 GATGTAGTGTGATGACCCAGCTCTCCACTCTCTTGGCCCGTTACCTTGGACAGCAGCTCC 60
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACACATTTTGAATTGG 120
DB 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTCAGCAGAGCCAGCCAGCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180
DB 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuLeuTyrLeuValSerLysLeuAsp 60
QY 181 TCTGAGTCCCTGACAGGTTTCAGCGCAGTGTGATCAGGACAGATTTTCACACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTTATTATTGCTGCAAGGTACACATTTTCG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTTGGACAGGACCCGACTGGAGATCAAG 336
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 14
US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02

US-09-809-739-15
; Sequence 15, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
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; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 112  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-10-766-773-13

Alignment Scores:  
Pred. No.: 4.62e-54 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x US-10-766-773-13 (1-112)

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Qy 1 GATGTAGTGTGACCCAGCTCTCCACTCTCCTTGCCCGTTACCTTGGACAGCCAGCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProIleSer 20

Qy 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATGATGAGAAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

Qy 121 TTTCAGCAGAGCCAGCCAGCTCTCCAGGCGCCTTAATCTATCTGGTCTTAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60

Qy 181 TCTGGAGTCCCTGACAGGTTTACGCGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80

Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGGCAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100

Qy 301 TACACGTTCCGACAGGACCGGACTGGAGATCAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112
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Search completed: January 28, 2006, 09:31:11  
Job time : 42.033 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:46:13 ; Search time 4.28829 Seconds  
(without alignments)  
1696.980 Million cell updates/sec

Title: US-10-733-563-109

Perfect score: 590

Sequence: 1 gatgtagtgtgaccagtc.....ggaccgcgactggatcaag 336

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=PublishedApplications\_AA\_New -OPMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10733563 @CNC 1.1.1 @runat\_27012006\_180008\_4917  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=3 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_AA\_New.\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pcp.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	577	97.8	112	7	US-11-075-184A-4
3	572	96.9	112	7	US-11-075-184A-7
4	570	96.6	112	7	US-11-075-184A-5
5	565	95.8	112	7	US-11-075-184A-6
6	542	91.9	132	6	US-10-789-273-11
7	536	90.8	112	7	US-11-075-184A-1
8	536	90.8	132	6	US-10-789-273-5
9	520	88.1	132	6	US-10-789-273-2
10	510	86.4	253	7	US-11-054-515-1964

11	507	85.9	112	6	US-10-477-950-4	Sequence 4, Appli
12	491.5	83.3	244	7	US-11-054-515-1991	Sequence 1991, Ap
13	490.5	83.1	261	7	US-11-056-825-2	Sequence 2, Appli
14	485.5	82.3	259	7	US-11-056-825-7	Sequence 7, Appli
15	483	81.9	113	7	US-11-054-689-122	Sequence 122, App
16	480	81.4	139	7	US-11-128-900-25	Sequence 25, Appl
17	480	81.4	139	7	US-11-128-900-114	Sequence 114, App
18	474	80.3	132	6	US-10-489-866-30	Sequence 30, Appl
19	470	79.7	100	7	US-11-054-669-75	Sequence 75, Appl
20	470	79.7	100	7	US-11-054-669-76	Sequence 76, Appl
21	470	79.7	100	7	US-11-084-554-103	Sequence 103, App
22	470	79.7	100	7	US-11-084-554-107	Sequence 107, App
23	470	79.7	100	7	US-11-128-900-113	Sequence 113, App
24	470	79.7	100	7	US-11-004-590-82	Sequence 82, Appl
25	470	79.7	100	7	US-11-004-590-83	Sequence 83, Appl
26	459	77.8	112	7	US-11-012-353-57	Sequence 57, Appl
27	457	77.5	112	7	US-11-012-353-61	Sequence 61, Appl
28	457	77.5	131	7	US-11-012-353-63	Sequence 63, Appl
29	456	77.3	112	7	US-11-012-353-65	Sequence 65, Appl
30	456	77.3	131	7	US-11-012-353-67	Sequence 67, Appl
31	451	76.4	112	7	US-11-012-353-60	Sequence 60, Appl
32	451	76.4	113	6	US-10-834-397-15	Sequence 15, Appl
33	447	75.8	113	6	US-10-932-334-60	Sequence 60, Appl
34	447	75.8	113	6	US-10-932-334-65	Sequence 65, Appl
35	447	75.8	131	7	US-11-125-837-23	Sequence 23, Appl
36	446	75.6	113	6	US-10-932-334-59	Sequence 59, Appl
37	445	75.4	112	7	US-11-012-353-55	Sequence 55, Appl
38	445	75.4	112	7	US-11-012-353-56	Sequence 56, Appl
39	445	75.4	263	7	US-11-089-286-66	Sequence 66, Appl
40	444	75.3	144	7	US-11-055-163-16	Sequence 16, Appl
41	443	75.1	113	6	US-10-932-334-61	Sequence 61, Appl
42	443	75.1	149	7	US-11-089-266-2	Sequence 2, Appli
43	443	75.1	239	7	US-11-139-499-6	Sequence 6, Appli
44	441	74.7	113	6	US-10-489-866-20	Sequence 20, Appl
45	441	74.7	116	7	US-11-065-943-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-11-075-184A-3  
; Sequence 3, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKA  
US-11-075-184A-3

Alignment Scores:		
Pred. No.:	2.96e-57	Length: 112
Score:	590.00	Matches: 112
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	7	Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-3 (1-112)

QY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60  
Db |||||  
1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGTAGTAGTGTGGAAGACATTTTGAATTGG 120  
Db |||||  
21 IleSerCysLysSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGGCGAGTCTCAAGGCGCTTAATCTATCTGGTGTCTAAACTGGAC 180  
Db |||||  
41 PheGlnGlnArgProGlyGlnSerProArgArgLeuLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGGAGTCCCTGACAGCTTACAGCGCAGTGGATCAGGACAGATTTTCACACTGAAATC 240  
Db |||||  
61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATTTATTTCTGTCGCAAGGTACACATTTCCG 300  
Db |||||  
81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGACAGGACCGAGCTCGAGATCAAG 336  
Db |||||  
101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 2

US-11-075-184A-4  
; Sequence 4, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE  
US-11-075-184A-4

Alignment Scores:  
Pred. No.: 7,81e-56 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-4 (1-112)

QY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60  
Db |||||  
1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGTAGTAGTGTGGAAGACATTTTGAATTGG 120  
Db |||||  
21 IleSerCysLysSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGGCGAGTCTCAAGGCGCTTAATCTATCTGGTGTCTAAACTGGAC 180  
Db |||||  
41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGGAGTCCCTGACAGCTTACAGCGCAGTGGATCAGGACAGATTTTCACACTGAAATC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATTTATTTCTGTCGCAAGGTACACATTTCCG 300  
Db |||||  
81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGACAGGACCGAGCTCGAGATCAAG 336  
Db |||||  
101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 3

US-11-075-184A-7  
; Sequence 7, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE  
US-11-075-184A-7

Alignment Scores:  
Pred. No.: 2,75e-55 Length: 112  
Score: 572.00 Matches: 109  
Percent Similarity: 97.32% Conservative: 0  
Best Local Similarity: 97.32% Mismatches: 3  
Query Match: 96.95% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-7 (1-112)

QY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60  
Db |||||  
1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyHisProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGTAGTAGTGTGGAAGACATTTTGAATTGG 120  
Db |||||  
21 IleSerCysLysSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGGCGAGTCTCAAGGCGCTTAATCTATCTGGTGTCTAAACTGGAC 180  
Db |||||  
41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGGAGTCCCTGACAGCTTACAGCGCAGTGGATCAGGACAGATTTTCACACTGAAATC 240  
Db |||||  
61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATTTATTTCTGTCGCAAGGTACACATTTCCG 300  
Db |||||  
81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGACAGGACCGAGCTCGAGATCAAG 336  
Db |||||  
101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 4

US-11-075-184A-5  
; Sequence 5, Application US/11075184A



```
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; TITLE OF INVENTION: Receptor Antagonists
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 112
; TYPE: PRP
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; OTHER INFORMATION: 1D9KK
US-11-075-184A-5
Alignment Scores:
Pred. No.: 4,55e-55 Length: 112
Score: 570.00 Matches: 109
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.61% Indels: 0
DB: Gaps: 0
US-10-733-563-109 (1-336) x US-11-075-184A-5 (1-112)
QY 1 GATGAGTGTGATGACCCAGGCTCTCCACTCTCTTGGCCCGTTACCTTGGACAGCAGCTCC 60
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATGATGATGAGAAAGACATTTTGAATTGG 120
DB 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180
DB 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGCAGTGTGATCAGGACAGATTTTCACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGAGATTATTATTCGTCGCAAGGTACACATTTTCG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
DB 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112
RESULT 5
US-11-075-184A-6
; Sequence 6, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
US-10-733-563-109 (1-336) x US-11-075-184A-6 (1-112)
QY 1 GATGAGTGTGATGACCCAGGCTCTCCACTCTCTTGGCCCGTTACCTTGGACAGCAGCTCC 60
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATGATGATGAGAAAGACATTTTGAATTGG 120
DB 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180
DB 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGCAGTGTGATCAGGACAGATTTTCACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGAGATTATTATTCGTCGCAAGGTACACATTTTCG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
DB 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112
RESULT 6
US-10-789-273-11
; Sequence 11, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)....(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-789-273-11
```

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; LENGTH: 112
; TYPE: PRP
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; OTHER INFORMATION: 1D9KK
US-11-075-184A-6
Alignment Scores:
Pred. No.: 1,6e-54 Length: 112
Score: 565.00 Matches: 108
Percent Similarity: 96.43% Conservative: 0
Best Local Similarity: 96.43% Mismatches: 4
Query Match: 95.76% Indels: 0
DB: Gaps: 0
US-10-733-563-109 (1-336) x US-11-075-184A-6 (1-112)
QY 1 GATGAGTGTGATGACCCAGGCTCTCCACTCTCTTGGCCCGTTACCTTGGACAGCAGCTCC 60
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyHisProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATGATGATGAGAAAGACATTTTGAATTGG 120
DB 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180
DB 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGCAGTGTGATCAGGACAGATTTTCACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGAGATTATTATTCGTCGCAAGGTACACATTTTCG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
DB 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112
RESULT 6
US-10-789-273-11
; Sequence 11, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)....(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-789-273-11
```

Alignment Scores:  
Pred. No.: 5,26e-52 Length: 132  
Score: 542.00 Matches: 102  
Percent Similarity: 96.43% Conservative: 6  
Best Local Similarity: 91.07% Mismatches: 4  
Query Match: 91.86% Indels: 0  
DB: 6 Gaps: 0

US-10-733-563-109 (1-336) x US-10-789-273-11 (1-132)

```
QY 1 GATGTAGTGAATGACCCAGCTCTCCACTCTCTGCGCGTTACCTTGGACAGCCCTCC 60
   |||
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
   |||
QY 61 ATCTCTTCAAGTCAAGTCAAGTCTTCAAGGCGCTTAATCTATCTGGTGTCTAAACTGG 120
   |||
Db 41 IleSerCysLysSerSerGlnSerLeuLeuAaspSerAaspGlyLysThrTyrLeuAasp 60
   |||
QY 121 TTTCAAGCAGGCGCAGGCGAGTCTCAAGGCGCTTAATCTATCTGGTGTCTAAACTGG 180
   |||
Db 61 LeuLeuGlnLysProGlyGlnSerProGlnArgLeuIleTyrLeuValSerLysLeuAasp 80
   |||
QY 181 TCTGAGTCCCTGACAGCTTCAAGGCGAGTGTGATCAGGACAGATTTTCAACTGGAATC 240
   |||
Db 81 SerGlyValProAaspArgPheSerGlySerGlyThrAaspPheThrLeuLysIle 100
   |||
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTTGCTGCGCAAGGTACACATTTCCG 300
   |||
Db 101 SerArgValGluAlaGluAaspValGlyValTyrCysTrpGlnGlyThrHisPhePro 120
   |||
QY 301 TACAGTTCGACAGGACCGGACTCGAGATCAAG 336
   |||
Db 121 ArgThrPheGlyGlnGlyThrLysValGluIleLys 132
```

## RESULT 7

US-11-075-184A-1  
; Sequence 1, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Murine 1D9 antibody kappa light chain variable (VK) region;  
; OTHER INFORMATION: Murine 1D9 antibody kappa light chain variable (VK) region;  
; OTHER INFORMATION: presumably Mus musculus

US-11-075-184A-1

Alignment Scores:  
Pred. No.: 2,38e-51 Length: 112  
Score: 536.00 Matches: 100  
Percent Similarity: 95.54% Conservative: 7  
Best Local Similarity: 89.29% Mismatches: 5  
Query Match: 90.85% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-1 (1-112)

```
QY 1 GATGTAGTGAATGACCCAGCTCTCCACTCTCTGCGCGTTACCTTGGACAGCCAGCCCTCC 60
   |||
Db 1 AspValValMetThrGlnThrProLeuThrProLeuSerValThrValGlyHisProAlaSer 20
   |||
```

```
QY 61 ATCTCTTCAAGTCAAGTCAAGTCTTCAAGGCGCTTCAAGTGTGATGGAAGACATTTTGAATTGG 120
   |||
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAaspSerAaspGlyLysThrPheLeuAaspTrp 40
   |||
QY 121 TTTCAAGCAGGCGCAGGCGAGTCTTCAAGGCGCTTAATCTATCTGGTGTCTAAACTGGAC 180
   |||
Db 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAasp 60
   |||
QY 181 TCTGAGTCCCTGACAGGTTTCAAGGCGAGTGTGATCAGGACAGATTTTCAACTGGAATC 240
   |||
Db 61 SerGlyValProAaspArgPheThrGlySerGlyThrAaspPheThrLeuLysIle 80
   |||
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTTGCTGCGCAAGGTACACATTTCCG 300
   |||
Db 81 SerArgValGluAlaGluAaspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100
   |||
QY 301 TACAGTTCGACAGGACCGGACTCGAGATCAAG 336
   |||
Db 101 TyrThrPheGlyGlyThrLysLeuGluIleLys 112
```

## RESULT 8

US-10-789-273-5  
; Sequence 5, Application US/10789273  
; Publication No. US20050249725A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/789,273  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(20)  
; OTHER INFORMATION: humanized 3D6 light chain variable region

US-10-789-273-5

Alignment Scores:  
Pred. No.: 2,38e-51 Length: 132  
Score: 536.00 Matches: 101  
Percent Similarity: 96.40% Conservative: 6  
Best Local Similarity: 90.99% Mismatches: 4  
Query Match: 90.85% Indels: 0  
DB: 6 Gaps: 0

US-10-733-563-109 (1-336) x US-10-789-273-5 (1-132)

```
QY 4 GTAGTGAATGACCCAGTCTCCACTCTCTGCGCGTTACCTTGGACAGCCAGCTCCATC 63
   |||
Db 22 ValValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSerIle 41
   |||
QY 64 TCTTGAAGTCAAGTCAAGCTTCTAGATAGTGTGAGACATTTTGAATTGGTTT 123
   |||
Db 42 SerCysLysSerSerGlnSerLeuLeuAaspSerAaspGlyLysThrTyrLeuAaspTrpLeu 61
   |||
QY 124 CAGCAGGCGCAGGCGAGTCTTCAAGGCGCTTAATCTATCTGGTGTCTAAACTGGACTCT 183
   |||
Db 62 LeuGlnLysProGlyGlnSerProGlnArgLeuIleTyrLeuValSerLysLeuAaspSer 81
   |||
```

QY 184 GGAGTCCCTGACAGGTTTCAGCGGCGAGTGGATCAGGACAGATTTCACATGAAATCAGC 243  
Db |||||||  
82 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 101  
QY 244 ACAGTGGAGGCTGAGGATCTGGAGTTTATTATTCCTGCGAGGTACACATTTCCGTAC 303  
Db |||||||  
102 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProArg 121  
QY 304 ACGTTTGGCAAGGACCGACTGGAGATCAAG 336  
Db |||||||  
122 ThrPheGlyGlnGlyThrLysValGluIleLys 132

RESULT 9  
US-10-789-273-2  
; Sequence 2, Application US/10789273  
; Publication No. US20050249725A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/789,273  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(20)  
US-10-789-273-2

Alignment Scores:  
Pred. No.: 1,34e-49 Length: 132  
Score: 520.00 Matches: 96  
Percent Similarity: 95.50% Conservative: 10  
Best Local Similarity: 86.43% Mismatches: 5  
Query Match: 88.14% Indels: 0  
DB: Gaps: 0

US-10-733-563-109 (1-336) x US-10-789-273-2 (1-132)  
QY 4 GTAGTGTGATGATGACCCAGTCTCCACTCTCTGCGCGTTACCTTGGACAGCAGCCTCCATC 63  
Db |||||||  
22 ValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSerIle 41  
QY 64 TCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGTGAAACACATTTTGAATGGTTT 123  
Db |||||||  
42 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrLeuAsnTrpLeu 61  
QY 124 CAGCAGAGCCAGGCGCAGTCTCCAGGCGCTTAATCTATCTGCTGTCTAAACTGGACTCT 183  
Db |||||||  
62 LeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAspSer 81  
QY 184 GGAGTCCCTGACAGGTTTCAGCGGCGAGTGGATCAGGACAGATTTCACATGAAATCAGC 243  
Db |||||||  
82 GlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIleSer 101  
QY 244 ACAGTGGAGGCTGAGGATCTGGAGTTTATTATTCCTGCGAGGTACACATTTCCGTAC 303  
Db |||||||  
102 ArgIleGluAlaGluAspLeuGlyLeuTyrCysTrpGlnGlyThrHisPheProArg 121  
QY 304 ACGTTTGGCAAGGACCGACTGGAGATCAAG 336

Db 122 ThrPheGlyGlyGlyThrLysLeuGluIleLys 132

RESULT 10  
US-11-054-515-1964  
; Sequence 1964, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind BlyS  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1964  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1964

Alignment Scores:  
Pred. No.: 1.67e-48 Length: 253  
Score: 510.00 Matches: 97  
Percent Similarity: 92.86% Conservative: 7  
Best Local Similarity: 86.61% Mismatches: 8  
Query Match: 86.44% Indels: 0  
DB: Gaps: 0

US-10-733-563-109 (1-336) x US-11-054-515-1964 (1-253)  
QY 1 GATGTAGTGTGATGACCCAGTCTCCACTCTCTGCGCGTTACCTTGGACAGCAGCCTCC 60  
Db |||||||  
141 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 160  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTGTGAAACACATTTTGAATGG 120  
Db |||||||  
161 IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 180  
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCTTAATCTATCTGCTGTCTAAACTGGAC 180  
Db |||||||  
181 PheGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 200  
QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGCGAGTGGATCAGGACAGATTTCACATGAAATC 240  
Db |||||||  
201 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 220  
QY 241 AGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTATTCCTGCGAGGTACACATTTCCG 300  
Db |||||||  
221 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaThrArgTrpPro 240  
QY 301 TACAGTTTGGCAAGGACCGACTGGAGATCAAG 336  
Db |||||||

iv

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-11-056-825-2

Alignment Scores:  
Pred. No.: 2,27e-46 Length: 261  
Score: 490.50 Matches: 93  
Percent Similarity: 92.92% Conservative: 12  
Best Local Similarity: 82.30% Mismatches: 7  
Query Match: 83.14% Indels: 1  
DB: Gaps: 1

US-10-733-563-109 (1-336) x US-11-056-825-2 (1-261)

```
QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTTCCCGTTACCTTGGACAGCCAGCTCC 60
      :::::::::::
Db 134 GluileValLeuThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 153

QY 61 ATCTTGTGCAAGTCAAGTCAGAGCTCTTAGATAGTGGAAAGACATTTTGAATTGG 120
      :::::::::::
Db 154 IleSerCysArgSerSerGlnAsnLeuValTyrSerAspGlyAsnThrTyrLeuSerTrp 173

QY 121 TTTTCAGCAGAGCCAGGCCAGTCTCCAAGCGCCTAATCTATCTGTGTCTAAACTGGAC 180
      :::::::::::
Db 174 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrIleValSerAsnArgAsp 193

QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGACGATGGATCAGGACAGATTTTCACACTGAAATC 240
      :::::::::::
Db 194 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuIle 213

QY 241 ACCAGATGGAGCTGAGATGTTGGAGTTTATTATTATGCTGCAAGGTACACATTTT--- 297
      :::::::::::
Db 214 SerArgValGluArgGluAspIleGlyValTyrCysMetGlnGlyThrHisTrpPro 233

QY 298 CGGTACACGTTCCGACAAAGGACCCGACTGGAGATCAAG 336
      :::::::::::
Db 234 ProArgThrPheGlyGlnGlyThrIleValGluIleLys 246
```

## RESULT 14

US-11-056-825-7  
; Sequence 7, Application US/11056825  
; Publication No. US20050255109A1  
; GENERAL INFORMATION:  
; APPLICANT: Feilding-Habermann, Brunhilde  
; APPLICANT: Janda, Kim D.  
; APPLICANT: Saven, Alan  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS  
; FILE REFERENCE: SCRP-0042  
; CURRENT APPLICATION NUMBER: US/11/056,825  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: US 60/626,726  
; PRIOR FILING DATE: 2004-11-10  
; PRIOR APPLICATION NUMBER: US 60/544,807  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7

Alignment Scores:  
Pred. No.: 7.98e-46 Length: 259  
Score: 485.50 Matches: 92  
Percent Similarity: 92.04% Conservative: 12

US-11-056-825-7  
; OTHER INFORMATION: Synthetic Construct

Best Local Similarity: 81.42% Mismatches: 8  
Query Match: 82.29% Indels: 1  
DB: Gaps: 1  
US-10-733-563-109 (1-336) x US-11-056-825-7 (1-259)

```
QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTTCCCGTTACCTTGGACAGCCAGCTCC 60
      :::::::::::
Db 134 GluileValLeuThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 153

QY 61 ATCTTGTGCAAGTCAAGTCAGAGCTCTTAGATAGTGGAAAGACATTTTGAATTGG 120
      :::::::::::
Db 154 IleSerCysArgSerSerGlnAsnLeuValTyrSerAspGlyAsnThrTyrLeuSerTrp 173

QY 121 TTTTCAGCAGAGCCAGGCCAGTCTCCAAGCGCCTAATCTATCTGTGTCTAAACTGGAC 180
      :::::::::::
Db 174 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrIleValSerAsnArgAsp 193

QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGACGATGGATCAGGACAGATTTTCACACTGAAATC 240
      :::::::::::
Db 194 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuIle 213

QY 241 ACCAGATGGAGCTGAGATGTTGGAGTTTATTATTATGCTGCAAGGTACACATTTT--- 297
      :::::::::::
Db 214 SerArgValGluArgGluAspIleGlyValTyrCysMetGlnGlyThrHisTrpPro 233

QY 298 CGGTACACGTTCCGACAAAGGACCCGACTGGAGATCAAG 336
      :::::::::::
Db 234 ProArgThrPheGlyGlnGlyThrIleValGluIleLys 246
```

## RESULT 15

US-11-054-669-122  
; Sequence 122, Application US/11054669  
; Publication No. US20050261480A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
; FILE REFERENCE: 30219/US/3  
; CURRENT APPLICATION NUMBER: US/11/054,669  
; CURRENT FILING DATE: 2005-02-08  
; PRIOR APPLICATION NUMBER: US 10/194,975  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 122  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-669-122

Alignment Scores:  
Pred. No.: 1.49e-45 Length: 113  
Score: 483.00 Matches: 93  
Percent Similarity: 90.18% Conservative: 8  
Best Local Similarity: 83.04% Mismatches: 11  
Query Match: 81.86% Indels: 0  
DB: Gaps: 0

US-10-733-563-109 (1-336) x US-11-054-669-122 (1-113)

```
QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTTCCCGTTACCTTGGACAGCCAGCTCC 60
      :::::::::::
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20

QY 61 ATCTTGTGCAAGTCAAGTCAGAGCTCTTAGATAGTGGAAAGACATTTTGAATTGG 120
      :::::::::::
Db 21 IleSerCysArgSerSerGlnSerLeuGluHisAsnAsnGlyAsnThrTyrLeuAsnTrp 40

QY 121 TTTTCAGCAGAGCCAGGCCAGTCTCCAAGCGCCTAATCTATCTGTGTCTAAACTGGAC 180
      :::::::::::
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrArgValSerAsnArgPhe 60
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 172.928 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-110  
Perfect score: 1765  
Sequence: 1 ASTGKPSVFPLAPSKSTSG.....MREALHNHYTKSLSPGK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*  
9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	100.0	330	8	Adq89332 Human imm
2	1765	100.0	330	9	Aeb09605 Human IgG
3	1765	100.0	333	8	Adj95914 Human IgG
4	1765	100.0	333	8	Adq89336 Human imm
5	1765	100.0	333	9	Aeb09609 Human IgG
6	1765	100.0	356	8	Adj95974 Humanised
7	1765	100.0	444	3	AAY32263 Immunoglob
8	1765	100.0	448	8	Adp88447 Antibody
9	1765	100.0	448	8	Adp88431 Antibody
10	1765	100.0	462	9	Aeb08800 Anti-NOGO
11	1765	100.0	467	6	AdA47334 TRX1 heavy
12	1765	100.0	467	6	AdA47336 TRX1 heavy
13	1765	100.0	467	8	Adp88446 Antibody
14	1765	100.0	467	8	Adp88430 Antibody
15	1765	100.0	467	8	Adq87966 Heavy Cha
16	1765	100.0	467	8	Adq87974 Heavy Cha
17	1765	100.0	473	5	Abg70743 Mouse/hum
18	1765	100.0	475	8	AdL23051 Mouse/hum
19	1765	100.0	475	8	AdL23054 Humanised
20	1765	100.0	475	8	AdS88803 Humanised
21	1765	100.0	475	8	AdS88792 A mouse/h
22	1758	99.6	469	7	AdL23199 Human ant
23	1756	99.5	330	4	Aab04071 Zcytor 10
24	1756	99.5	330	5	Aam47856 Human Ig-

## ALIGNMENTS

## RESULT 1

ID	ADQ89332	standard; protein; 330 AA.
XX	AC	ADQ89332;
XX	DT	21-OCT-2004 (first entry)
XX	DE	Human immunoglobulin protein #44.
XX	KW	Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2; inflammatory disease; autoimmune disorder; graft rejection;
KW	KW	HIV infection; atherosclerosis; antinflammatory; immunosuppressive;
KW	KW	anti-HIV; virucide; antiarteriosclerotic.
XX	OS	Homo sapiens.
XX	FN	US2004151721-A1.
XX	PD	05-AUG-2004.
XX	PF	10-DEC-2003; 2003US-00733563.
XX	PR	19-OCT-2001; 2001US-0350166P.
PR	PR	26-JUN-2002; 2002US-0392364P.
XX	XX	17-OCT-2002; 2002US-00272899.
XX	PA	(OKEE/) O'KEEFE T.
XX	PA	(PONA/) PONA P.
PI	PI	O'Keefe T, Ponath P;
XX	XX	WPI; 2004-580175/56.
XX	XX	New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists, useful for diagnosing and/or treating inflammatory or autoimmune diseases, and HIV infection.
PT	PT	Claim 1; SEQ ID NO 110; 128pp; English.
XX	XX	The invention relates to humanised immunoglobulin heavy and light chains which have specificity for the CC-chemokine receptor 2 (CCR2) and an immunoglobulin or its antigen binding fragment comprising the chains. The humanised immunoglobulin or its antigen binding fragment preferably comprises two heavy chains and two light chains. The humanised immunoglobulin and its heavy and light chains are useful for the diagnosis, prevention and/or treatment of diseases or conditions

25	1756	99.5	330	5	AAE21960 Human dea
26	1756	99.5	330	5	ABB81641 Human IGG
27	1756	99.5	330	5	ABB05736 Human imm
28	1756	99.5	330	6	ABP71856 Human IGG
29	1756	99.5	330	6	AAE32915 Human imm
30	1756	99.5	330	6	AAE32627 Human imm
31	1756	99.5	330	6	ABR82103 Human DR6
32	1756	99.5	330	6	AAO31102 Human A2-
33	1756	99.5	330	6	ABR55836 Anti-Ang-
34	1756	99.5	330	6	AAO30893 Human imm
35	1756	99.5	330	7	ADP11389 Anti-OPGL
36	1756	99.5	330	7	ADP97351 Human IGG
37	1756	99.5	330	7	ADF83605 Cytokine
38	1756	99.5	330	7	ADF75001 Human Ig
39	1756	99.5	330	8	ADM41537 Anti-inte
40	1756	99.5	330	8	ADM68911 Human IgG
41	1756	99.5	330	8	ADR43460 Heavy cha
42	1756	99.5	330	8	ADR31605 Human IGG
43	1756	99.5	330	8	ADN87909 Anti-IFN-
44	1756	99.5	330	8	ADN33230 IgG1-CH h
45	1756	99.5	330	8	ADS94906 Anti-IFN-

CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a human  
 CC immunoglobulin protein of the invention.

XX Sequence 330 AA;

Query Match 100.0%; Score 1765; DB 8; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 Db 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
 Db 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
 Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSPFLYSLKLTVDKSRW 300  
 Db 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSPFLYSLKLTVDKSRW 300  
 Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
 Db 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330

# RESULT 2

AEBO9605  
 ID AEB09605 standard; protein; 330 AA.

XX AEB09605;

XX 08-SEP-2005 (first entry)

XX Human IgG1 constant region FcRmut SEQ ID NO 110.

XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW heavy chain constant region.

XX Homo sapiens.

XX WO2005060368-A2.

XX 07-JUL-2005.

XX 10-DEC-2003; 2003WO-US039599.

XX 10-DEC-2003; 2003WO-US039599.

XX (MILL-) MILLENNIUM PHARM INC.

XX Okeefe T, Ponath P;

XX WPI; 2005-488561/49.

XX N-PSDB; AEB09605.

XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.

XX

PS Claim 1; SEQ ID NO 110; 192pp; English.

CC The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for  
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
 CC construct comprising nucleic acid molecule encoding (I); and host cell  
 CC comprising the nucleic acid molecule. (I) is useful as a therapeutic  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of human IgG1 constant  
 CC region FcRmut used in the creation of a humanized anti-CCR2-antibody.

XX Sequence 330 AA;

Query Match 100.0%; Score 1765; DB 9; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 Db 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
 Db 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
 Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSPFLYSLKLTVDKSRW 300  
 Db 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSPFLYSLKLTVDKSRW 300  
 Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
 Db 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330

# RESULT 3

ADJ95914

ID ADJ95914 standard; protein; 333 AA.

XX ADJ95914;

XX 06-MAY-2004 (first entry)

XX Human IgG heavy chain constant region FcRmut.

XX cytostatic; antibody therapy; immunoglobulin cassette construct;



KW immunoglobulin leader molecule; immunoglobulin domain;  
 KW immunoglobulin therapeutic molecule; monobody; cancer; immunoglobulin G;  
 KW IGG; heavy chain constant region; FCRMut; human.

XX Homo sapiens.  
 OS Synthetic.

PN US2004033561-A1.

PD 19-FEB-2004.

XX 17-OCT-2002; 2002US-00272899.

XX 19-OCT-2001; 2001US-0350166P.

PR 26-JUN-2002; 2002US-0392364P.

XX (MILL-) MILLENNIUM PHARM INC.

PI O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;

XX WPI; 2004-180050/17.

DR N-PSDB; ADJ95913.

PT New isolated nucleic acid molecules having an immunoglobulin cassette  
 PT construct, useful for producing immunoglobulin therapeutic molecules  
 PT termed monobodies, used as a therapeutic group in cancer disorders.

XX Example 2; SEQ ID NO 10; 84pp; English.

CC The invention describes an isolated nucleic acid molecule comprising an  
 CC immunoglobulin cassette construct, wherein the immunoglobulin cassette  
 CC comprises an immunoglobulin leader molecule operably linked to a stable  
 CC immunoglobulin domain region. The methods and compositions of the present  
 CC invention are useful for producing immunoglobulins, in particular  
 CC immunoglobulin therapeutic molecules termed monobodies, used as a  
 CC therapeutic group in cancer disorders. This is the amino acid sequence of  
 CC the human immunoglobulin G (IgG) heavy chain constant region mutant  
 CC FCRMut used in the creation of immunoglobulin DNA cassette constructs.

XX Sequence 333 AA;

Query Match 100.0%; Score 1765; DB 8; Length 333;

Best Local Similarity 100.0%; Pred. No. 4.9e-124;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 60

Db 4 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 63

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPELAGA 120

Db 64 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPELAGA 123

Qy 121 PSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180

Db 124 PSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 183

Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSRDE 240

Db 184 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSRDE 243

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 300

Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 303

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

Db 304 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 333

RESULT 4

ADQ89336

ID ADQ89336 standard; protein; 333 AA.

XX

AC

XX

DT

XX

DE

XX

KW

KW

KW

KW

XX

OS

XX

PN

XX

XX

PD

XX

PF

XX

XX

PR

PR

PR

PR

XX

PA

PA

XX

PI

XX

DR

XX

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 333 AA;

Query Match

Best Local Similarity

Matches 330;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 60

Db

4

ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 63

Qy

61

GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPELAGA 120

Db

64

GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPELAGA 123

Qy

121

PSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180

Db

124

PSVFLPPPKQDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 183

Qy

181

STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSRDE 240

Db

184

STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGPQEPQVYTLPPSRDE 243

Qy

241

LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 300



CC comprises an immunoglobulin leader molecule operably linked to a stable  
 CC immunoglobulin domain region. The methods and compositions of the present  
 CC invention are useful for producing immunoglobulins, in particular  
 CC immunoglobulin therapeutic molecules termed monobodies, used as a  
 CC therapeutic group in cancer disorders. This is the amino acid sequence of  
 CC an immunoglobulin DNA cassette construct.

XX SQ Sequence 356 AA;

Query Match 100.0%; Score 1765; DB 8; Length 356;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 DB |||||  
 27 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 86  
 |||||  
 QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120  
 DB |||||  
 87 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 146  
 |||||  
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 DB |||||  
 147 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 206  
 |||||  
 QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 DB |||||  
 207 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 266  
 |||||  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
 DB |||||  
 267 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 326  
 |||||  
 QY 301 QQQNVFSCSVNHEALHNYTKQSLSPGK 330  
 DB |||||  
 327 QQQNVFSCSVNHEALHNYTKQSLSPGK 356  
 |||||

# RESULT 7

AAV32263

ID AAV32263 standard; protein; 444 AA.

XX AC AAV32263;

XX 15-FEB-2000 (first entry)

DT Humanised anti-CD23 Mab C11 heavy chain.

XX CD23; FCERII; Igb receptor; monoclonal antibody; C11; mouse; human;

XX monoclonal antibody; chimeric antibody; humanised antibody;

XX complementarity determining region; CDR; autoimmune disease;

XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX urticaria; nephrotic syndrome; glomerulonephritis;

XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy.

XX Homo sapiens.

OS Synthetic.

XX Key

XX Location/Qualifiers

FT Region 1..30

FT /note= "framework region 1"

FT Region 31..35

FT /note= "CDR 1"

FT Region 36..49

FT /note= "framework region 2"

FT Region 50..68

FT /note= "CDR 2"

FT Region 69..100

FT /note= "framework region 3"

FT Region 101..103  
 FT /note= "CDR 3"  
 FT Region 104..111  
 FT /note= "framework region 4"  
 FT Region 112..144  
 FT /note= "constant region"

XX WO9958679-A1.  
 XX 18-NOV-1999.  
 XX 07-MAY-1999; 99WO-GB001434.  
 XX 09-MAY-1998; 98GB-00009839.  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 PI WPI; 2000-053101/04.  
 DR N-PSDB; AAZ34748.  
 DR Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX Claim 9; Fig 4; 81pp; English.

XX This amino acid sequence represents the heavy chain of humanised anti-  
 CC CD23 (FCERII) monoclonal antibody C11, composed of a human framework  
 CC (HISGRVII) and the heavy chain complementarity determining regions (see  
 CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice  
 CC overlap PCR. The invention provides altered antibodies, such as chimeric  
 CC or humanised antibodies, which comprise sufficient of the amino acid  
 CC sequences of the C11 light and heavy chain complementarity determining  
 CC regions to render them capable of binding to the CD23 type II molecule  
 CC expressed on haematopoietic cells. The antibodies are used to block  
 CC soluble CD23 formation in human therapy, for the treatment of arthritis,  
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,  
 CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
 CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 CC malignancies (claimed). They are also useful for studying interactions  
 CC between CD23 and various ligands and determining the binding agents

XX SQ Sequence 444 AA;

Query Match 100.0%; Score 1765; DB 3; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 7e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 DB |||||  
 115 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 174  
 |||||  
 QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120  
 DB |||||  
 175 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 234  
 |||||  
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 DB |||||  
 235 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 294  
 |||||  
 QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 DB |||||  
 295 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 354  
 |||||  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
 DB |||||  
 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 414  
 |||||

Qy 301 QQGNVFCVSMHEALHNHYTKQSLSPGK 330  
Db 415 QQGNVFCVSMHEALHNHYTKQSLSPGK 444

RESULT 8  
ADP88447  
ID ADP88447 standard; protein; 448 AA.  
AC ADP88447;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Antibody TRX1 heavy chain SEQ ID NO: 24.  
XX  
XX immunosuppressive; transplant rejection; antigen tolerance; antibody;  
XX TRX1.  
XX  
XX Unidentified.  
XX  
XX WO2004052398-A1.  
XX  
XX 24-JUN-2004.  
XX  
XX 09-DEC-2003; 2003WO-US039165.  
XX  
XX 09-DEC-2002; 2002US-0431839P.  
XX  
XX (TOLE-) TOLERRX INC.  
XX  
XX Windsor-Hines D, Rao P, Ringler DJ;  
XX WPI; 2004-468712/44.  
XX  
XX Treating a primate to induce tolerance to at least one antigen comprises  
XX administering at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells.  
XX  
XX Disclosure; SEQ ID NO 24; 113pp; English.  
XX  
XX The present invention relates to a process of treating a primate to  
XX induce tolerance to at least one antigen, which comprises administering  
XX to the primate at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
XX the primate when the antigen is present in the primate. The method is  
XX useful in treating a primate to induce tolerance to at least one foreign  
XX antigen to prevent transplant rejection. The present sequence is an  
XX antibody fragment used in the exemplification of the invention.  
XX  
XX Sequence 448 AA;  
XX  
Query Match 100.0%; Score 1765; DB 8; Length 448;  
Best Local Similarity 100.0%; Pred. No. 7e-124;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPVAVLQSS 60  
Db 119 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPVAVLQSS 178

Qy 61 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPELAGA 120  
Db 179 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPELAGA 238

Qy 121 PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180  
Db 239 PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 298

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 299 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 358

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSEFELYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSEFELYSKLTVDKSRW 418

Qy 301 QQGNVFCVSMHEALHNHYTKQSLSPGK 330  
Db 419 QQGNVFCVSMHEALHNHYTKQSLSPGK 448

RESULT 9  
ADP88431  
ID ADP88431 standard; protein; 448 AA.  
XX  
XX ADP88431;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Antibody TRX1 heavy chain SEQ ID NO: 8.  
XX  
XX immunosuppressive; transplant rejection; antigen tolerance; antibody;  
XX TRX1.  
XX  
XX Unidentified.  
XX  
XX WO2004052398-A1.  
XX  
XX 24-JUN-2004.  
XX  
XX 09-DEC-2003; 2003WO-US039165.  
XX  
XX 09-DEC-2002; 2002US-0431839P.  
XX  
XX (TOLE-) TOLERRX INC.  
XX  
XX Windsor-Hines D, Rao P, Ringler DJ;  
XX WPI; 2004-468712/44.  
XX  
XX Treating a primate to induce tolerance to at least one antigen comprises  
XX administering at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells.  
XX  
XX Disclosure; SEQ ID NO 8; 113pp; English.  
XX  
XX The present invention relates to a process of treating a primate to  
XX induce tolerance to at least one antigen, which comprises administering  
XX to the primate at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
XX the primate when the antigen is present in the primate. The method is  
XX useful in treating a primate to induce tolerance to at least one foreign  
XX antigen to prevent transplant rejection. The present sequence is an  
XX antibody fragment used in the exemplification of the invention.  
XX  
XX Sequence 448 AA;  
XX  
Query Match 100.0%; Score 1765; DB 8; Length 448;  
Best Local Similarity 100.0%; Pred. No. 7e-124;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPVAVLQSS 60  
Db 119 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPVAVLQSS 178

Qy 61 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPELAGA 120  
Db 179 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPELAGA 238

Qy 121 PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180  
Db 239 PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 298

QY 191 STYRVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQRPFPVYVTLPPSRDE 240  
Db 299 STYRVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQRPFPVYVTLPPSRDE 358  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 418  
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
Db 419 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 448  
RESULT 10  
AEB08800  
ID AEB08800 standard; protein; 462 AA.  
XX  
AC AEB08800;  
XX  
DT 08-SEP-2005 (first entry)  
XX  
DE Anti-NOGO-antibody heavy chain SEQ ID NO 88.  
XX  
KW cerebroprotective; vasotropic; neuroprotective; vulnerable; neurotropic; nontropic;  
KW antiparkinsonian; anticonvulsant; neuroleptic; antibody engineering;  
KW pharmaceutical; cerebrovascular ischemia; cardiovascular disease;  
KW neurological disease; brain injury; injury; spinal cord injury;  
KW Alzheimers disease; degeneration; dementia; neuropathy;  
KW parkinsons disease; Huntingtons chorea; genetic disorder;  
KW multiple sclerosis; immune disorder; Creutzfeldt Jakob disease;  
KW infection; schizophrenia; psychiatric disorder; motor neurone disease;  
KW cns-gen.; muscular-gen.  
XX  
OS Synthetic.  
XX  
PN WO2005061544-A2.  
XX  
PD 07-JUL-2005.  
XX  
PF 20-DEC-2004; 2004WO-GB005325.  
XX  
PR 22-DEC-2003; 2003GB-00029684.  
PR 22-DEC-2003; 2003GB-00029711.  
XX  
PA (GLAXO) GLAXO GROUP LTD.  
XX  
PI Ellis JH, Bon-Duval A, Grundy RI, Hussain F, Mcadam R;  
PI Plumpton C, Prinjha RK, Wilson PA;  
XX  
DR N-PSDB; AEB08802.  
XX  
PT WPI; 2005-479448/48.  
PT New antibody or its functional fragment that binds with and neutralizes  
PT human neurite outgrowth useful for treating or prophylaxis of stroke and  
PT other neurological disease e.g. traumatic brain injury, spinal cord  
PT injury, Alzheimer's disease.  
XX  
PS Example 8; SEQ ID NO 88; 143pp; English.  
XX  
CC The invention describes an antibody (A1) or its functional fragment, that  
CC binds with and neutralizes human neurite outgrowth (NOGO). Also described  
CC are: providing a first vector encoding a heavy chain of the antibody;  
CC providing a second vector encoding a light chain of the antibody; co-  
CC transfecting a mammalian host cell with the first and second vectors;  
CC culturing the host cell in culture media (preferably serum free) under  
CC conditions permissive to the secretion of the antibody from the host cell  
CC into the culture media; and recovering (and optionally purifying) the  
CC secreted antibody; and promoting axonal sprouting involving contacting a  
CC human axon with an anti-NOGO antibody. The antibody is useful in the  
CC preparation of a medicament for treating or prophylaxis of stroke and  
CC other neurological disease/disorders (e.g. traumatic brain injury, spinal  
CC cord injury, Alzheimer's disease, frontotemporal dementias (tauopathies),  
CC peripheral neuropathy, Parkinson's disease, Huntington's disease and

CC multiple sclerosis); Creutzfeldt-jakob disease (CJD), Schizophrenia,  
CC amyotrophic lateral sclerosis (ALS), inclusion body myositis. The  
CC antibody inhibits neurodegeneration and/or promotes functional recovery  
CC in a human patient suffering, or at risk of developing, stroke or other  
CC neurological diseases/disorder. This is the amino acid sequence of an  
CC anti-NOGO-antibody heavy chain created in the invention.  
XX  
SQ Sequence 462 AA;  
Query Match 100.0%; Score 1765; DB 9; Length 462;  
Best Local Similarity 100.0%; Pred. No. 7.3e-124; Indels 0; Gaps 0;  
Matches 330; Conservative 0; Mismatches 0;  
QY 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVLYKDYFPEPVTWNSGALTSVGVHFFPAVLQSS 60  
Db 133 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVLYKDYFPEPVTWNSGALTSVGVHFFPAVLQSS 192  
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELAGA 120  
Db 193 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELAGA 252  
QY 121 PSVFLPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 180  
Db 253 PSVFLPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 312  
QY 181 STYRVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQRPFPVYVTLPPSRDE 240  
Db 313 STYRVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQRPFPVYVTLPPSRDE 372  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 432  
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
Db 433 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 462  
RESULT 11  
ADA47334  
ID ADA47334 standard; protein; 467 AA.  
XX  
AC ADA47334;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE TRX1 heavy chain encoding DNA #SEQ ID 7.  
XX  
KW Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;  
KW graft rejection; autoimmune disease; humanised.  
XX  
OS Homo sapiens.  
XX  
PN WO2002102853-A2.  
XX  
PD 27-DEC-2002.  
XX  
PF 14-JUN-2002; 2002WO-GB002796.  
XX  
PR 14-JUN-2001; 2001GB-00014517.  
PR 20-SEP-2001; 2001GB-00022724.  
PR 19-OCT-2001; 2001US-0345194P.  
PR 18-APR-2002; 2002US-0373470P.  
PR 18-APR-2002; 2002US-0373471P.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
PA (TOLE-) TOLERRX INC.  
XX  
PI Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;  
PI Ringler D, Cobbold S, Winsor-Hines D;  
XX  
DR WPI; 2003-175228/17.

DR N-PSDB; ADA47336.  
XX Treating a primate to induce tolerance to at least one antigen, useful  
PT for inhibiting graft rejection or treating an autoimmune disease,  
PT comprises administering a TRX1 antibody to reduce the amount of CD4+  
PT CD25+ cells produced.  
XX  
XX  
PS Claim 26; Fig 1D; 131pp; English.  
XX  
XX The invention relates to a method for treating a primate to induce  
CC tolerance to at least one antigen. The method of the invention comprises  
CC administering at least one compound which in a primary mixed  
CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells  
CC produced. The preferred compound is a humanised antibody or its fragment,  
CC that does not bind to the FC receptor, and includes CDRs that are free of  
CC a glycosylation site. The method of the invention is useful for inducing  
CC tolerance to at least one antigen, specifically for inhibiting,  
CC ameliorating or reducing an immune response to an antigen. The antibody  
CC is useful for manufacturing a medicament for inducing tolerance to an  
CC antigen (possibly in the form of a vaccine), for inhibiting an immune  
CC response, for inhibiting the rejection of a graft (such as an organ) in a  
CC human patient, and for treating an autoimmune disease. The current  
CC sequence represents the TRX1 heavy chain.  
XX  
XX  
SQ Sequence 467 AA;  
  
Query Match 100.0%; Score 1765; DB 6; Length 467;  
Best Local Similarity 100.0%; Pred. No. 7.4e-124;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTTFAVLQSS 60  
Db |||||  
Qy 138 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTTFAVLQSS 197  
Db |||||  
Qy 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120  
Db |||||  
Qy 198 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELAGA 257  
Db |||||  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREPQYN 180  
Db |||||  
Qy 258 PSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREPQYN 317  
Db |||||  
Qy 181 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db |||||  
Qy 318 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377  
Db |||||  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRW 437  
Db |||||  
Qy 301 QQGNVPSCSVMHEALHNYTKQSLSPGK 330  
Db |||||  
Qy 438 QQGNVPSCSVMHEALHNYTKQSLSPGK 467  
  
RESULT 12  
ADA47336  
ID ADA47336 standard; protein; 467 AA.  
XX  
XX ADA47336;  
AC  
DT 20-NOV-2003 (first entry)  
XX  
DE TRX1 heavy chain #SEQ ID 9.  
XX  
XX Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;  
KW graft rejection; autoimmune disease; humanised.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
PT /label= leader peptide

Region 50..54  
/label= CDR  
Region 69..85  
/label= CDR  
Region 118..126  
/label= CDR  
XX  
XX WO2002102853-A2.  
XX  
XX 27-DEC-2002.  
XX  
XX 14-JUN-2002; 2002WO-GB002796.  
XX  
XX 14-JUN-2001; 2001GB-00014517.  
XX 20-SEP-2001; 2001GB-00022724.  
XX 19-OCT-2001; 2001US-0345194P.  
XX 18-APR-2002; 2002US-0373470P.  
XX 18-APR-2002; 2002US-0373471P.  
XX  
XX (ISIS-) ISIS INNOVATION LTD.  
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX (TOLE-) TOLERRX INC.  
XX  
XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;  
XX Ringler D, Cobbold S, Winsor-Hines D;  
XX  
XX WPI; 2003-175228/17.  
XX  
XX Treating a primate to induce tolerance to at least one antigen, useful  
PT for inhibiting graft rejection or treating an autoimmune disease,  
PT comprises administering a TRX1 antibody to reduce the amount of CD4+  
PT CD25+ cells produced.  
XX  
XX Claim 27; Fig 1F; 131pp; English.  
XX  
XX The invention relates to a method for treating a primate to induce  
CC tolerance to at least one antigen. The method of the invention comprises  
CC administering at least one compound which when in a primary mixed  
CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells  
CC produced. The preferred compound is a humanised antibody or its fragment,  
CC that does not bind to the FC receptor, and includes CDRs that are free of  
CC a glycosylation site. The method of the invention is useful for inducing  
CC tolerance to at least one antigen, specifically for inhibiting,  
CC ameliorating or reducing an immune response to an antigen. The antibody  
CC is useful for manufacturing a medicament for inducing tolerance to an  
CC antigen (possibly in the form of a vaccine), for inhibiting an immune  
CC response, for inhibiting the rejection of a graft (such as an organ) in a  
CC human patient, and for treating an autoimmune disease. The current  
CC sequence represents the TRX1 heavy chain amino acid sequence.  
XX  
XX  
SQ Sequence 467 AA;  
  
Query Match 100.0%; Score 1765; DB 6; Length 467;  
Best Local Similarity 100.0%; Pred. No. 7.4e-124;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTTFAVLQSS 60  
Db |||||  
Qy 138 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTTFAVLQSS 197  
Db |||||  
Qy 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120  
Db |||||  
Qy 198 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELAGA 257  
Db |||||  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREPQYN 180  
Db |||||  
Qy 258 PSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREPQYN 317  
Db |||||  
Qy 181 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db |||||  
Qy 318 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377  
Db |||||  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRW 300  
Db |||||

Db 378 LTKNOVSLTCLVKGYPSPDIAVEWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 437  
Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330  
Db 438 QQGNVFCSCVMHEALHNNHYTKSLSPGK 467

RESULT 13  
ADP88446  
ID ADP88446 standard; protein; 467 AA.  
XX ADP88446;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 23.  
XX  
XX immunosuppressive; transplant rejection; antigen tolerance; antibody;  
XX TRX1.  
XX  
XX Unidentified.  
XX  
XX WO2004052398-A1.  
XX  
XX 24-JUN-2004.  
XX  
XX 09-DEC-2003; 2003WO-US039165.  
XX  
XX 09-DEC-2002; 2002US-0431839P.  
XX  
XX (TOLE-) TOLERRX INC.  
XX  
XX Windsor-Hines D, Rao P, Ringler DJ;  
XX  
XX WPI; 2004-468712/44.  
XX  
XX N-PSDB; ADP88444, ADP88445.  
XX  
XX Treating a primate to induce tolerance to at least one antigen comprises  
XX administering at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells.  
XX  
XX Disclosure; SEQ ID NO 23; 113pp; English.  
XX  
XX The present invention relates to a process of treating a primate to  
XX induce tolerance to at least one antigen, which comprises administering  
XX to the primate at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
XX the primate when the antigen is present in the primate. The method is  
XX useful in treating a primate to induce tolerance to at least one foreign  
XX antigen to prevent transplant rejection. The present sequence is an  
XX antibody fragment used in the exemplification of the invention.  
XX  
XX Sequence 467 AA;  
XX  
XX Query Match 100.0%; Score 1765; DB 8; Length 467;  
XX Best Local Similarity 100.0%; Pred. No. 7.4e-124; Indels 0; Gaps 0;  
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 60  
Db 138 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 197  
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPCPAPELAGA 120  
Db 198 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPCPAPELAGA 257  
Qy 121 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNVTVDGVGVHNAKTKPREQYN 180  
Db 258 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNVTVDGVGVHNAKTKPREQYN 317

Qy 181 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240  
Db 318 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 377  
Qy 241 LTKNOVSLTCLVKGYPSPDIAVEWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 300  
Db 378 LTKNOVSLTCLVKGYPSPDIAVEWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 437  
Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330  
Db 438 QQGNVFCSCVMHEALHNNHYTKSLSPGK 467

RESULT 14  
ADP88430  
ID ADP88430 standard; protein; 467 AA.  
XX ADP88430;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 7.  
XX  
XX immunosuppressive; transplant rejection; antigen tolerance; antibody;  
XX TRX1.  
XX  
XX Unidentified.  
XX  
XX WO2004052398-A1.  
XX  
XX 24-JUN-2004.  
XX  
XX 09-DEC-2003; 2003WO-US039165.  
XX  
XX 09-DEC-2002; 2002US-0431839P.  
XX  
XX (TOLE-) TOLERRX INC.  
XX  
XX Windsor-Hines D, Rao P, Ringler DJ;  
XX  
XX WPI; 2004-468712/44.  
XX  
XX N-PSDB; ADP88429, ADP88428.  
XX  
XX Treating a primate to induce tolerance to at least one antigen comprises  
XX administering at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells.  
XX  
XX Disclosure; SEQ ID NO 7; 113pp; English.  
XX  
XX The present invention relates to a process of treating a primate to  
XX induce tolerance to at least one antigen, which comprises administering  
XX to the primate at least one anti-CD4 antibody or its fragment in an  
XX initial dose of at least 40 mg/kg and at least one compound that inhibits  
XX CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
XX the primate when the antigen is present in the primate. The method is  
XX useful in treating a primate to induce tolerance to at least one foreign  
XX antigen to prevent transplant rejection. The present sequence is an  
XX antibody fragment used in the exemplification of the invention.  
XX  
XX Sequence 467 AA;  
XX  
XX Query Match 100.0%; Score 1765; DB 8; Length 467;  
XX Best Local Similarity 100.0%; Pred. No. 7.4e-124; Indels 0; Gaps 0;  
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 60  
Db 138 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKSRW 197  
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPCPAPELAGA 120  
Db 198 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPCPAPELAGA 257







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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:23:14 ; Search time 33.69377 Seconds  
(without alignments)  
942.358 Million cell updates/sec

Title: US-10-733-563-110  
Perfect score: 1765  
Sequence: 1 ASTKGPSVFPLAPSKSTSG.....MHEALHNYTKSLSPGK 330  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	99.5	330	1 GHU	Ig gamma-1 chain C
2	1619.5	91.8	377	2 A23511	Ig gamma-3 chain C
3	1617.5	91.6	377	2 A0764	Ig gamma-3 chain C
4	1608	91.1	326	1 G2HU	Ig gamma-2 chain C
5	1579.5	89.5	327	1 G4HU	Ig gamma-4 chain C
6	1259	71.3	328	2 I47159	Ig gamma 2a chain
7	1253	71.0	328	2 I47160	Ig gamma 2b chain
8	1252.5	71.0	374	2 S69339	Ig heavy chain V r
9	1249	70.8	255	4 S31866	Ig gamma-1 chain C
10	1243	70.4	234	2 P70207	Ig gamma chain C r
11	1235	70.0	328	2 I47158	Ig gamma 1 chain c
12	1231	69.7	328	2 I47161	Ig gamma 3 chain c
13	1219.5	69.1	323	1 GHRB	Ig gamma chain C r
14	1201.5	68.1	329	1 G2GP	Ig gamma-2 chain C
15	1195.5	67.7	472	2 S31459	Ig gamma-1 chain -
16	1176.5	66.7	470	2 S22080	Ig heavy chain pre
17	1157.5	65.6	308	2 C30554	Ig heavy chain C r
18	1156	65.5	444	2 PC4436	monoclonal antibod
19	1154	65.4	326	2 PS0017	Ig gamma-1 chain C
20	1144	64.8	324	1 G3MS	Ig gamma-1 chain C
21	1140	64.6	289	1 G3HWT	Ig gamma-3 heavy c
22	1139	64.5	393	1 GLMSW	Ig gamma-1 chain C
23	1135.5	64.3	333	2 PS0018	Ig gamma-2b chain
24	1130	64.0	329	1 G3MSC	Ig gamma-3 chain C
25	1119	63.4	398	1 G3MSM	Ig gamma-3 chain C
26	1115	63.2	330	1 G2MSA	Ig gamma-2a chain
27	1115	63.2	469	2 S37483	Ig gamma-2a chain
28	1114.5	63.1	329	2 S00847	Ig gamma-2c chain
29	1114	63.1	322	2 PS0019	Ig gamma-2a chain

RESULT 1  
GHU

Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370  
A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, ;  
A:Note: Lys-330 is removed after translation  
R:Haris, L.J.  
submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a ;  
A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C.

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Cross-references: UNIPARC:UPI000017378D

A:Note: This sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'

A:Cross-references: UNIPARC:UPI000017378E

A:Note: This sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.



A;Residues: 1-377 <HUC>  
A;Cross-references: UNIPROT:Q8NAY9; UNIPARC:UPI0000176F0B  
C;Superfamily: immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMW>

```
Query Match      91.6%; Score 1617.5; DB 2; Length 377;
Best Local Similarity 81.4%; Pred. No. 4e-104;
Matches 307; Conservative 10; Mismatches 13; Indels 47; Gaps 1;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVQDYFFPPVTVVSNWNGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVQDYFFPPVTVVSNWNGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVVTVVPSSSLGTTQTYICNVNHPKSNKVDKKV----- 98
Db 61 GLYSLSVVTVVPSSSLGTTQTYICNVNHPKSNKVDKRVELKTPGLDTHTCPCPEPKSC 120

Qy 99 -----EPKSCDKTHTCPCPAPELAGPSVFLFPPKPKDT 133
Db 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPAPELAGPSVFLFPPKPKDT 180

Qy 134 LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVSVLTVLH 193
Db 181 LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVSVLTVLH 240

Qy 194 QDWLNGKEYKCKVSNKALPAPIETKISKAKQPREPVYITLPPSRDELTKNQVSLTCLVK 253
Db 241 QDWLNGKEYKCKVSNKALPAPIETKISKAKQPREPVYITLPPSRDEWTKNQVSLTCLVK 300

Qy 254 GFYPDSIAVEHESGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQGNVFPSCVMHE 313
Db 301 GFYPDSIAVEHESGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQGNVFPSCVMHE 360

Qy 314 ALHNHYTQKSLSLSPGK 330
Db 361 ALHNRYTQKSLSLSPGK 377
```

## RESULT 4

G2HU

Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con-

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 &lt;ELL&gt;

A;Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:932

A;Note: Lys-326 is probably removed posttranslationally

E;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f

A;Reference number: A92809; MUID:81007873; PMID:6774012

A;Contents: myeloma protein Til

A;Accession: A92809

A;Molecule type: protein

A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 &lt;WAN&gt;

A;Cross-references: UNIPARC:UPI0000173791

A;Note: Trp-156 is at or near the complement-binding site

R;Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of a

A;Reference number: A90752; MUID:80001357; PMID:113060

A;Contents: myeloma protein Zie

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-

A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793

A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A;Reference number: A93132; MUID:80114419; PMID:118920

A;Contents: Zie

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <HOF>

A;Cross-references: UNIPARC:UPI0000173794

R;Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A;Reference number: A94591

A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic

ned

R;Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Reference number: A90253; MUID:72033500; PMID:4940472

A;Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A;Title: Structural studies of immunoglobulin G.

A;Reference number: A93157; MUID:69064124; PMID:5782707

A;Contents: annotation; Sa, disulfide bonds

C;Genetics:

A;Gene: GDB:IGHG2

A;Cross-references: GDB:119338; OMIM:147110

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la;

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>

F;133-202/Domain: immunoglobulin homology <IM2>

F;239-306/Domain: immunoglobulin homology <IM3>

F;14/Disulfide bonds: interchain (to light chain) #status experimental

F;27-83,140-200,246-304/Disulfide bonds: #status experimental

F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.1%; Score 1608; DB 1; Length 326;

Best Local Similarity 91.5%; Pred. No. 1.5e-103;

Matches 302; Conservative 12; Mismatches 12; Indels 4; Gaps 2;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVQDYFFPPVTVVSNWNGALTSGVHTFPAVLQSS 60

Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVQDYFFPPVTVVSNWNGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVVTVVPSSSLGTTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELAGA 120

Db 61 GLYSLSVVTVVPSNFGTYITCNVDHHPKSNKVDKTVKCCVE---CPPCPAPPVAG- 116

Qy 121 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

Db 117 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFN 176

Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKQPREPVYITLPPSRDE 240

Db 177 STFRVSVLTVLHODWLNKGEYKCKVSNKGLPAPIETKISKAKQPREPVYITLPPSRDE 236

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRW 300

Db 237 MTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRW 296

Qy 301 QQGNVFPSCVMHEALHNHYTQKSLSLSPGK 330

Db 297 QQGNVFPSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 5

G4HU

Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
C/Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83151704; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A/Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30,81-326 <PIN>  
A/Cross-references: UNIPARC:UPI00000173795; UNIPARC:UPI00000173796  
C:Genetics:  
A:Gene: GDB:IGHG4  
A/Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.5%; Score 1579.5; DB 1; Length 327;  
Best Local Similarity 90.3%; Pred. No. 1.4e-101;  
Matches 298; Conservative 12; Mismatches 17; Indels 3; Gaps 1;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120  
Db 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 117

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
Db 118 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFN 177

Qy 181 STYRVSVLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 240  
Db 178 STYRVSVLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 237

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 238 MTNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 297

Qy 301 QQGNVFSCSVHMEALHNHYTQKSLSLSPGK 330  
Db 298 QEGNVFSCSVHMEALHNHYTQKSLSLSPGK 327

RESULT 6  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C/Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3563-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A/Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:9433123; PIDN:AAAS2217.1; PII  
C:Genetics:  
A:Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 1259; DB 2; Length 328;  
Best Local Similarity 70.2%; Pred. No. 1.6e-79;  
Matches 233; Conservative 42; Mismatches 51; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
Db 1 APTAPLSVYPLAPCSRDTSGPNVALGCLASSYPPEPTVTWNSGALSSGVHTTPEPSVLQPS 60

Qy 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120  
Db 61 GLYSLSSVWTVTPASSLSKSYTCNVNHPATTTKVDKRVGKTKT---KPCCPICACESFG- 116

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
Db 117 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFN 176

Qy 181 STYRVSVLTCLVKGFYPSDIAVEHESNGQ--PNNYKTPPVLDSDGSFPLYSKLTVDKSR 240  
Db 177 STYRVSVLTCLVKGFYPSDIAVEHESNGQ--PNNYKTPPVLDSDGSFPLYSKLTVDKSR 236

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PNNYKTPPVLDSDGSFPLYSKLTVDKSR 298  
Db 237 LSRKSVISLTCLVKGFYPSDIAVEHESNGQ--PNNYKTPPVLDSDGSFPLYSKLTVDKSR 296

Qy 299 RWOQGNVFSCSVHMEALHNHYTQKSLSLSPGK 330  
Db 297 SWDGGGIFQCAVHMEALHNHYTQKSLSLSPGK 328

RESULT 7  
Ig gamma 2b chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C/Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47160  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A/Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:9433125; PIDN:AAAS2218.1; PII  
C:Genetics:  
A:Gene: IGG2b  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 1253; DB 2; Length 328;  
Best Local Similarity 69.9%; Pred. No. 4.2e-79;  
Matches 232; Conservative 41; Mismatches 53; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
Db 1 APTAPLSVYPLAPCSRDTSGPNVALGCLASSYPPEPTVTWNSGALSSGVHTTPEPSVLQPS 60

Qy 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120

```
Db 61 GLYSLSWVTPASSLSKSYTCNNHPATTKVDRVGTKT---KPPCPICPACESPG- 116
Qy 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 117 PSVIFPPPKDPTLMISRTPTQVTCVVVDVSDQENPEVQSWYVDGVEVHNAKTRPKEEQFN 176
Qy 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
Db 177 STYRVSVLPIQHQLDLNGKEFKCKVNNKOLPAPITRIISKAKGQTRPEPQVYTLPPHAE 236
Qy 241 LTKQVSLTCLVKGPYSDIAVESNGQ--PENNYKTPPVLDSDGSPFLYSLKLTVDKS 298
Db 237 LRSKVSITCLVIGFYPPDIIVQWRNQGPPEGNYRTTPQQDVGDFYFLYSKFSVDKA 296
Qy 299 RWQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
Db 297 SWQGGIFQCAVMHEALHNNHYTKQSLTPGK 328

RESULT 8
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176P24; EMBL:X81695
R:Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176P25; EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 71.0%; Score 1252.5; DB 2; Length 374;
Best Local Similarity 89.0%; Pred. No. 5.4e-79;
Matches 235; Conservative 3; Mismatches 15; Indels 11; Gaps 2;

Qy 78 TQTYICNNV-----HK-PSNTKVDKVEPKSCDKHTCCPPAPELAGAPSVFLF 126
Db 111 TATYVCGSVBVGQGYRHFHWSGQGLTVTVSSEPKSCDKHTCCPPAPELAGAPSVFLF 170
Qy 127 PPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRV 186
Db 171 PPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRV 230
Qy 187 SVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNOV 246
Db 231 SVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNOV 290
Qy 247 SLTCLVKGFYPSDIAVESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNV 306
Db 291 SLTCLVKGFYPSDIAVESNGQPENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNV 350
Qy 307 SCVMHEALHNNHYTKQSLSPGK 330
Db 351 SCVMHEALHNNHYTKQSLSPGK 374

RESULT 9
S31866
Ig gamma-1 chain C region - synthetic
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C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 70.8%; Score 1249; DB 4; Length 255;
Best Local Similarity 96.7%; Pred. No. 5.9e-79;
Matches 231; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 92 TKVDKVEPKSCDKHTCCPPAPELAGAPSVFLPFPKPKDPTLMISRTPEVTCVVVDVSH 151
Db 17 TVAQADVESKSCDKHTCCPPAPELAGAPSVFLPFPKPKDPTLMISRTPEVTCVVVDVSH 76
Qy 152 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNKAL 211
Db 77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNKAL 136
Qy 212 PAPIETKISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVESNGQPE 271
Db 137 PAPIETKISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVESNGQPE 196
Qy 272 NNYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
Db 197 NNYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 255

RESULT 10
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (Chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Cc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
A:Cross-references: UNIPARC:UPI0000176F05
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 1243; DB 2; Length 234;
Best Local Similarity 97.9%; Pred. No. 1.4e-78;
Matches 229; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 90 SNTKVDKVEPKSCDKHTCCPPAPELAGAPSVFLPFPKPKDPTLMISRTPEVTCVVVDV 149
Db 1 SNTKVDKVEPKSCDKHTCCPPAPELAGAPSVFLPFPKPKDPTLMISRTPEVTCVVVDV 60
Qy 150 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNK 209
Db 61 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNK 120
Qy 210 ALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVESNGQ 269
Db 121 ALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVESNGQ 180
Qy 270 PENNYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKS 323
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Db 181 PENNYKTTTPVLDSGDFLYSLKLVTDKSRQGVFSCSVMEALHNHYTQKS 234

RESULT 11  
147158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a swine IgG heavy chain  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47158  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:G433121; PIDN:AAAS2216.1; PID:133-202/Domain: immunoglobulin homology <IMM>  
C:Genetics:  
A:Gene: IGH1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 1235; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 7.4e-78;  
Matches 231; Conservative 39; Mismatches 56; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFFLAPSKSTSGTAALGCLVDKYPPEVTVSNWNSGALTSVGHVTFPAVLQSS 60  
Db 1 AKTPASVYFLAPCGRDVSGPNVALGCLASSYFPPEVTVTNWNSGALTSVGHVTFPAVLQSS 60  
Qy 61 GLYSLSWVTVTPSSSLGTQTYICNNHKNPTKVKVEPKSCDKHTCCPCPAPELAGA 120  
Db 61 GLYSLSWVTVTPSSSLGTQTYICNNHKNPTKVKVEPKSCDKHTCCPCPAPELAGA 120  
Qy 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHDEPKVFNWYVDGVVHNAKTKPREQYN 180  
Db 117 PSVFLPPKPKDLMISRTPEVTCVVDVSHDEPKVFNWYVDGVVHNAKTKPREQYN 180  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 240  
Db 177 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 240  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYYKTTTPVLDSDGSPFLYSLKLTVDKS 298  
Db 237 LSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPEGVNRTTPPQQDVGDTFFLYSLKLVDA 296  
Qy 299 RWQGVNFVSCSVMEALHNHYTQKSLSLSPGK 330  
Db 297 RWDHGDKEFCVMEALHNHYTQKSISKTQK 328

RESULT 12  
147161  
Ig gamma 3 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47161  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a swine IgG heavy chain  
A:Reference number: I47161; MUID:95015845; PMID:7930579  
A:Accession: I47161  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:G433127; PIDN:AAAS2219.1; PID:133-202/Domain: immunoglobulin homology <IMM>  
C:Genetics:  
A:Gene: IGK3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 1231; DB 2; Length 328;

Best Local Similarity 69.3%; Pred. No. 1.4e-77;  
Matches 230; Conservative 40; Mismatches 56; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFFLAPSKSTSGTAALGCLVDKYPPEVTVSNWNSGALTSVGHVTFPAVLQSS 60  
Db 1 AKTPASVYFLAPCGRDVSGPNVALGCLASSYFPPEVTVTNWNSGALTSVGHVTFPAVLQSS 60  
Qy 61 GLYSLSWVTVTPSSSLGTQTYICNNHKNPTKVKVEPKSCDKHTCCPCPAPELAGA 120  
Db 61 GLYSLSWVTVTPSSSLGTQTYICNNHKNPTKVKVEPKSCDKHTCCPCPAPELAGA 120  
Qy 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHDEPKVFNWYVDGVVHNAKTKPREQYN 180  
Db 117 PSVFLPPKPKDLMISRTPEVTCVVDVSHDEPKVFNWYVDGVVHNAKTKPREQYN 180  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 240  
Db 177 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 240  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYYKTTTPVLDSDGSPFLYSLKLTVDKS 298  
Db 237 LSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPEGVNRTTPPQQDVGDTFFLYSLKLVDA 296  
Qy 299 RWQGVNFVSCSVMEALHNHYTQKSLSLSPGK 330  
Db 297 RWDHGDKEFCVMEALHNHYTQKSISKTQK 328

RESULT 13  
GHRB  
Ig gamma chain C region - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
C:Accession: A91749; A93928; A90245; A94416; A02161  
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
Immunogenetics 18, 387-397, 1983  
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype  
A:Reference number: A91749; MUID:84030930; PMID:6133520  
A:Accession: A91749  
A:Molecule type: mRNA  
A:Residues: 1-323 <BER>  
A:Cross-references: UNIPARC:UPI000012337D  
C:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
R:Pratt, D.M.; Mole, L.E.  
Biochem. J. 151, 337-349, 1975  
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G  
A:Reference number: A90290; MUID:76135469; PMID:1243651  
A:Accession: A90290  
A:Molecule type: protein  
A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>  
A:Cross-references: UNIPARC:UPI00001737AB  
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
A:Reference number: A93928; MUID:83299917; PMID:6193512  
A:Accession: A93928  
A:Molecule type: mRNA  
A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
A:Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:G165111; PIDN:AAA31289.1; PID:133-202/Domain: immunoglobulin homology <IMM>  
C:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker  
R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
Biochem. J. 116, 249-259, 1970  
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C  
A:Reference number: A90245; MUID:70110015; PMID:5461106  
A:Accession: A90245  
A:Molecule type: protein  
A:Residues: 132-143, 'E', 145-161 <FRU>  
A:Cross-references: UNIPARC:UPI00001737AC  
R:Hill, R.D.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, 1968  
A:Reference number: A94416  
A:Accession: A94416  
A:Molecule type: protein



A:Residues: 129-131;155-172,'D','174-184','A','186','E','188-200','D','202-217','E','219-232','Q'.  
 A:Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE  
 A:Note: this has the e15 allotypic marker, 185-Ala  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-82/Domain: immunoglobulin homology <IM1>  
 F:130-199/Domain: immunoglobulin homology <IM2>  
 F:236-303/Domain: immunoglobulin homology <IM3>  
 F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.1%; Score 1219.5; DB 1; Length 323;  
 Best Local Similarity 69.4%; Pred. No. 8.4e-77;  
 Matches 227; Conservative 34; Mismatches 59; Indels 7; Gaps 2;

Qy 4 KGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSNWNSGALTSVHTFPAVLQSSGLY 63  
 Db 4 KAPSVFPLAPCGDTPSTTVIGCLVKGILPEPTVTVNSGTLNGVTRPSPVRSQSSGLY 63

Qy 64 SLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGAPSV 123  
 Db 64 SLSSVSVTSSS---QPVTCNVAPATNTKVDKTVAPSTCSK----PTCPPPELLGGPSV 116

Qy 124 FLPPPKPDMLISRTPEVTCVVDVSHEDPEKFNWYDGVVEVHNATKPRBEQYNSTY 183  
 Db 117 FIFPPKPDMLISRTPEVTCVVDVSDDEPEVQFTYINNEQVTRAPPLREQQPNSTI 176

Qy 184 RVSVSLTVLHODWLNGEYKCKVSNKALPAPIETKISKAKQPREPQVYTLPPSRDELTK 243  
 Db 177 RVVSTLPIHODWLNGEYKCKVSNKALPAPIETKISKAKQPREPQVYTLPPSRDELTK 236

Qy 244 NQVSLTCLVKGFPYSDIAVESNGOPNNYKTPPVLDSDGSPFLYSKLTVDKSRWQOG 303  
 Db 237 RVSLSLTCMNGFYSDISVEKNGKAEDNTKTPPAVLDSGSPFLYNKLSVPTSEWQRG 296

Qy 304 NVFSCSVNHEALHNHYTKSLSPGK 330  
 Db 297 DVFTCSVNHEALHNHYTKSLSPGK 323

RESULT 14  
 GzGP  
 Ig gamma-2 chain C region - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 07-May-1991 #sequence revision 07-May-1991 #text change 09-Jul-2004  
 C:Accession: A94553; A90352; A90359; A90384; A90385; A02151  
 R:Trischmann, T.M.  
 submitted to the Atlae, April 1975  
 A:Reference number: A94553  
 A:Accession: A94553  
 A:Molecule type: protein  
 A:Residues: 1-3 <TRI>  
 A:Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E  
 R:Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
 Biochemistry 10, 18-25, 1971  
 A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
 A:Reference number: A90352; MUID:71058471; PMID:5538606  
 A:Accession: A90352  
 A:Molecule type: protein  
 A:Residues: 4-68 <BIR>  
 A:Cross-references: UNIPARC:UPI000017379F  
 R:Turner, K.J.; Cebra, J.J.  
 Biochemistry 10, 9-17, 1971  
 A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
 A:Reference number: A90359; MUID:71058486; PMID:5538616  
 A:Accession: A90359  
 A:Molecule type: protein  
 A:Residues: 69-133;312-329 <TUR>  
 A:Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1  
 R:Tracey, D.E.; Cebra, J.J.  
 Biochemistry 13, 4796-4803, 1974  
 A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A:Reference number: A90384; MUID:75036072; PMID:4429665  
 A:Accession: A90384  
 A:Molecule type: protein  
 A:Residues: 134-256 <TRA>  
 A:Cross-references: UNIPARC:UPI00001737A2  
 R:Trischmann, T.M.; Cebra, J.J.  
 Biochemistry 13, 4804-4811, 1974  
 A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
 A:Reference number: A90385; MUID:75036073; PMID:4609467  
 A:Accession: A90385  
 A:Molecule type: protein  
 A:Residues: 227-311 <TR2>  
 A:Cross-references: UNIPARC:UPI00001737A3  
 R:Oliveira, B.; Lamm, M.B.  
 Biochemistry 10, 26-31, 1971  
 A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
 A:Reference number: A90354; MUID:71058474; PMID:4922544  
 A:Contents: annotation; disulfide bonds  
 A:Note: Cys-16 is involved in a heavy-light chain bond  
 A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
 C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:21-81/Domain: immunoglobulin homology <IM1>  
 F:135-204/Domain: immunoglobulin homology <IM2>  
 F:241-310/Domain: immunoglobulin homology <IM3>  
 F:28-79/Disulfide bonds: #status experimental  
 F:142-202/Disulfide bonds: #status experimental  
 F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 1201.5; DB 1; Length 329;  
 Best Local Similarity 69.7%; Pred. No. 1.5e-75;  
 Matches 232; Conservative 28; Mismatches 64; Indels 9; Gaps 4;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSNWNSGALTSVHTFPAVLQSS 60  
 Db 2 ARTTAPSVFPLAPSCVDTSGSMVTGLCLVKGYPPEPTVSNWNSGALTSVHTFPAVLQ-S 60

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH--TCPPCPAPELA 118  
 Db 61 GLYSLTSMVTPSSSQAT---CNVAHPASSTKVDKTVPEIRTPZPBCTCPKCPPENL 116

Qy 119 GAPSVFLPPPKPDMLISRTPEVTCVVDVSHEDPEKFNWYDGVVEVHNATKPRREQ 178  
 Db 117 GGPSVFIPPPKPDMLISLTPRVTCVVDVSDDEPEVQFTYINNEQVTRAPPLREQQPNSTI 176

Qy 179 YNSTYRVSVSLTVLHODWLNGEYKCKVSNKALPAPIETKISKAKQPREPQVYTLPPSR 238  
 Db 177 YNTYRVSVSLTVLHODWLNGEYKCKVSNKALPAPIETKISKAKQPREPQVYTLPPSR 236

Qy 239 DELTKNQVSLTCLVKGFPYSDIAVESNGOP--ENNYKTPPVLDSDGSPFLYSKLTVD 296  
 Db 237 DELSKSVSVTCLINFPADIIHVEASNRVPVSEKEYKNTPTPIEDADGSPFLYSKLTVD 296

Qy 297 KSRWQOGNVFSCSVNHEALHNHYTKSLSPG 329  
 Db 297 KSAWDOGTVTYTCVSNHEALHNHYTKSLSPG 329

RESULT 15  
 S31459

Ig gamma-1 chain - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
 C:Accession: S31459  
 R:Patric, S.; Nau, P.  
 submitted to the EMBL Data Library, December 1992  
 A:Reference number: S31459  
 A:Accession: S31459  
 A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-472 <PAT>  
C:Cross-references: UNIPARC:UPI0000176F35; EMBL:X69797  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
P:277-346/Domain: immunoglobulin homology <IMM>

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Query Match      67.7%; Score 1195.5; DB 2; Length 472;
Best Local Similarity 67.2%; Pred. No. 6e-75;
Matches 223; Conservative 38; Mismatches 68; Indels 3; Gaps 2;

Qy 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVADYFPEPTVSWNSGALTSGVHTFPVILQSS 60
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 142 ASITPPKVPYPLTSCCGDTSSSIVTLGCLVSSYMFPEPTVTVNSGALTSGVHTFPAILQSS 201
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 GLXSLSSVVTVPSSSLGTQTYICNVNKKPSNTKVDKVPKSCDKTHTCPPCPAPELAGA 120
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 202 GLXSLSSVVTVPASTSGAQTFCNVAFHSPASSTKVDKRVPGCPDPCKHC-RCPPPELPGG 260
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 121 PSVPLPPPKPDITLMISRTPEVTCVVDVSHEDPEVKENWTVDGVEVHNATKPREBOYN 180
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 261 PSVFIFPPPKPDITLTISGTPEVTCVVDVGGDDPEVQFSWFVDNVEVTRTARKPREBOFN 320
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 181 STYRVSVLTVLHQDLNKGKCKVSNKALPAIEKTISKAKGQPREPOVYTLPPSRDE 240
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 321 STFRVVSALPIQHQDWLGGKEFKCKVNEALPAFIVRTISRTKGQAREPQVYVLAPQSE 380
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDSDGSFFLYSKLTVDKS 298
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 381 LSKSTLSVTCLVTGYPDYIAVEWQKNGQPESDKYGTTSQLDADGSGYFLYSRLRYDKN 440
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 299 RWQGNVFCSVMEHALNHHYTKSLSPGK 330
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 441 SWQEGDTYACVVMHEALNHHYTKSLSPGK 472
Db ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: January 28, 2006, 09:45:39  
Job time : 34.6937 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:21:24 ; Search time 174.91 Seconds  
(without alignments)  
1331.110 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765

Sequence: 1 ASTKGPSVFLAPSSKSTSG.....MHEALHNHYTKSLSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05\_80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	99.5	330	1	IGHG1 HUMAN
2	1756	99.5	465	2	Q6MX6 HUMAN
3	1756	99.5	469	2	Q569F4 HUMAN
4	1756	99.5	469	2	Q727P5 HUMAN
5	1756	99.5	470	2	Q7Z5W1 HUMAN
6	1756	99.5	470	2	Q6FJA4 HUMAN
7	1756	99.5	475	2	Q5BFB5 HUMAN
8	1756	99.5	475	2	Q6GMW7 HUMAN
9	1756	99.5	476	2	Q6MX1 HUMAN
10	1753	99.3	466	2	Q6IN78 HUMAN
11	1753	99.3	472	2	Q6N089 HUMAN
12	1752	99.3	473	2	Q6P055 HUMAN
13	1752	99.3	475	2	Q6MZ06 HUMAN
14	1752	99.3	480	2	Q6N094 HUMAN
15	1752	99.3	481	2	Q6N097 HUMAN
16	1752	99.3	482	2	Q7Z351 HUMAN
17	1749	99.1	466	2	Q6N096 HUMAN
18	1747	99.0	348	2	Q6PYX1 HUMAN
19	1747	99.0	478	2	Q6PI81 HUMAN
20	1747	99.0	480	2	Q6PJF1 HUMAN
21	1745	98.9	475	2	Q6N095 HUMAN
22	1745	98.9	544	2	Q6PJ95 HUMAN
23	1737	98.4	473	2	Q6MZV7 HUMAN
24	1687	95.6	475	2	Q3RE17 PONPY
25	1619.5	91.8	519	2	Q6N030 HUMAN
26	1619.5	91.8	518	2	Q5EBM2 HUMAN
27	1615.5	91.5	521	2	Q6N4V9 HUMAN
28	1608	91.1	326	1	IGHG2 HUMAN
29	1608	91.1	417	2	Q6N093 HUMAN
30	1604.5	90.9	509	2	Q6NF17 HUMAN
31	1603	90.8	465	2	Q6P6C4 HUMAN

32	1594	90.3	470	2	Q68CN4 HUMAN	Q68cn4 homo sapien
33	1593	90.3	464	2	Q6MZU6 HUMAN	Q6mzu6 homo sapien
34	1579.5	89.5	327	1	IGHG4 HUMAN	P01861 homo sapien
35	1579.5	89.5	473	2	Q8TC63 HUMAN	Q8tc63 homo sapien
36	1570.5	89.0	476	2	Q6MZT7 HUMAN	Q6mzx7 homo sapien
37	1513.5	85.8	354	2	Q86TT2 HUMAN	Q86tt2 homo sapien
38	1255.5	71.1	337	2	Q95M34 HORSE	Q95m34 equus cabal
39	1253	71.0	679	2	Q96PQ8 HUMAN	Q96pq8 homo sapien
40	1237.5	70.1	487	2	Q65ZL2-9MURI	Q65zl2 mus sp. fv/
41	1219.5	69.1	323	1	GC RABIT	P01870 oryctolagus
42	1201.5	68.1	329	1	IGHG2 CAVPO	P01862 cavia porce
43	1157	65.6	463	2	Q99LC4 MOUSE	Q99lc4 mus musculu
44	1156	65.5	458	2	Q65ZQ1 HUMAN	Q65zq1 homo sapien
45	1154	65.4	326	1	GC1 RAT	P20759 rattus norv

#### ALIGNMENTS

RESULT 1  
IGHG1 HUMAN  
ID IGHG1 HUMAN STANDARD; PRT; 330 AA.  
AC P01857; 1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DB IG gamma-1 chain C region.  
CN Name=IGHG1;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA MEDLINE=82274238; PubMed=6287432;  
RX Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RX Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP PROTEIN SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RX Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponsingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.

RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RN Biochemistry 9:3188-3196(1970).  
 RP [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC GIM(3) marker and the GIM (non-1) markers.  
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; J00228; AAC8527.1; ALT\_INIT; Genomic\_DNA.  
 DR PIR; A93433; GHU.  
 DR PDB; 1AJ7; X-ray; H=1-103.  
 DR PDB; 1AQK; X-ray; H=1-103.  
 DR PDB; 1DSB; X-ray; B/H=1-101.  
 DR PDB; 1DSI; X-ray; H=1-101.  
 DR PDB; 1D6V; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1E4K; X-ray; A/B=106-330.  
 DR PDB; 1FC1; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCC; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I72; X-ray; B/D=1-103.  
 DR PDB; 1IIS; X-ray; A/B=107-330.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1LOQ; X-ray; A/B=119-330.  
 DR PDB; 1T83; X-ray; A/B=107-330.  
 DR PDB; 2RCS; X-ray; H=1-103.  
 DR HGNC; HGNC:5525; IGHG1.  
 DR MIM; 147100; .  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; P:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR Pfam; PF07654; C1-set; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW immunoglobulin C region; Immunoglobulin domain.  
 FT REGION 1 98 CH1.

FT	REGION	99	110	Hinge.
FT	REGION	111	223	CH2.
FT	REGION	224	330	CH3.
FT	CARBOHYD	180	180	N-linked (GlcNAc...).
FT	DISULFID	27	83	Interchain (with light chain).
FT	DISULFID	103	103	Interchain (with heavy chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	Interchain (with heavy chain).
FT	DISULFID	250	308	Interchain (with heavy chain).
FT	VARIANT	97	97	K -> R (in GIM(3) marker).
FT	VARIANT	239	239	/FTId=VAR_003886.
FT	VARIANT	241	241	D -> E (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTId=VAR_003887.
FT	VARIANT	241	241	L -> M (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTId=VAR_003888.
FT	NON TER	1	1	
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	STRAND	176	177	
FT	TURN	179	180	
FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
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FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	STRAND	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 99.5%; Score 1756; DB 1; Length 330;  
 Best Local Similarity 99.4%; Pred. No. 5.8e-120;  
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ASTKGPSPFLAPSSKSTSGTAALGLVKDYPPETVTSWNSGALTSQVHTFPVAVLQSS 60

Db 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVKPEKSCDKTHTCPCPAPELAGA 120  
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVKPEKSCDKTHTCPCPAPELGG 120  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEQYN 180  
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEQYN 180  
QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPPEPQVYTLPPSRDE 240  
Db 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPPEPQVYTLPPSRDE 240  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330  
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

## RESULT 2

Q6GMX6 HUMAN  
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.  
AC Q6GMX6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN RNP  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
[2]  
RN RNP  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
[3]  
RN RNP  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG-Like; 4.  
DR PROSITE; PS00290; IG-MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; B3A9B7D0FDB1386E CRC64;  
Query Match 99.5%; Score 1756; DB 2; Length 465;  
Best Local Similarity 99.4%; Pred. No. 9.1e-120;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQSS 60  
Db 136 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQSS 195  
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVKPEKSCDKTHTCPCPAPELAGA 120  
Db 196 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVKPEKSCDKTHTCPCPAPELGG 255  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEQYN 180  
Db 256 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEQYN 315  
QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPPEPQVYTLPPSRDE 240  
Db 316 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGPPEPQVYTLPPSRDE 375  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 376 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 435  
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330  
Db 436 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 465

## RESULT 3

Q569F4 HUMAN  
ID Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.  
AC Q569F4  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE IGHG1 protein.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN RNP  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

```
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 469;
Best Local Similarity 99.4%; Pred. No. 9.2e-120;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 140 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 199
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 200 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELGG 259
Qy 121 PSVFLPPPKPD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 260 PSVFLPPPKPD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 319
Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 320 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 379
Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 380 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 439
Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 440 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 469

RESULT 4
Q727P5 HUMAN
ID Q727P5 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haie H.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -; mRNA.
DR HSSP; P01857; IHZH.
DR SMR; Q727P5; 20-469.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8DSBE12BAAF795C CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 469;
Best Local Similarity 99.4%; Pred. No. 9.2e-120;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 140 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 199
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 200 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSN TKVDKVEPKSCDKTHTCPPCPAPELGG 259
Qy 121 PSVFLPPPKPD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 260 PSVFLPPPKPD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 319
Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 320 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 379
Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 380 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 439
Qy 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330
Db 440 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 469

RESULT 5
Q725W1 HUMAN
ID Q725W1 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
```

RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA	Schmerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE-Spleen;
RA	Straussberg R.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.
DR	EMBL; BC053984; AAHS3984.1; -; mRNA.
DR	HSSP; P01857; 1H2H.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig MHC.
DR	InterPro; IPR003596; Ig v.
DR	Pfam; PF07654; CI-set; 3.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG LIKE; 4.
DR	PROSITE; PS02090; IG MHC; UNKNOWN 2.
KW	Hypothetical protein; Immunoglobulin domain.
QO	SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
Query Match	99.5%; Score 1756; DB 2; Length 470;
Best Local Similarity	99.4%; Pred. No. 9,2e-120;
Matches 328; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 ASTKGPSVFLAPLSKSTSGGTAALGLCLVKDYFPEPTVTSWNNSGALTSGVHTFPAVLQSS 60
Db	141 ASTKGPSVFLAPLSKSTSGGTAALGLCLVKDYFPEPTVTSWNNSGALTSGVHTFPAVLQSS 200
QY	61 GLYSLSVVTVTPSSSLGTQTGYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db	201 GLYSLSVVTVTPSSSLGTQTGYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGG 260
QY	121 PSVFLLPPKPDTLMISRTEPTCVVDVSHDEPVKFNWTVDGVEVINATKPREQYN 180
Db	261 PSVFLLPPKPDTLMISRTEPTCVVDVSHDEPVKFNWTVDGVEVINATKPREQYN 320
QY	181 STYRVSVLVTLVHDWLNGKEVKCKVSNKALPAPIEKTIISKAGQPREPOVYITLPSPRDE 240
Db	321 STYRVSVLVTLVHDWLNGKEYKCKVSNKALPAPIEKTIISKAGQPREPOVYITLPSPRDE 380
QY	241 LTQNQVSLTCLVKGPYPDSIDIAVESNESQPNENNYKTTPPVLDSDGSFPFLYSKLTVDKSRW 300
Db	381 LTQNQVSLTCLVKGPYPDSIDIAVESNESQPNENNYKTTPPVLDSDGSFPFLYSKLTVDKSRW 440
QY	301 QQGNNVFCFSVMHEALHNHYTKQSLSLSPGK 330
Db	441 QQGNNVFCFSVMHEALHNHYTKQSLSLSPGK 470
RESULT 6	
Q6PJAA4_HUMAN	
ID	Q6PJAA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC	Q6PJAA4;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DN	IIGH1 protein.
GN	Name=IGHG1;

OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
NC	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Primary B-Cells;
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altechul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalius D.E.,
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
NC	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Primary B-Cells;
RG	NIH MGC Project;
RL	Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC018747; AAH18747.1; --; mRNA.
DR	HSSP; P01861; 1ADQ.
DR	SMR; Q6PJ44; 20-470.
DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003597; IG cl.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF07654; CI-set; 3.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGcl; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG_LIKE; 4.
DR	PROSITE; PS0290; IG_MHC; UNKNOWN 2.
SQ	SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;
Query Match 99.5%; Score 1756; DB 2; Length 470;	
Best Local Similarity 99.4%; Pred. No. 9.2e-120;	
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
QY	1 ASTKGPSVFLPAPSCKSTSGCTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
DB	141 ASTKGPSVFLPAPSCKSTSGCTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 200
QY	61 GLYSLSSVTVTPSSSLGTQTVICNNHKKPSNTKVDKKVPEKSKDKTHTCPCPAPELAGA 120
DB	201 GLYSLSSVTVTPSSSLGTQTVICNNHKKPSNTKVDKKVPEKSKDKTHTCPCPAPELGG 260
QY	121 PSVFLPPKPKDGLMIKRTPEVTCVVDVSHEDPEVKFNVTVDGVGVHNAKTKPREQYN 180
DB	261 PSVFLPPKPKDGLMIKRTPEVTCVVDVSHEDPEVKFNVTVDGVGVHNAKTKPREQYN 320
QY	181 STYRVSVLTVLHDWLNKGEYCKKVSNKALPAPIEKTISKAKGPREFQVYTLPPSRDE 240
DB	321 STYRVSVLTVLHDWLNKGEYCKKVSNKALPAPIEKTISKAKGPREFQVYTLPPSRDE 380
QY	241 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
DB	381 LTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 440

```
Qy 301 OQGNVFCVSMHEALHNHYTKQSLSPGK 330
Db 441 OQGNVFCVSMHEALHNHYTKQSLSPGK 470

RESULT 7
QSEPF5_HUMAN
ID QSEPF5_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEPF5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Belliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RL antibody T125."
EMBL: AY894992; AAWB2028.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL.
FT CHAIN
FT FT
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 19 Potential.
Best Local Similarity 20 475 anti-Rhd monoclonal T125 gammal heavy
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAAALGLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 146 ASTKGPSVFPPLAPSSKSTSGGTAAALGLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 205

Qy 61 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 206 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELLGG 265

Qy 121 PSVFLFPPPKDGLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 266 PSVFLFPPPKDGLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 325

Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 326 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385

Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
Db 386 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 445

Qy 301 OQGNVFCVSMHEALHNHYTKQSLSPGK 330
Db 446 OQGNVFCVSMHEALHNHYTKQSLSPGK 475
```

```
RESULT 8
Q6GMW7_HUMAN
ID Q6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL: BC073782; AAH73782.1; -, mRNA.
GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 475;
Best Local Similarity 99.4%; Pred. No. 9.3e-120;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAAALGLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 146 ASTKGPSVFPPLAPSSKSTSGGTAAALGLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 205

Qy 61 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 206 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVKKVEPKSCDKTHTCPPCPAPELLGG 265

Qy 121 PSVFLFPPPKDGLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 266 PSVFLFPPPKDGLMISRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 325
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QY 191 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAKGPRPQVYTLPPSRDE 240  
 DB 326 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAKGPRPQVYTLPPSRDE 385  
 QY 241 LTKNQVSLTCLVKGPYPSPDIAVEWESNGQPNNTKTPPVLDSGSPFLYSKLTVDKSRW 300  
 DB 386 LTKNQVSLTCLVKGPYPSPDIAVEWESNGQPNNTKTPPVLDSGSPFLYSKLTVDKSRW 445  
 QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330  
 DB 446 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 475

RESULT 9  
 Q6GMX1\_HUMAN  
 ID Q6GMX1\_HUMAN PRELIMINARY; PRT; 476 AA.  
 AC Q6GMX1  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Splice;  
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Splice;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073773; AAH73773.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.cl.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR003596; IG.V.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.  
 KW Hypothetical protein  
 SQ SEQUENCE 476 AA; 5286 MW; 622AABA5C62DDE9D CRC64;

Query Match

99.5%; Score 1756; DB 2; Length 476;

Best Local Similarity 99.4%; Pred. No. 9.3e-120;  
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAAAGCLVADKVPFPPVTVSWNSGALTSGVHTFPAVLQSS 60  
 DB 147 ASTKGPSVFPLAPSSKSTSGGTAAAGCLVADKVPFPPVTVSWNSGALTSGVHTFPAVLQSS 206  
 QY 61 GLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELAGA 120  
 DB 207 GLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELAGG 266  
 QY 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVFVFNNAKTKPREQYN 180  
 DB 267 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVFVFNNAKTKPREQYN 326  
 QY 181 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAKGPRPQVYTLPPSRDE 240  
 DB 327 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAKGPRPQVYTLPPSRDE 386  
 QY 241 LTKNQVSLTCLVKGPYPSPDIAVEWESNGQPNNTKTPPVLDSGSPFLYSKLTVDKSRW 300  
 DB 387 LTKNQVSLTCLVKGPYPSPDIAVEWESNGQPNNTKTPPVLDSGSPFLYSKLTVDKSRW 446  
 QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330  
 DB 447 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 476

## RESULT 10

Q6IN78\_HUMAN  
 ID Q6IN78\_HUMAN PRELIMINARY; PRT; 466 AA.  
 AC Q6IN78;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE IGHG1 protein.  
 GN Name=IGHG1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RC NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC072419; AAH72419.1; -; mRNA.  
 DR HSSP; P01861; 1ADQ.

DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig-MHC.  
 DR InterPro; IPR003596; Ig.v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
 SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCEDE81076E CRC64;

Query Match 99.3%; Score 1753; DB 2; Length 466;  
 Best Local Similarity 99.1%; Pred. No. 1.5e-119;  
 Matches 327; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSVGHVTFPAVLQSS 60  
 |||||  
 Db 137 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSVGHVTFPAVLQSS 196  
 |||||

Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 |||||  
 Db 197 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 256  
 |||||

Qy 121 PSVPLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 |||||  
 Db 257 PSVPLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 316  
 |||||

Qy 181 STYRVSVLTVLHQDLNGLNGEYKCKVSNKALPAPIETISKAKQPREPOVYITLPPSRDE 240  
 |||||  
 Db 317 STYRVSVLTVLHQDLNGLNGEYKCKVSNKALPAPIETISKAKQPREPOVYITLPPSRDE 376  
 |||||

Qy 241 LTRNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300  
 |||||  
 Db 377 LTRNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 436  
 |||||

Qy 301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330  
 |||||  
 Db 437 QQGNVFCSCVMHEALHNHYTKSLSPGK 466  
 |||||

## RESULT 11

O6N089\_HUMAN  
 AC Q6N089;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein DKFZp686P15220.  
 GN Name=DKFZp686P15220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Rectum tumor;  
 RG The German cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640627; CA545781.1; -; mRNA.  
 DR HSSP; P01861; 1ADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig-MHC.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 99.3%; Score 1753; DB 2; Length 472;  
 Best Local Similarity 99.1%; Pred. No. 1.5e-119;  
 Matches 327; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSVGHVTFPAVLQSS 60  
 |||||  
 Db 143 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSVGHVTFPAVLQSS 202  
 |||||

Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 |||||  
 Db 203 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 262  
 |||||

Qy 121 PSVPLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
 |||||  
 Db 263 PSVPLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 322  
 |||||

Qy 181 STYRVSVLTVLHQDLNGLNGEYKCKVSNKALPAPIETISKAKQPREPOVYITLPPSRDE 240  
 |||||  
 Db 323 STYRVSVLTVLHQDLNGLNGEYKCKVSNKALPAPIETISKAKQPREPOVYITLPPSRDE 382  
 |||||

Qy 241 LTRNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300  
 |||||  
 Db 383 LTRNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 442  
 |||||

Qy 301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330  
 |||||  
 Db 443 QQGNVFCSCVMHEALHNHYTKSLSPGK 472  
 |||||

## RESULT 12

O6P055\_HUMAN  
 ID Q6P055\_HUMAN PRELIMINARY; PRT; 473 AA.  
 AC Q6P055;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match          99.3%; Score 1752; DB 2; Length 473;
Best Local Similarity 99.1%; Pred. No. 1.8e-119;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203
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Db 204 GLYSLSSVTVTPSSSLGQTTCYICNVNHPKSTKVDKKVEPKSCDKHTCCPCPAPELGG 263
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Db 264 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEOYN 323
QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 324 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 383
QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 384 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 443
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Db 444 QQGNVFCVSMHEALHNYHTQKSLSLSPGK 473

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AC Q6MZQ6_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6MZQ6; 20-475.

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match          99.3%; Score 1752; DB 2; Length 473;
Best Local Similarity 99.1%; Pred. No. 1.8e-119;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203
QY 61 GLYSLSSVTVTPSSSLGQTTCYICNVNHPKSTKVDKKVEPKSCDKHTCCPCPAPELAGA 120
Db 204 GLYSLSSVTVTPSSSLGQTTCYICNVNHPKSTKVDKKVEPKSCDKHTCCPCPAPELGG 263
QY 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEOYN 180
Db 264 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEOYN 323
QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240
Db 324 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 383
QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Db 384 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 443
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Db 444 QQGNVFCVSMHEALHNYHTQKSLSLSPGK 473

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AC Q6N094_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G001196.
GN Name=DKFZp686G001196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 48.586 seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/PC/US COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1756	99.5	371	1	US-08-236-311-7
2	1756	99.5	371	2	US-08-457-918-7
3	1756	99.5	371	2	US-10-157-408-7
4	1756	99.5	446	2	US-08-397-411-7
5	1756	99.5	449	1	US-08-458-516-13
6	1756	99.5	467	2	US-08-030-175-41
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8	1756	99.5	470	2	US-10-104-047-3730
9	1756	99.5	476	1	US-08-378-939-10
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33	1751	99.2	470	2	US-09-238-741-4
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ALIGNMENTS

RESULT 1  
US-08-236-311-7  
; Sequence 7, Application US/08236311  
; Patent No. 5565335  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,311  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 444PIC2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-236-311-7

Query Match 99.5%; Score 1756; DB 1; Length 371;  
Best Local Similarity 99.4%; Pred. No. 6e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 102 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCTCPCPAPELAGG 161  
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Db 222 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 281  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
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Db 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

## RESULT 2

US-10-457-918-7  
; Sequence 7, Application US/08457918  
; Patent No. 6117655  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,918  
; FILING DATE: 1-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/236311  
; FILING DATE: 02-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.

; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0444P1C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8228  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-457-918-7

Query Match 99.5%; Score 1756; DB 2; Length 371;  
Best Local Similarity 99.4%; Pred. No. 6e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 42 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 101  
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Db 102 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCTCPCPAPELAGG 161  
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Db 162 PSVFLPPPKPDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 221  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 222 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 281  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
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Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
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## RESULT 3

US-10-457-408-7  
; Sequence 7, Application US/10157408  
; Patent No. 6710169  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/157,408  
; FILING DATE: 28-MAY-2002  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,918  
; FILING DATE: 1-JUN-1995  
; APPLICATION NUMBER: 08/236311  
; FILING DATE: 02-MAY-1994  
; APPLICATION NUMBER: 07/936190

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 99.5%; Score 1756; DB 2; Length 371;  
Best Local Similarity 99.4%; Pred. No. 68-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 102 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSTKVDKKVEPKSCDKHTCCPPCPAPELAG 161  
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DB 162 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 221  
QY 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240  
DB 222 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 281  
QY 241 LTRNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300  
DB 282 LTRNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 341  
QY 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330  
DB 342 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 371

RESULT 4  
US-08-397-411-7  
; Sequence 7, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 99.5%; Score 1756; DB 2; Length 446;  
Best Local Similarity 99.4%; Pred. No. 7.9e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
DB 117 ASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176  
QY 61 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSTKVDKKVEPKSCDKHTCCPPCPAPELAG 120  
DB 177 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSTKVDKKVEPKSCDKHTCCPPCPAPELAG 236  
QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
DB 237 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 296  
QY 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240  
DB 297 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 356  
QY 241 LTRNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300  
DB 357 LTRNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 416  
QY 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330  
DB 417 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 446

RESULT 5  
US-08-458-516-13  
; Sequence 13, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIb/IIIa  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

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Query Match      99.5%; Score 1756; DB 1; Length 449;
Best Local Similarity 99.4%; Pred. No. 7.9e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSWNSGALTSGVHTTFAVLQSS 60
DB 120 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSWNSGALTSGVHTTFAVLQSS 179
QY 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTCTCPCPAPELAGA 120
DB 180 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTCTCPCPAPELAGG 239
QY 121 PSVFLFPKPKDITLMSRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNATKPREQYN 180
DB 240 PSVFLFPKPKDITLMSRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNATKPREQYN 299
QY 181 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 240
DB 300 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 359
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
DB 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 419
QY 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
DB 420 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

```

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RESULT 6
US-08-030-175-41
; Sequence 41, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.

```

```

; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Dos Text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,175
; FILING DATE: 17-MAY-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-030-175-41

Query Match      99.5%; Score 1756; DB 2; Length 467;
Best Local Similarity 99.4%; Pred. No. 8.4e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSWNSGALTSGVHTTFAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSWNSGALTSGVHTTFAVLQSS 197
QY 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTCTCPCPAPELAGA 120
DB 198 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTCTCPCPAPELAGG 257
QY 121 PSVFLFPKPKDITLMSRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNATKPREQYN 180
DB 258 PSVFLFPKPKDITLMSRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNATKPREQYN 317
QY 181 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 240
DB 318 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 437
QY 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
DB 438 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 467

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RESULT 7
US-08-030-175-42
; Sequence 42, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.

```



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; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Dos Text)
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAY-1993
; CLASSIFICATION: 424
; APPLICATION NUMBER: US/08/030,175
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-030-175-42

; Query Match 99.5%; Score 1756; DB 2; Length 467;
; Best Local Similarity 99.4%; Pred. No. 8.4e-157;
; Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELAGG 257
Qy 121 PSVFLPPPKDQTLMIKSTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180
Db 258 PSVFLPPPKDQTLMIKSTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 317
Qy 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTIISKAKGQPRPQVYTLPPSRDE 240
Db 318 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTIISKAKGQPRPQVYTLPPSRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNNHYTKSLSPGK 467

RESULT 8
US-10-104-047-3730
; Sequence 3730, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cdna
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3730

; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Dos Text)
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAY-1993
; CLASSIFICATION: 424
; APPLICATION NUMBER: US/08/030,175
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-030-175-42

; Query Match 99.5%; Score 1756; DB 2; Length 467;
; Best Local Similarity 99.4%; Pred. No. 8.4e-157;
; Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTHTCPCPAPELAGG 257
Qy 121 PSVFLPPPKDQTLMIKSTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180
Db 258 PSVFLPPPKDQTLMIKSTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 317
Qy 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTIISKAKGQPRPQVYTLPPSRDE 240
Db 318 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTIISKAKGQPRPQVYTLPPSRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNNHYTKSLSPGK 467

RESULT 9
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
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;  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-378-939-10

Query Match 99.5%; Score 1756; DB 1; Length 476;  
Best Local Similarity 99.4%; Pred. No. 8.7e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLIQSS 60  
Db 147 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLIQSS 206  
Qy 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPAPLAGA 120  
Db 207 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPAPLAGA 266  
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREPOYN 180  
Db 267 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREPOYN 326  
Qy 181 STRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240  
Db 327 STRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 386  
Qy 241 LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 387 LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 446  
Qy 301 QOQNVFSCSVMEALHNHYTQKSLSLSPGK 330  
Db 447 QOQNVFSCSVMEALHNHYTQKSLSLSPGK 476

RESULT 10

US-09-746-359A-54  
; Sequence 54, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaepers, Stephen R.  
; APPLICANT: Chandrasekher, Yasmin A.  
; APPLICANT: No. 6610286ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746.359A  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 54  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-54

Query Match 99.5%; Score 1756; DB 2; Length 547;  
Best Local Similarity 99.4%; Pred. No. 1.1e-156;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLIQSS 60  
Db 218 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLIQSS 277

Qy 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPAPLAGA 120  
Db 278 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPAPLAGA 337  
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREPOYN 180  
Db 338 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREPOYN 397  
Qy 181 STRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240  
Db 398 STRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 457  
Qy 241 LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 458 LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 517  
Qy 301 QOQNVFSCSVMEALHNHYTQKSLSLSPGK 330  
Db 518 QOQNVFSCSVMEALHNHYTQKSLSLSPGK 547

RESULT 11

US-09-825-561A-16  
; Sequence 16, Application US/09825561A  
; Patent No. 677539  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: No. 677539ak, Julia E.  
; APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22  
; CURRENT APPLICATION NUMBER: US/09/825.561A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/194,731  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/222,121  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: soluble zalpha11/IgGgamma1 polypeptide  
US-09-825-561A-16

Query Match 99.5%; Score 1756; DB 2; Length 567;  
Best Local Similarity 99.4%; Pred. No. 1.1e-156;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLIQSS 60  
Db 238 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLIQSS 297  
Qy 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPAPLAGA 120  
Db 298 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPAPLAGA 357  
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREPOYN 180  
Db 358 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREPOYN 417  
Qy 181 STRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240  
Db 418 STRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 477  
Qy 241 LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 478 LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 537

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QY 301 QQGNVFCVSMHEALHNNHYTKLSLSPGK 330
|||||
Db 538 QQGNVFCVSMHEALHNNHYTKLSLSPGK 567

RESULT 12
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jasper, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-53

Query Match 99.5%; Score 1756; DB 2; Length 571;
Best Local Similarity 99.4%; Pred. No. 1.1e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
|||||
Db 242 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 301

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
|||||
Db 302 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 361

QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 180
|||||
Db 362 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 421

QY 181 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
|||||
Db 422 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 481

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
|||||
Db 482 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 541

QY 301 QQGNVFCVSMHEALHNNHYTKLSLSPGK 330
|||||
Db 542 QQGNVFCVSMHEALHNNHYTKLSLSPGK 571

RESULT 13
US-09-313-942-9
; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-9

Query Match 99.5%; Score 1756; DB 2; Length 951;
Best Local Similarity 99.4%; Pred. No. 2.4e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
|||||
Db 622 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 681

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
|||||
Db 682 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 741

QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 180
|||||
Db 742 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 801

QY 181 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
|||||
Db 802 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 861

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
|||||
Db 862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 921

QY 301 QQGNVFCVSMHEALHNNHYTKLSLSPGK 330
|||||
Db 922 QQGNVFCVSMHEALHNNHYTKLSLSPGK 951

RESULT 14
US-10-282-162-9
; Sequence 9, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-9

Query Match 99.5%; Score 1756; DB 2; Length 951;
Best Local Similarity 99.4%; Pred. No. 2.4e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAAGCLIVKDYPPEPVTVSNWNGALTSQVHTFPVAVLQSS 60
Db |||||||
Qy 622 ASTKGPSVFPPLAPSSKSTSGGTAAGCLIVKDYPPEPVTVSNWNGALTSQVHTFPVAVLQSS 681
Db |||||||
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db |||||||
Qy 682 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 741
Db |||||||
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db |||||||
Qy 742 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 801
Db |||||||
Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db |||||||
Qy 802 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 861
Db |||||||
Qy 241 LTRNQVSLTCLIVKGFIYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300
Db |||||||
Qy 862 LTRNQVSLTCLIVKGFIYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 921
Db |||||||
Qy 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330
Db |||||||
Qy 922 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 951
Db |||||||
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RESULT 15
US-09-289-942A-7
; Sequence 7, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pai, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab'-EPTOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; FILE OF INVENTION: MONOCLONAL ANTIBODY 2F5
; FILE REFERENCE: 1038-926 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-289-942A-7
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Query Match 99.3%; Score 1752; DB 2; Length 462;
Best Local Similarity 99.1%; Pred. No. 2e-156;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAAGCLIVKDYPPEPVTVSNWNGALTSQVHTFPVAVLQSS 60
Db |||||||
Qy 133 ASTKGPSVFPPLAPSSKSTSGGTAAGCLIVKDYPPEPVTVSNWNGALTSQVHTFPVAVLQSS 192
Db |||||||
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELAGA 120
Db |||||||
Qy 193 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 252
Db |||||||
Qy 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db |||||||
Qy 253 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 312
Db |||||||
Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db |||||||
Qy 313 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 372
Db |||||||
Qy 241 LTRNQVSLTCLIVKGFIYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300
Db |||||||
Qy 373 LTRNQVSLTCLIVKGFIYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 432
Db |||||||
Qy 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330
Db |||||||
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Db 433 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 462

Search completed: January 28, 2006, 09:47:29

Job time : 49.5586 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 140.721 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765

Sequence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNHYTQKSLSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA\_Main:
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1765	100.0	330	4	US-10-733-563-110
2	1765	100.0	333	4	US-10-272-899A-10
3	1765	100.0	333	4	US-10-733-563-114
4	1765	100.0	356	4	US-10-272-899A-70
5	1765	100.0	448	4	US-10-171-452A-42
6	1765	100.0	448	4	US-10-171-452A-54
7	1765	100.0	448	4	US-10-353-708-42
8	1765	100.0	448	4	US-10-353-708-54
9	1765	100.0	448	4	US-10-731-984-8
10	1765	100.0	448	4	US-10-731-984-24
11	1765	100.0	467	4	US-10-171-452A-53
12	1765	100.0	467	4	US-10-353-708-53
13	1765	100.0	467	4	US-10-731-984-7
14	1765	100.0	467	4	US-10-731-984-23
15	1759	99.7	473	4	US-10-467-253-13
16	1758	99.6	469	4	US-10-404-724-72
17	1756	99.5	330	3	US-09-995-898A-15
18	1756	99.5	330	3	US-09-892-949-38
19	1756	99.5	330	4	US-10-047-542-20
20	1756	99.5	330	4	US-10-269-805-68
21	1756	99.5	330	4	US-10-310-719-8
22	1756	99.5	330	4	US-10-112-582-1
23	1756	99.5	330	4	US-10-320-231A-81
24	1756	99.5	330	4	US-10-363-902A-6
25	1756	99.5	330	4	US-10-408-901-2
26	1756	99.5	330	4	US-10-420-034A-15
27	1756	99.5	330	4	US-10-257-907-5

28	1756	99.5	330	4	US-10-656-769-2	Sequence 2, Appli
29	1756	99.5	330	4	US-10-772-531-38	Sequence 38, Appli
30	1756	99.5	330	4	US-10-479-326-1	Sequence 1, Appli
31	1756	99.5	330	5	US-10-815-449-8	Sequence 8, Appli
32	1756	99.5	330	5	US-10-684-957-2	Sequence 2, Appli
33	1756	99.5	330	5	US-10-886-838-6	Sequence 6, Appli
34	1756	99.5	330	5	US-10-822-300-3	Sequence 3, Appli
35	1756	99.5	330	5	US-10-822-300-7	Sequence 7, Appli
36	1756	99.5	330	5	US-10-687-118-3	Sequence 3, Appli
37	1756	99.5	330	5	US-10-687-118-7	Sequence 7, Appli
38	1756	99.5	330	5	US-10-901-735-2	Sequence 2, Appli
39	1756	99.5	330	5	US-10-698-907-22	Sequence 22, Appli
40	1756	99.5	330	5	US-10-928-305-7	Sequence 7, Appli
41	1756	99.5	330	5	US-10-480-109-5	Sequence 5, Appli
42	1756	99.5	330	5	US-10-891-658-2	Sequence 2, Appli
43	1756	99.5	330	5	US-10-867-506-81	Sequence 81, Appli
44	1756	99.5	330	5	US-10-937-596-31	Sequence 31, Appli
45	1756	99.5	330	5	US-10-893-576-45	Sequence 45, Appli

ALIGNMENTS

RESULT 1  
US-10-733-563-110  
; Sequence 110, Application US/10733563  
; Publication No. US20040151721A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa  
; APPLICANT: Ponath, Paul  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 10448-213001  
; CURRENT APPLICATION NUMBER: US/10733.563  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: US 10/272,899  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 110  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human IgG1-FcRmut protein  
US-10-733-563-110

Query Match	100.0%	Score	1765;	DB	4;	Length	330;
Best Local Similarity	100.0%	Pred. No.	1.3e-128;	Indels	0;	Gaps	0;
Matches	330;	Conservative	0;	Mismatches	0;		
Oy	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA	1
Db	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA	1
Oy	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61
Db	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61
Oy	121	PSVFLPPPKPDMLMISRTPEVTCVV	121	PSVFLPPPKPDMLMISRTPEVTCVV	121	PSVFLPPPKPDMLMISRTPEVTCVV	121
Db	121	PSVFLPPPKPDMLMISRTPEVTCVV	121	PSVFLPPPKPDMLMISRTPEVTCVV	121	PSVFLPPPKPDMLMISRTPEVTCVV	121
Oy	181	STYRWVSVLTVLHODWLNKGEYCKV	181	STYRWVSVLTVLHODWLNKGEYCKV	181	STYRWVSVLTVLHODWLNKGEYCKV	181
Db	181	STYRWVSVLTVLHODWLNKGEYCKV	181	STYRWVSVLTVLHODWLNKGEYCKV	181	STYRWVSVLTVLHODWLNKGEYCKV	181
Oy	241	LTKNQVSLTCLVKGFYPSDIAVEWES	241	LTKNQVSLTCLVKGFYPSDIAVEWES	241	LTKNQVSLTCLVKGFYPSDIAVEWES	241
Db	241	LTKNQVSLTCLVKGFYPSDIAVEWES	241	LTKNQVSLTCLVKGFYPSDIAVEWES	241	LTKNQVSLTCLVKGFYPSDIAVEWES	241

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Db      241 LTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 300
Qy      301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330
Db      301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330

RESULT 2
US-10-272-899A-10
; Sequence 10, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MEI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-FcRmut protein
US-10-272-899A-10

Query Match      100.0%; Score 1765; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db      4 ASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 63
Qy      61 GLYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPPCPAPELAGA 120
Db      64 GLYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPPCPAPELAGA 123
Qy      121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db      124 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 183
Qy      181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Db      184 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 243
Qy      241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 300
Db      244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 303
Qy      301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330
Db      304 QQGNVFCSCVMHEALHNHYTKSLSPGK 333

RESULT 3
US-10-733-563-114
; Sequence 114, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
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; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-FcRmut protein
US-10-733-563-114

Query Match      100.0%; Score 1765; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db      4 ASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 63
Qy      61 GLYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPPCPAPELAGA 120
Db      64 GLYSLSVSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPPCPAPELAGA 123
Qy      121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db      124 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 183
Qy      181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Db      184 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 243
Qy      241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 300
Db      244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 303
Qy      301 QQGNVFCSCVMHEALHNHYTKSLSPGK 330
Db      304 QQGNVFCSCVMHEALHNHYTKSLSPGK 333

RESULT 4
US-10-272-899A-70
; Sequence 70, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MP101-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
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Db 119 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 178  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 179 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 238  
Qy 121 PSVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYN 180  
Db 239 PSVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYN 298  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 299 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGFYPSDIAVHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 418  
Qy 301 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 330  
Db 419 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 448

RESULT 7  
US-10-353-708-42  
; Sequence 42, Application US/10353708  
; Publication No. US20030219403A1  
; GENERAL INFORMATION:  
; APPLICANT: Frewin, Mark  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Gorman, Scott  
; APPLICANT: Hale, Geoff  
; APPLICANT: Rao, Patricia  
; APPLICANT: Kornaga, Tadeusz  
; APPLICANT: Ringler, Douglas  
; APPLICANT: Cobbold, Stephen  
; APPLICANT: Winsor-Hines, Dawn  
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen  
; FILE REFERENCE: 695458-73  
; CURRENT APPLICATION NUMBER: US/10/353,708  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: US10/171,452  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US60/373,471  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: GB0122724.8  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/373,470  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB0114517.6  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 60  
; SEQ ID NO 42  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Heavy chain of humanized antibody  
US-10-353-708-42

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60  
Db 119 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 178  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 179 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 238

Qy 121 PSVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYN 180  
Db 239 PSVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYN 298  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 299 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGFYPSDIAVHESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 418  
Qy 301 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 330  
Db 419 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 448

RESULT 8  
US-10-353-708-54  
; Sequence 54, Application US/10353708  
; Publication No. US20030219403A1  
; GENERAL INFORMATION:  
; APPLICANT: Frewin, Mark  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Gorman, Scott  
; APPLICANT: Hale, Geoff  
; APPLICANT: Rao, Patricia  
; APPLICANT: Kornaga, Tadeusz  
; APPLICANT: Ringler, Douglas  
; APPLICANT: Cobbold, Stephen  
; APPLICANT: Winsor-Hines, Dawn  
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen  
; FILE REFERENCE: 695458-73  
; CURRENT APPLICATION NUMBER: US/10/353,708  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: US10/171,452  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US60/373,471  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/373,470  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: GB0122724.8  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB0114517.6  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 60  
; SEQ ID NO 54  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Heavy chain of humanized antibody  
US-10-353-708-54

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60  
Db 119 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 178  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 179 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 238  
Qy 121 PSVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYN 180  
Db 239 PSVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREBOYN 298



Qy 181 STYRVSVLTCLVHODWLNKGEYCKKVSNAKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240  
Db 299 STYRVSVLTCLVHODWLNKGEYCKKVSNAKALPAPIEKTISKAKGPREPQVYTLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTTPVLDSDGSFPFLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTTPVLDSDGSFPFLYSKLTVDKSRW 418  
Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330  
Db 419 QQGNVFCSCVMHEALHNNHYTKSLSPGK 448

## RESULT 9

US-10-731-984-8  
; Sequence 8, Application US/10731984  
; Publication No. US20040175381A1  
; GENERAL INFORMATION:  
; APPLICANT: WINDSOR-HINES, Dawn  
; APPLICANT: RAO, Patricia  
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES  
; FILE REFERENCE: TLN-022  
; CURRENT APPLICATION NUMBER: US/10/731,984  
; PRIOR FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: 60/431839  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric Sequence  
US-10-731-984-8

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLSS 60  
Db 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLSS 178  
Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCPCPAPELAGA 120  
Db 179 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCPCPAPELAGA 238  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
Db 239 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 298  
Qy 181 STYRVSVLTCLVHODWLNKGEYCKKVSNAKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240  
Db 299 STYRVSVLTCLVHODWLNKGEYCKKVSNAKALPAPIEKTISKAKGPREPQVYTLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTTPVLDSDGSFPFLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTTPVLDSDGSFPFLYSKLTVDKSRW 418  
Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330  
Db 419 QQGNVFCSCVMHEALHNNHYTKSLSPGK 448

## RESULT 10

US-10-731-984-24  
; Sequence 24, Application US/10731984  
; Publication No. US20040175381A1  
; GENERAL INFORMATION:  
; APPLICANT: WINDSOR-HINES, Dawn  
; APPLICANT: RAO, Patricia

; APPLICANT: RINGLER, Douglas J.  
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES  
; FILE REFERENCE: TLN-022  
; CURRENT APPLICATION NUMBER: US/10/731,984  
; PRIOR FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: 60/431839  
; PRIOR FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric Sequence  
US-10-731-984-24

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLSS 60  
Db 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLSS 178  
Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCPCPAPELAGA 120  
Db 179 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCPCPAPELAGA 238  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
Db 239 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 298  
Qy 181 STYRVSVLTCLVHODWLNKGEYCKKVSNAKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240  
Db 299 STYRVSVLTCLVHODWLNKGEYCKKVSNAKALPAPIEKTISKAKGPREPQVYTLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTTPVLDSDGSFPFLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTTPVLDSDGSFPFLYSKLTVDKSRW 418  
Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSPGK 330  
Db 419 QQGNVFCSCVMHEALHNNHYTKSLSPGK 448

## RESULT 11

US-10-171-452A-53  
; Sequence 53, Application US/10171452A  
; Publication No. US20030108518A1  
; GENERAL INFORMATION:  
; APPLICANT: Frewin, Mark  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Gorman, Scott  
; APPLICANT: Hale, Geoff  
; APPLICANT: Rao, Patricia  
; APPLICANT: Kornaga, Tadeusz  
; APPLICANT: Ringler, Douglas  
; APPLICANT: Cobboid, Stephen  
; APPLICANT: Winsor-Hines, Dawn  
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor  
; FILE REFERENCE: 695458-59  
; CURRENT APPLICATION NUMBER: US/10/171,452A  
; PRIOR FILING DATE: 2003-02-10  
; PRIOR APPLICATION NUMBER: US60/373,471  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/373,470  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: GB0122724.8  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB0114517.6

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; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-53

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSN TKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSN TKVDKKVEPKSCDKTHCTCPCPAPELAGA 257
Qy 121 PSVFLPPPKPD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 258 PSVFLPPPKPD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 438 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 12
US-10-353-708-53
; Sequence 53, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
;
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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-53

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSN TKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSN TKVDKKVEPKSCDKTHCTCPCPAPELAGA 257
Qy 121 PSVFLPPPKPD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 258 PSVFLPPPKPD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 438 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 13
US-10-731-984-7
; Sequence 7, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-731-984-7

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSN TKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSN TKVDKKVEPKSCDKTHCTCPCPAPELAGA 257
Qy 121 PSVFLPPPKPD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 258 PSVFLPPPKPD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317
;
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Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 437  
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 330  
Db 438 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 467

## RESULT 14

US-10-731-984-23  
; Sequence 23, Application US/10731984  
; Publication No. US20040175381A1  
; GENERAL INFORMATION:  
; APPLICANT: WINDSOR-HINES, Dawn  
; APPLICANT: RAO, Patricia  
; APPLICANT: RINGLER, Douglas J.  
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES  
; FILE REFERENCE: TILN-022  
; CURRENT APPLICATION NUMBER: US/10/731.984  
; CURRENT FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: 60/431839  
; PRIOR FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric Sequence  
US-10-731-984-23

Query Match 100.0%; Score 1765; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 2e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197  
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCTPCPAPELAGA 120  
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCTPCPAPELAGA 257  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
Db 258 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 377  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 437  
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 330  
Db 438 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 467

## RESULT 15

US-10-467-253-13  
; Sequence 13, Application US/10467253  
; Publication No. US20040170627A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham plc

; APPLICANT: Irving, Elaine A  
; APPLICANT: Vinson, Mary  
; TITLE OF INVENTION: Novel Method of Treatment  
; FILE REFERENCE: SAL/P32763  
; CURRENT APPLICATION NUMBER: US/10/467.253  
; CURRENT FILING DATE: 2003-08-05  
; PRIOR APPLICATION NUMBER: GB 0103174.9  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: mouse/human  
; OTHER INFORMATION: chimeric anti-MAG antibody heavy chain  
US-10-467-253-13

Query Match 99.7%; Score 1759; DB 4; Length 473;  
Best Local Similarity 99.7%; Pred. No. 5.9e-128;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
Db 144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203  
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCTPCPAPELAGA 120  
Db 204 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCTPCPAPELAGA 263  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
Db 264 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 323  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 324 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 383  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 384 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 443  
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 330  
Db 444 QQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 473

Search completed: January 28, 2006, 10:11:23

Job time : 141.721 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 19.8198 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-110  
Perfect score: 1765  
Sequence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNYTKSLSPGK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	100.0	448	7	US-11-158-505-8
2	1765	100.0	448	7	US-11-158-505-24
3	1765	100.0	467	7	US-11-158-505-5
4	1765	100.0	467	7	US-11-158-505-7
5	1765	100.0	467	7	US-11-158-505-21
6	1765	100.0	467	7	US-11-158-505-23
7	1756	99.5	330	6	US-10-886-383-6
8	1756	99.5	330	7	US-10-493-909-20
9	1756	99.5	330	7	US-11-022-289-11
10	1756	99.5	330	7	US-11-075-351-1
11	1756	99.5	330	7	US-11-165-141-15
12	1756	99.5	330	7	US-11-102-621-3
13	1756	99.5	330	7	US-11-102-621-7
14	1756	99.5	335	7	US-11-024-251-35
15	1756	99.5	444	7	US-11-172-320-6
16	1756	99.5	444	7	US-11-173-969-6
17	1756	99.5	451	7	US-11-158-505-33
18	1756	99.5	551	7	US-11-022-289-7
19	1756	99.5	551	7	US-11-022-289-8
20	1756	99.5	557	7	US-11-022-289-4
21	1756	99.5	557	7	US-11-022-289-5
22	1756	99.5	557	7	US-11-022-289-6
23	1754	99.4	592	6	US-10-016-686-4
24	1753	99.3	330	7	US-11-102-621-71
25	1753	99.3	446	7	US-11-102-621-121

26	1753	99.3	447	7	US-11-102-621-132	Sequence 132, Appl
27	1752	99.3	476	7	US-11-139-499-4	Sequence 4, Appl
28	1752	99.3	476	7	US-11-139-499-12	Sequence 12, Appl
29	1752	99.3	478	7	US-11-139-499-8	Sequence 8, Appl
30	1751	99.2	330	7	US-11-102-621-70	Sequence 70, Appl
31	1750	99.2	330	7	US-11-022-289-1	Sequence 1, Appl
32	1750	99.2	330	7	US-11-102-621-67	Sequence 67, Appl
33	1750	99.2	330	7	US-11-102-621-68	Sequence 68, Appl
34	1750	99.2	330	7	US-11-102-621-69	Sequence 69, Appl
35	1750	99.2	446	7	US-11-102-621-119	Sequence 119, Appl
36	1750	99.2	446	7	US-11-102-621-120	Sequence 120, Appl
37	1750	99.2	447	7	US-11-102-621-130	Sequence 130, Appl
38	1750	99.2	447	7	US-11-102-621-131	Sequence 131, Appl
39	1750	99.2	449	7	US-11-154-337-17	Sequence 17, Appl
40	1750	99.2	451	6	US-10-923-327-7	Sequence 7, Appl
41	1750	99.2	451	6	US-10-923-327-9	Sequence 9, Appl
42	1750	99.2	451	6	US-10-923-327-11	Sequence 11, Appl
43	1750	99.2	452	7	US-11-120-338-14	Sequence 14, Appl
44	1750	99.2	452	7	US-11-107-028-32	Sequence 32, Appl
45	1750	99.2	452	7	US-11-106-820-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-11-158-505-8  
; Sequence 8, Application US/11158505  
; Publication No. US20060002921A1  
; GENERAL INFORMATION:  
; APPLICANT: WINSOR-HINES, DAWN  
; APPLICANT: RAO, PATRICIA  
; APPLICANT: RINGLER, DOUGLAS J  
; APPLICANT: POWATH, PAUL  
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE  
; FILE OF INVENTION: INDUCTION IN PRIMATES  
; FILE REFERENCE: TLN-031  
; CURRENT APPLICATION NUMBER: US/11/158,505  
; PRIOR FILING DATE: 2005-06-21  
; PRIOR APPLICATION NUMBER: 60/582,181  
; PRIOR FILING DATE: 2004-06-22  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 8  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1  
; OTHER INFORMATION: antibody heavy chain construct  
US-11-158-505-8

Query Match 100.0%; Score 1765; DB 7; Length 448;  
Best Local Similarity 100.0%; Pred. No. 2.4e-133;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSNWNSGALTSGVHTFPAVLQSS 60
Db	119	ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSNWNSGALTSGVHTFPAVLQSS 178
Qy	61	GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKVPKSCDKTKHTTCCPPAPELAGA 120
Db	179	GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKVPKSCDKTKHTTCCPPAPELAGA 238
Qy	121	PSVFLPPPKDITLMISRTPEVTCVVDVSHEDDEVKFNVTVDGVGVNNAKTKPREQYN 180
Db	239	PSVFLPPPKDITLMISRTPEVTCVVDVSHEDDEVKFNVTVDGVGVNNAKTKPREQYN 298
Qy	181	STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQPREPQVYITLPPSRDE 240
Db	299	STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQPREPQVYITLPPSRDE 358
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300

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Db 359 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 418
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Db 419 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448

RESULT 2
US-11-158-505-24
; Sequence 24, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-24

Query Match 100.0%; Score 1765; DB 7; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.4e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 178
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKHTCTCPPELAPLAGA 120
Db 179 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKHTCTCPPELAPLAGA 238
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 239 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 298
Qy 181 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 240
Db 299 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 358
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 418
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 419 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448

RESULT 3
US-11-158-505-5
; Sequence 5, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
```

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; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-5

Query Match 100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKHTCTCPPELAPLAGA 120
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKHTCTCPPELAPLAGA 257
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 258 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 317
Qy 181 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 240
Db 318 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 4
US-11-158-505-7
; Sequence 7, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-7
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Query Match      100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 257

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317

QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 5
US-11-158-505-21
; Sequence 21, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-21

Query Match      100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 257

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317

QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 6
US-11-158-505-23
; Sequence 23, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-23

Query Match      100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
DB 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 257

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317

QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 7
US-10-886-383-6
; Sequence 6, Application US/10886383
; Publication No. US20060005571A1
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; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-165-141-15

Query Match      99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
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Db 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330

RESULT 12
US-11-102-621-3
; Sequence 3, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-3

Query Match      99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330

RESULT 11
US-11-165-141-15
; Sequence 15, Application US/11165141
; Publication No. US20050266485A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Novak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/11/165,141
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US/09/995,898
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
US-11-075-351-1
; Sequence 1, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-1

Query Match      99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
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Db 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 13
US-11-102-621-7
; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 059882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-11-102-621-7

Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Db 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 14
US-11-102-621-7
; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 059882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-11-102-621-7

Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Db 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 15
US-11-172-320-6
; Sequence 6, Application US/111172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
US-11-172-320-6

Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.8e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 6 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 65
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 66 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 125
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Db 126 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 185
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 186 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 245
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 305
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 306 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 335

RESULT 16
US-11-172-320-6
; Sequence 6, Application US/111172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
US-11-172-320-6

Query Match 99.5%; Score 1756; DB 7; Length 335;
Best Local Similarity 99.4%; Pred. No. 8.8e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 6 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 65
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 66 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 125
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Db 126 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 185
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 186 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 245
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 305
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 306 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 335
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US-11-024-251-35
; Sequence 35, Application US/11024251
; Publication No. US20050266425A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Paris, Mark
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
; FILE REFERENCE: 1843.0230001
; CURRENT APPLICATION NUMBER: US/11/024,251
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: 60/533,241
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 35
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: IgG Secreted Constant Domain
US-11-024-251-35

Query Match 99.5%; Score 1756; DB 7; Length 335;
Best Local Similarity 99.4%; Pred. No. 8.8e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 6 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 65
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 66 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 125
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Db 126 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 185
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 186 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 245
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 305
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 306 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 335

RESULT 17
US-11-172-320-6
; Sequence 6, Application US/111172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
US-11-172-320-6

Query Match 99.5%; Score 1756; DB 7; Length 335;
Best Local Similarity 99.4%; Pred. No. 8.8e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 6 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 65
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 66 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 125
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 180
Db 126 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDVEKKNVYDGVGVNNAKTKPREQYN 185
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 186 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 245
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 305
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 306 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 335
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; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

Query Match          99.5%; Score 1756; DB 7; Length 444;
Best Local Similarity 99.4%; Pred. No. 1.2e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 115 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 174

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 175 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG 234

QY 121 PSVFLFPPPKPDTLISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 235 PSVFLFPPPKPDTLISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 294

QY 181 STYRVVSVLTVQLHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 295 STYRVVSVLTVQLHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 354

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 414

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 415 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 444
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GenCore version 5.1.6  
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OM nucleic - protein search using frame\_plus\_n2p model

Run on: January 28, 2006, 08:12:21 ; Search time 154.595 Seconds  
(without alignments)  
5627.428 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797

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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGEOBURY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	98.2	333	8	Adj95914 Human Igg
2	1765	98.2	333	8	Adq89336 Human Imm
3	1765	98.2	333	9	Aeb09609 Human Igg
4	1765	98.2	356	8	Adj95974 Immunoglo
5	1765	98.2	444	3	Aay32263 Humanised
6	1765	98.2	448	8	Adp88447 Antibody
7	1765	98.2	448	8	Adp88431 Antibody
8	1765	98.2	467	6	Ada47334 TRX1 heav
9	1765	98.2	467	6	Ada47336 TRX1 heav

10	1765	98.2	467	8	ADP88446	Adp88446 Antibody
11	1765	98.2	467	8	ADP88430	Adp88430 Antibody
12	1765	98.2	467	8	ADQ87966	Adq87966 Heavy cha
13	1765	98.2	467	8	ADQ87974	Adq87974 Heavy cha
14	1765	98.2	473	5	ABG70743	Abg70743 Mouse/hum
15	1765	98.2	475	8	ADL23051	Adl23051 Mouse/hum
16	1765	98.2	475	8	ADL23054	Adl23054 Humanised
17	1765	98.2	475	8	ADS88803	Ads88803 Humanised
18	1765	98.2	475	8	ADS88792	Ads88792 A mouse/h
19	1760	97.9	330	8	ADQ89332	Adq89332 Human Imm
20	1760	97.9	330	9	AEB09605	Aeb09605 Human Igg
21	1760	97.9	462	9	AEB08800	Aeb08800 Anti-NOGO
22	1758	97.8	469	7	ADL23199	Adl23199 Human ant
23	1756	97.7	332	8	ADL35095	Adl35095 Human Igg
24	1756	97.7	332	9	ADM07455	Adm07455 Human Igg
25	1756	97.7	333	8	ADJ95912	Adj95912 Human Igg
26	1756	97.7	333	8	ADL22761	Adl22761 Human ant
27	1756	97.7	335	9	AEC22665	Aec22665 Secreted
28	1756	97.7	351	2	AAR43685	Aar43685 Human Kap
29	1756	97.7	356	8	ADJ95976	Adj95976 Immunoglo
30	1756	97.7	371	1	AAP91918	Aap91918 Sequence
31	1756	97.7	444	6	AAE35327	Aae35327 Humanised
32	1756	97.7	444	6	AAE34876	Aae34876 BIWA4/8 a
33	1756	97.7	444	8	ADL15443	Adl15443 Humanised
34	1756	97.7	444	8	ADO0851	Ado0851 Humanised
35	1756	97.7	444	9	AEB29789	Aeb29789 Humanized
36	1756	97.7	444	9	AEB29780	Aeb29780 Humanized
37	1756	97.7	445	6	AAO31101	Aao31101 Human A2-
38	1756	97.7	445	7	ADP11421	Adp11421 2B11 anti
39	1756	97.7	445	7	ADP11429	Adp11429 18B2 anti
40	1756	97.7	445	9	ADY74778	Ady74778 Rat anti-
41	1756	97.7	447	2	AAV31669	Aav31669 Human Igg
42	1756	97.7	447	8	ADQ31274	Adq31274 Humanised
43	1756	97.7	447	8	ADQ31271	Adq31271 Murine 11
44	1756	97.7	447	8	ADQ31276	Adq31276 Humanised
45	1756	97.7	447	8	ADS87928	Ads87928 Anti-IFN-

ALIGNMENTS

RESULT 1

ADJ95914

ID ADJ95914 standard; protein; 333 AA.

XX AC ADJ95914;

XX AC ADJ95914;

DT 06-MAY-2004 (first entry)

XX DB Human Igg heavy chain constant region FCRmut.

XX DB Human Igg heavy chain constant region FCRmut.

XX KW cytostatic; antibody therapy; immunoglobulin cassette construct;

XX KW immunoglobulin leader molecule; immunoglobulin domain;

XX KW immunoglobulin therapeutic molecule; monoclonal antibody; cancer; immunoglobulin G;

XX KW Igg; heavy chain constant region; FCRmut; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN US2004033561-A1.

XX PD 19-FEB-2004.

XX PF 17-OCT-2002; 2002US-00272899.

XX PR 19-OCT-2001; 2001US-0350166P.

XX PR 26-JUN-2002; 2002US-0392364P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI O'keefe TL, Heasley JJ, Newman W, Ponath PD, Keyt BA;

XX WPI; 2004-180050/17.

XX DR N-PSDE; ADJ95913.

XX New isolated nucleic acid molecules having an immunoglobulin cassette  
PT construct, useful for producing immunoglobulin therapeutic molecules  
PT termed monobodies, used as a therapeutic group in cancer disorders.

XX Example 2; SEQ ID NO 10; 84pp; English.

XX The invention describes an isolated nucleic acid molecule comprising an  
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette  
CC comprises an immunoglobulin leader molecule operably linked to a stable  
CC immunoglobulin domain region. The methods and compositions of the present  
CC invention are useful for producing immunoglobulins, in particular  
CC immunoglobulin therapeutic molecules termed monobodies, used as a  
CC therapeutic group in cancer disorders. This is the amino acid sequence of  
CC the human immunoglobulin G (IgG) heavy chain constant region mutant  
CC FCKmut used in the creation of immunoglobulin DNA cassette constructs.

XX SQ Sequence 333 AA;

Alignment Scores:  
Pred. No.: 5.89e-113 Length: 333  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADJ95914 (1-333)

QY 1 GCCTCCACCAAGGCGCCATCGTCTTCCCTCGCACCTCTCCCAAGAGCACCTCTGGG 60  
DB 4 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23  
QY 61 GGCAACAGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTG 120  
DB 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43  
QY 121 TGGAACTCAGCGCGCTGACGAGCGGGGTGACACCTTCCCGGTGCTCTACAGTCTCA 180  
DB 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 63  
QY 181 GGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCGCACCTCTGGGCGACCCAGCC 240  
DB 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83  
QY 241 TACATCTGCAACGTGAATCAACAGCCGACCAACCAAGGTGGACAAGAAGTTGAGCCC 300  
DB 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 103  
QY 301 AAATCTTGTGACAAACTCAACATGCCACCGTCCCGACCTGAACTCGCGGGGCA 360  
DB 104 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 123  
QY 361 CCGTCAGTCTTCTCTTCCCGCAACCAAGGACACCTCTCATGATCTCCCGGACCCCT 420  
DB 124 ProSerValPheLeuPheProProLysPheLysAspThrLeuMetIleSerArgThrPro 143  
QY 421 GAGGTCACTCGTGGTGGAGCGTGAAGCCAGCAACCTGAGGTCAAGTTCACCTGG 480  
DB 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 163  
QY 481 TAGCTGACCGCGTGGAGGTGCATAATGCCAGACAAAGCCGCGGAGGAGCAGTACAC 540  
DB 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluInTrpAsn 183  
QY 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
DB 184 SerThrTyrArgValValSerValValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 203  
QY 601 GAGTACAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660  
DB 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 223

QY 661 AAGCCAAAGGCGAGCCCGAGACACAGCTGTACACCTGCGCCCATCCCGGATGAG 720  
DB 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerArgAspGlu 243  
QY 721 CTGACCAAGAACAGGTCAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780  
DB 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263  
QY 781 GCCCTGAGTGGAGAGCAATGGGAGCCCGAGAACAACTACAGACACGCTCCCGTG 840  
DB 264 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProVal 283  
QY 841 CTGACTCCCGAGCGCTCTTCTCTCTACAGCAAGCTCACCTGGACAGACGAGTGG 900  
DB 284 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303  
QY 901 CAGCAGGGGAACTCTTCTCATGCTCGTGCATGATGAGGCTTGCAACACCTACACG 960  
DB 304 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 323  
QY 961 CAGAAGAGCTCTCCCTGCTCCCGGTAAA 990  
DB 324 GlnLysSerLeuSerLeuSerProGlyLys 333  
RESULT 2  
ADQ89336  
ID ADQ89336 standard; protein; 333 AA.  
XX AC ADQ89336;  
XX DT 21-OCT-2004 (first entry)  
XX DE Human immunoglobulin protein #46.  
XX KW Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;  
KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX OS Homo sapiens.  
XX PN US2004151721-A1.  
XX PD 05-AUG-2004.  
XX PF 10-DEC-2003; 2003US-00733563.  
XX PR 19-OCT-2001; 2001US-0350166P.  
XX PR 26-JUN-2002; 2002US-0392364P.  
XX PR 17-OCT-2002; 2002US-00272899.  
XX PA (OKEE/) O'KEEFE T.  
XX PA (PONA/) PONATH P.  
XX PI O'keefe T, Ponath P;  
XX DR WPI; 2004-580175/56.  
XX PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX PS Disclosure; SEQ ID NO 114; 128pp; English.  
XX CC The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV

CC infection and atherosclerosis. This sequence represents a human  
XX immunoglobulin protein of the invention.

SQ Sequence 333 AA;

Alignment Scores:

Pred. No.: 5,89e-113 Length: 333  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADQ89336 (1-333)

QY 1 GCCTCCACCAAGGCGCCATCGTCTTCCCTCCCTGGCAGCCCTCTCTCCAGAGCACCTCTCTGGG 60  
DB 4 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23  
QY 61 GGCACAGCGCGCTGGCTGGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTGTGC 120  
DB 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43  
QY 121 TGGAACTCAGCGCCCTCAGCAGCGCGGTGACACCTTCCCGGTGCTCTACAGTCTCA 180  
DB 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 63  
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGCGCACCCAGACC 240  
DB 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83  
QY 241 TACATCTGCAAGTGAATCAAGCCCGAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300  
DB 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 103  
QY 301 AAATCTTGTGCAAAACTCACACATGCCACCGTCCCGACCTGAACCTCGCGGGGCA 360  
DB 104 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 123  
QY 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
DB 124 ProSerValPheLeuPheProProlysProLysAspThrLeuMetIleSerArgThrPro 143  
QY 421 GAGTCAATCGTGGTGGAGCTGAGCCACGAGACCTCGAGGTCAAGTTCACATCGG 480  
DB 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 163  
QY 481 TACGTGACGCGGTGGAGTGCATAATCCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540  
DB 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 183  
QY 541 AGCAGTACCGTGGTGGAGTCTCTACCGTCTCTGACACAGGACTGGCTCAATGGCAAG 600  
DB 184 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 203  
QY 601 GAGTCAAGTCAAGGTCTCAACAAAGCCCTCCAGCGCCCATCGAGAAACCATCTCC 660  
DB 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 223  
QY 661 AAAGCCAAGGCGCCCGAGAACCAAGTGTACACCTGCCCCCTCCCGGATGAG 720  
DB 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 243  
QY 721 CTGACCAAGAACCAAGTTCAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATC 780  
DB 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263  
QY 781 GCCGTGAGTGGGAGCAATGGGAGCGCGAGAACCACTACAAGACCAACCCCTCCCGT 840  
DB 264 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 283  
QY 841 CTGACCTCCGACGGTCTCTTCTCTTACAGCAAGTTCACCGTGGACAGAGCGGTGG 900

Db 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303  
QY 901 CAGCAGGCGGAACGTCTTCTCATGCTCCGTCATGATGATGAGGCTCTGCACAACCACTACACG 960  
DB 304 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 323  
QY 961 CAGAAGACCTCTCCCTGCTCTCCCGGTAA 990  
DB 324 GlnLysSerLeuSerLeuSerProGlyLys 333

RESULT 3

AEBO9609

ID ABB09609 standard; protein; 333 AA.

XX AEB09609;

AC 08-SEP-2005 (first entry)

DT 08-SEP-2005 (first entry)

XX Human IgG1 constant region FcRmut SEQ ID NO 114.

DE antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;

XX antibody engineering; therapeutic; diagnosis; inflammation;

KW autoimmune diseases; immune disorder; graft rejection; HIV infection;

KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;

KW light chain constant region.

OS Homo sapiens.

XX WO2005060368-A2.

PN 07-JUL-2005.

XX 10-DEC-2003; 2003WO-US039599.

PF 10-DEC-2003; 2003WO-US039599.

PR (MILL-) MILLENNIUM PHARM INC.

PA Okeefe T, Ponath P;

PI WPI; 2005-488561/49.

XX N-PSDB; AEB09610.

DR New humanized immunoglobulin or its antigen binding portion having

XX binding specificity for CC-chemokine receptor 2 and having a heavy chain

PT and light chain, for treating inflammatory diseases, HIV, and autoimmune

PT diseases.

XX Disclosure; SEQ ID NO 114; 192pp; English.

XX The invention describes a humanized immunoglobulin (I) or its antigen

CC binding portion having binding specificity for CC-chemokine receptor 2

CC (CCR2) and having a heavy chain and a light chain, where the heavy chain

CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)

CC sequence, given in specification or its portion, and the light chain

CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given

CC in specification. Also described are: a humanized immunoglobulin heavy

CC chain, or its antigen binding fragment, having binding specificity for

CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the

CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized

CC immunoglobulin light chain, or its antigen binding fragment, having

CC binding specificity for CCR2 and comprising the amino acid sequence of

CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)

CC sequence, given in specification. The following are disclosed: isolated

CC nucleic acid molecules comprising nucleic acid sequence encoding (i); a

CC construct comprising nucleic acid molecule encoding (i); and host cell

CC comprising the nucleic acid molecule. (i) Is useful as a therapeutic

CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus

CC reducing inflammatory response, for use in the treatment of diseases

CC associated with leukocyte infiltration of tissue, e.g. in the treatment

CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV

CC infection and monocyte-mediated disorders such as atherosclerosis. (i) Is

CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.

CC

CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
CC fluid), and for modulating binding function and/or leukocyte trafficking  
CC modulated by CCR2. This is the amino acid sequence of human I9G1 constant  
CC region FcRmut used in the creation of a humanized anti-CCR2-antibody.  
XX  
SQ Sequence 333 AA;

Alignment Scores:  
Pred. No.: 5.89e-113 Length: 333  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 9 Gaps: 0

US-10-733-563-111 (1-990) x ABB09609 (1-333)

Qy 1 GCCTCCACCAAGGCGCCATCGTCTTCCCTGGCAGCCCTCTCCACAGACACCTCTGGG 60  
Db 4 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23  
Qy 61 GGCAAGCGGCGCTGGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGCTGTCG 120  
Db 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43  
Qy 121 TGGAACTCAGGCGCTGACAGCGGCGTGACACCTTCCCGGCTGCTCAAGTCTCA 180  
Db 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 63  
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGTGACCTGCGCTCCAGCAGCTGGGCGACCCAGCC 240  
Db 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83  
Qy 241 TACATCTGCAACGTGAATCACAGCCCAAGCCAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300  
Db 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 103  
Qy 301 AAATCTGTGCAAAATCACACATGCCACCGTGGCCAGCACCTGAACCTCGCGGGGCA 360  
Db 104 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 123  
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
Db 124 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 143  
Qy 421 GAGTCTCATCGTGGTGGAGCTGAGCCACGACCAAGACCTTGAGGTCAAGTTCAACTGG 480  
Db 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 163  
Qy 481 TACGTGACGCGGTGGAGTGCATATGCGCAAGCAAAAGCCGCGGAGGACGAGTACAC 540  
Db 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 183  
Qy 541 AGCAGTACCGTGTGGTGGAGTCTCTACCGTCTCGCACAGGACTGTGCTAAATGGCAAG 600  
Db 184 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 203  
Qy 601 GAGTACAAGTGCAGGTTCTCAACAAAGCCCTCCAGCCGCCATCGAGAAACCATCTCC 660  
Db 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 223  
Qy 661 AAAGCCAAAGGCGGCGCCGAGACCAACGAGTGTACACCTGCGCCCTCCCGGAGTAG 720  
Db 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 243  
Qy 721 CTGACCAAGAACACGAGTGCAGCTGACCTGCTGTCAAGAGTCTTATCCAGGACATC 780  
Db 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263  
Qy 781 GCCGTGAGTGGGAGAGCAATGGCGAGCGGAGAACACTACAAGACCAAGCCCTCCCGTG 840  
Db 264 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAentyrLysThrThrProProVal 283

Qy 841 CTGACCTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCCTGGGACAGAGCAGGTGG 900  
Db 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303  
Qy 901 CAGCAGGGGAACGTCTTCTCATGCTCGTGATGATGATGATGATGATGATGATGATGAT 960  
Db 304 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 323  
Qy 961 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990  
Db 324 GlnLysSerLeuSerLeuSerProGlyLys 333  
RESULT 4  
ADJ95974  
ID ADJ95974 standard; protein; 356 AA.  
XX  
AC ADJ95974;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DB Immunoglobulin DNA cassette polypeptide seqid 70.  
XX  
KW cytostatic; antibody therapy; immunoglobulin cassette construct;  
KW immunoglobulin leader molecule; immunoglobulin domain;  
KW immunoglobulin therapeutic molecule; monobody; cancer.  
OS Synthetic.  
XX  
FN US2004033561-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 17-OCT-2002; 2002US-00272899.  
XX  
PR 19-OCT-2001; 2001US-0350166P.  
PR 26-JUN-2002; 2002US-0392364P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA,  
XX  
XX WPI: 2004-180050/17.  
DR N-PSDB; ADJ95973.  
XX  
PT New isolated nucleic acid molecules having an immunoglobulin cassette  
PT construct, useful for producing immunoglobulin therapeutic molecules  
PT termed monobodies, used as a therapeutic group in cancer disorders.  
XX  
PS Disclosure; SEQ ID NO 70; 84pp; English.  
XX  
CC The invention describes an isolated nucleic acid molecule comprising an  
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette  
CC comprises an immunoglobulin leader molecule operably linked to a stable  
CC immunoglobulin domain region. The methods and compositions of the present  
CC invention are useful for producing immunoglobulins, in particular  
CC immunoglobulin therapeutic molecules termed monobodies, used as a  
CC therapeutic group in cancer disorders. This is the amino acid sequence of  
XX an immunoglobulin DNA cassette construct.  
SQ Sequence 356 AA;

Alignment Scores:  
Pred. No.: 5.96e-113 Length: 356  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADJ95974 (1-356)

Qy 1 GCCTCCACCAAGGCGCCATCGTCTTCCCTGGCAGCCCTCTCCACAGACACCTCTGGG 60  
|||||



Db 27 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 46  
Qy 61 GGCACAGCGCGCTGCTGCTGCTCAAGAGTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 47 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 66  
Qy 121 TGGAACTCAGCGCGCTGACAGCGGGGTGCACACTTCCCGGTGCTTACAGTCTCA 180  
Db 67 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 86  
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGTCAGCTGCTCCCTCCAGCAGCTGGGACCCAGCC 240  
Db 87 GlyLeuTyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThr 106  
Qy 241 TACATCTGCAAGCTGAATCAACAAGCCCAAGCAACCAAGGTGGACAAAGTTGAGCCC 300  
Db 107 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 126  
Qy 301 AAATCTTGTCACAAACTCACATGCCCCACCGTGCAGCACCTGAATCCGCGGGGCA 360  
Db 127 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 146  
Qy 361 CCGTCAGTCTCTCTTCCCTCCCAACCAAGCAAGCACCTCATGATCTCCCGACCCCT 420  
Db 147 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 166  
Qy 421 GAGGTCAATCGTGGTGGAGCTGAGCCCAAGCAAGCACCTGAGGTCAAGTTCACATGG 480  
Db 167 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 186  
Qy 481 TACGTGACCGCGTGGAGGTGCATATATGCCAAGCAAAAGCCGCGGAGGACGACTACAAC 540  
Db 187 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 206  
Qy 541 AGCAGTACCGTGGTGGTGGAGCTCTCACCGTCTGACACAGGACTGGTGAATGGCAAG 600  
Db 207 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 226  
Qy 601 GAGTACAGTGAAGTGTCTCAACAAGAGCCCTCCAGCCGCCCATCGAGAAACCATCTCC 660  
Db 227 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 246  
Qy 661 AAAGCCAAAGCGACCGCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGATGAG 720  
Db 247 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 266  
Qy 721 CTGACCAAGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 780  
Db 267 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 286  
Qy 781 GCCGTGAGTGGGAGAGCAATGGGCGAGCGAGAACCAACTACAAGACCGCCCTCCCGTG 840  
Db 287 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 306  
Qy 841 CTGACCTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGACAAGCAGGTGG 900  
Db 307 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 326  
Qy 901 CAGCAGGGGAACGTCTTCTATGCTCCGTGTATGATGATGATGATGATGATGATGATGAT 960  
Db 327 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 346  
Qy 961 CAGAAGAGCTCTCCCTGCTCCCGGTAAA 990  
Db 347 GlnLysSerLeuSerLeuSerProGlyLys 356

RESULT 5  
AAV32263  
ID AAV32263 standard; protein; 444 AA.  
XX  
AC AAV32263;  
XX  
DT 15-FEB-2000 (first entry)

XX DE Humanised anti-CD23 MAB C11 heavy chain.  
XX KW CD23; FCRII; IgG receptor; monoclonal antibody; C11; mouse; human;  
KW monoclinal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;  
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
therapy.  
XX OS Homo sapiens.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Region 1..30  
FT /note= "framework region 1"  
FT Region 31..35  
FT /note= "CDR 1"  
FT Region 36..49  
FT /note= "framework region 2"  
FT Region 50..68  
FT /note= "CDR 2"  
FT Region 69..100  
FT /note= "framework region 3"  
FT Region 101..103  
FT /note= "CDR 3"  
FT Region 104..111  
FT /note= "framework region 4"  
FT Region 112..444  
FT /note= "constant region"  
XX MO9958679-A1.  
FN 18-NOV-1999.  
XX PD 07-MAY-1999; 99WO-GB001434.  
XX PP 09-MAY-1998; 98GB-00009839.  
XX PR (GLAX ) GLAXO GROUP LTD.  
XX PA Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
PI WPI; 2000-053101/04.  
XX DR N-PSDB; AA234748.  
XX PS Cell receptor specific antibodies useful for treating e.g. arthritis,  
diabetes, multiple sclerosis and psoriasis.  
XX Claim 9; Fig 4; 81pp; English.  
XX This amino acid sequence represents the heavy chain of humanised anti-  
CD23 (FCRII) monoclonal antibody C11, composed of a human framework  
(H5IGKV1) and the heavy chain complementarity determining regions (see  
AAV32257-59) of murine antibody C11. The DNA was constructed by splice  
overlap PCR. The invention provides altered antibodies, such as chimeric  
or humanised antibodies, which comprise sufficient of the amino acid  
sequences of the C11 light and heavy chain complementarity determining  
regions to render them capable of binding to the CD23 type II molecule  
expressed on haematopoietic cells. The antibodies are used to block  
soluble CD23 formation in human therapy, for the treatment of arthritis,  
lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,  
glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
malignancies (claimed). They are also useful for studying interactions

CC between CD23 and various ligands and determining the binding agents

XX Sequence 444 AA;

Alignment Scores:  
Pred. No.: 6.19e-113 Length: 444  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-111 (1-990) x AAV32263 (1-444)

```
Qy 1 GCCTCCACCAAGGCGCCATCGCTCTCCCTCGGACCCCTCTCCACAGAGCACCTCTGGG 60
Db 115 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 134
Qy 61 GGACAGCGCCCTGGCTGCTCGTCAAGGACTACTTCCCGAACCCTGACGGTGCCTG 120
Db 135 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 154
Qy 121 TGGAACTCAGCGCCCTGACACAGCGGGGTGCACACTTCCCGGTGCTCTACAGTCTCA 180
Db 155 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 174
Qy 181 GGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCCAGCAGCTGGGACCCAGCAC 240
Db 175 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 194
Qy 241 TACATCTGCACGTAATCAACAGCCAGCAACCAAGTGGGACAGAGTTGAGCCC 300
Db 195 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 214
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
Db 215 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 234
Qy 361 CCGTCAGTCTTCTTCTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGACCCCT 420
Db 235 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 254
Qy 421 GAGTCACTGCGTGGTGGAGTGGAGTGGCCAGCAAGCCCTGAGTCAAGTTCAGTGG 480
Db 255 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 274
Qy 481 TACGTGACGCGGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAC 540
Db 275 TyrValAspGlyValGluValHisAsnAlaLysThrLysProAspGluGluGlnTyrAsn 294
Qy 541 AGCAGGTACCGTGTGGTCAAGCTCTCAGCTCTGTGACACAGGACTGGCTGAATGGCAAG 600
Db 295 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 314
Qy 601 GAGTACAAAGTCAAGGTCTCAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCATCC 660
Db 315 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 334
Qy 661 AAAGCCAAAGGCGCCGAGAACCAACAGGTGTACACCCCTGCGCCCTCCAGGAGTGG 720
Db 335 LysAlaLysGlyGlnProAspGluProGlnValTyrThrLeuProProSerArgAspGlu 354
Qy 721 CTGACCAAGAACCAAGTCAAGCTGCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780
Db 355 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 374
Qy 781 GCCTGTGAGTGGGAGAGCAATGGCAGCCGAGAACCAACTACAGACCAAGCCCTCCGCTG 840
Db 375 AlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProProVal 394
Qy 841 CTGACTCCGACGGCTCTCTTCTCTCTTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGG 900
Db 395 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 414
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Qy 901 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACAG 960
Db 415 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 434
Qy 961 CAGAGAGGCTCTCCCTGCTCTCCGGGTAAA 990
Db 435 GlnLysSerLeuSerLeuSerProGlyLys 444
```

RESULT 6

ADP88447

ID ADP88447 standard; protein; 448 AA.

XX AC ADP88447;

XX DT 09-SEP-2004 (first entry)

XX DE Antibody TRX1 heavy chain SEQ ID NO: 24.

XX KW immunosuppressive; transplant rejection; antigen tolerance; antibody;

XX OS Unidentified.

XX PN W02004052398-A1.

XX PD 24-JUN-2004.

XX PF 09-DEC-2003; 2003WO-US039165.

XX PR 09-DEC-2002; 2002US-0431839P.

XX PA (TOLE-) TOLERRX INC.

XX PI Windsor-Hines D, Rao P, Ringler DJ;

XX DR WPI; 2004-468712/44.

XX PT Treating a primate to induce tolerance to at least one antigen comprises administering at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits CD8+ T cells.

XX PS Disclosure; SEQ ID NO 24; 113pp; English.

XX CC The present invention relates to a process of treating a primate to induce tolerance to at least one antigen, which comprises administering to the primate at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits CD8+ T cells, where the anti-CD4 antibody or its fragment is present in the primate when the antigen is present in the primate. The method is useful in treating a primate to induce tolerance to at least one foreign antigen to prevent transplant rejection. The present sequence is an antibody fragment used in the exemplification of the invention.

XX SQ Sequence 448 AA;

Alignment Scores:

Pred. No.: 6.2e-113 Length: 448  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADP88447 (1-448)

Qy 1 GCCTCCACCAAGGCGCCATCGCTCTCCCTCGGACCCCTCTCCAGAGCACCTCTGGG 60

Db 119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138

Qy 61 GGACAGCGCCCTGGGCTGCTCGTCAAGGACTACTTCCCGAACCCTGAGTGGTGGTCTCG 120

Db 139 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158  
Qy 121 TGGAACTCAGGCGCCTGACAGCGCGGTGACACCTTCCCGGTGCTCTACAGTCCTCA 180  
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178  
Qy 181 GGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198  
Qy 241 TACATCTGCAAGCTCAATCACAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300  
Db 199 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218  
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCAGCAGCAGCAGCAGCAG 360  
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238  
Qy 361 CGTCAGTCTTCTTCCCTCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420  
Db 239 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 258  
Qy 421 GAGTTCACATCGTGTGCTGAGCGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 480  
Db 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278  
Qy 481 TACGTGAGCGCGTGGAGGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540  
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 298  
Qy 541 AGCAGTACCGTGTGCTCAGCGTCTCCACCGTCTGACAGGACTGCTGAATGGCAAG 600  
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318  
Qy 601 GAGTACAGTCCAGGTCTCCACAAAGCCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660  
Db 319 GluTyrLysCysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 338  
Qy 661 AAAGCAAAGCGCAGCGCCGAGAACACAGGTGTACACCTGCCCGCCATCCCGGATCAG 720  
Db 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358  
Qy 721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378  
Qy 781 GCCGTGGAGTGGGAGCAATGGCGAGCGGAGGAGCACTACAGACCAAGCAGCAGCAGC 840  
Db 379 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398  
Qy 841 CTGGACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGAAGCAGGAGTGG 900  
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418  
Qy 901 CAGCAGGGGAAGCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCAACCACTTACACG 960  
Db 419 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 438  
Qy 961 CAGAGAGCCCTCCTCTCTCCGGTAAA 990  
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448

## RESULT 7

ADP88431

ID ADP88431 standard; protein; 448 AA.

XX AC ADP88431;

XX DT 09-SEP-2004 (first entry)

XX DE Antibody TRX1 heavy chain SEQ ID NO: 8.

XX KW immunosuppressive; transplant rejection; antigen tolerance; antibody;

KW TRX1.  
XX Unidentified.  
XX WO2004052398-A1.  
XX 24-JUN-2004.  
XX 09-DEC-2003; 2003WO-US039165.  
XX 09-DEC-2002; 2002US-0431839P.  
XX (TOLLE-) TOLERRX INC.  
XX Windsor-Hines D, Rao P, Ringler DJ;  
XX WPI; 2004-468712/44.  
XX Treating a primate to induce tolerance to at least one antigen comprises administering at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits CD8+ T cells.  
XX Disclosure; SEQ ID NO 8; 113pp; English.  
XX The present invention relates to a process of treating a primate to induce tolerance to at least one antigen, which comprises administering to the primate at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits CD8+ T cells, where the anti-CD4 antibody or its fragment is present in the primate when the antigen is present in the primate. The method is useful in treating a primate to induce tolerance to at least one foreign antigen to prevent transplant rejection. The present sequence is an antibody fragment used in the exemplification of the invention.  
XX SQ Sequence 448 AA;  
Alignment Scores:  
Pred. No.: 6,2e-113 Length: 448  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0  
US-10-733-563-111 (1-990) x ADP88431 (1-448)  
Qy 1 GCCTCCACCAAGGCGCCATCGTCTTCCCTGGCACCTCTCTCAAGAGACCTCTGGG 60  
Db 119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138  
Qy 61 GGCACAGGCGCCCTGGCTGCTGCTCAGAGACTACTTCCCGAACCGGTGACGGTGTGG 120  
Db 139 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158  
Qy 121 TGGAACTCAGGCGCCTGACAGCGCGGTGACACCTTCCCGGTGCTCTACAGTCCTCA 180  
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178  
Qy 181 GGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198  
Qy 241 TACATCTGCAAGCTCAATCACAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300  
Db 199 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218  
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCAGCAGCAGCAGCAGCAG 360  
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238  
Qy 361 CGTCAGTCTTCTTCCCTCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420

Db 239 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 258  
 Qy 421 GAGGTCAATCGTGGTGGTGGAGCGTGGAGCCACGACGACCTGAGTCAAGTTCACCTGG 480  
 Db 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278  
 Qy 481 TACGTGACGCGGTGGAGTGCATTAATGCCAAGACAAAGCCGCGGAGGACGAGTACAAAC 540  
 Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 298  
 Qy 541 AGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
 Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318  
 Qy 601 GAGTACAGTGCAGGTCTCAACAAAGCCCTCCAGCCGCCATCGAGAAACCATCTCC 660  
 Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 338  
 Qy 661 AAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTACACCTCCCTCCATCCCGGGATGAG 720  
 Db 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358  
 Qy 721 CTGACCAAGAACGAGTGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378  
 Qy 781 GCCGTGAGTGGAGAGCAATGGGAGCGCGAGAGCAACTACAGACCAACGCTCCCGTG 840  
 Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398  
 Qy 841 CTGACTCCGACGCT 900  
 Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysArgTrp 418  
 Qy 901 CAGCAGGGAGACGCTTCT 960  
 Db 419 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438  
 Qy 961 CAGAAGACCT 990  
 Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448  
 RESULT 8  
 ID ADA47334 standard; protein; 467 AA.  
 AC ADA47334;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE TRX1 heavy chain encoding DNA #SEQ ID 7.  
 XX  
 KW Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;  
 KW graft rejection; autoimmune disease; humanised.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2002102853-A2.  
 XX  
 PD 27-DEC-2002.  
 XX  
 PF 14-JUN-2002; 2002WO-GB002796.  
 XX  
 PR 14-JUN-2001; 2001GB-00014517.  
 PR 20-SEP-2001; 2001GB-00022724.  
 PR 19-OCT-2001; 2001US-0345194P.  
 PR 18-APR-2002; 2002US-0373470P.  
 PR 18-APR-2002; 2002US-0373471P.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
 PA (TOLE-) TOLERRX INC.  
 XX

PI Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;  
 PI Ringler D, Cobbold S, Winsor-Hines D;  
 DR WPI; 2003-175228/17.  
 DR N-PSDB; ADA47333.  
 XX  
 PT Treating a primate to induce tolerance to at least one antigen, useful  
 PT for inhibiting graft rejection or treating an autoimmune disease,  
 PT comprises administering a TRX1 antibody to reduce the amount of CD4+  
 PT CD25+ cells produced.  
 XX  
 PS Claim 26; Fig 1D; 131pp; English.  
 XX  
 CC The invention relates to a method for treating a primate to induce  
 CC tolerance to at least one antigen. The method of the invention comprises  
 CC administering at least one compound which when in a primary mixed  
 CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells  
 CC produced. The preferred compound is a humanised antibody or its fragment,  
 CC that does not bind to the FC receptor, and includes CDRs that are free of  
 CC a glycosylation site. The method of the invention is useful for inducing  
 CC tolerance to at least one antigen, specifically for inhibiting,  
 CC ameliorating or reducing an immune response to an antigen. The antibody  
 CC is useful for manufacturing a medicament for inducing tolerance to an  
 CC antigen (possibly in the form of a vaccine), for inhibiting an immune  
 CC response for inhibiting the rejection of a graft (such as an organ) in a  
 CC human patient, and for treating an autoimmune disease. The current  
 CC sequence represents the TRX1 heavy chain.  
 XX  
 SQ Sequence 467 AA;  
 Alignment Scores:  
 Pred. No.: 6,24e-113 Length: 467  
 Score: 1765.00 Matches: 330  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.22% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-733-563-111 (1-990) x ADA47334 (1-467)  
 Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCTGACCTCTCTCCAGAGCACCTCTGGG 60  
 Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 157  
 Qy 61 GGCACAGCGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177  
 Qy 121 TGGAACTCAGCGCGCTGACAGCGCGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA 180  
 Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
 Qy 181 GGACTCTACTCTCTCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240  
 Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217  
 Qy 241 TACATCTGCAACGTGAATCAAGCCCGACCAACACCAAGTGGACAAAGATTGAGCCC 300  
 Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
 Qy 301 AAATCTTGTGACAAACTCACATGCCCCACCGTCCGACACCTGACCTGCGGGGCGCA 360  
 Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
 Qy 361 CCGTCAGTCT 420  
 Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277  
 Qy 421 GAGTCAATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
 Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
 Qy 481 TACGTGACGCGGTGGAGTGCATTAATGCCAAGACAAAGCCGCGGAGGACGAGTACAAAC 540

Db	298	TyrValAspGlyValIguValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn	317
Qy	541	AGCAGCTACCGTGTGGTCAGCGCTCTCCACGCTCCCTGCACCGACTGGCTGAATGCGAAG	600
Db	318	SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	337
Qy	601	GAGTACAAAGTCAAGGTTCTCAACAAGACCCCTCCAGCGCCCTCCAGAGAAAACCATCTCC	660
Db	338	GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer	357
Qy	661	AAAGCCAAAGGCGCCCGAGMACCAGAGTGATACACCTGCCCCCATCCCGGATGAG	720
Db	358	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu	377
Qy	721	CTGACCAAGAACCGAGTCTGACCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGCACATC	780
Db	378	LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle	397
Qy	781	GCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAAACAATCAAGACACGCTCCCGTG	840
Db	398	AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal	417
Qy	841	CTGAGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGG	900
Db	418	LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp	437
Qy	901	CAGCAGGGGAACGCTCTCTCATGCTCCGCTGATGCATGAGGCTCTGCACACCACTACACG	960
Db	438	GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr	457
Qy	961	CAGAAGAGCCCTCTCCCTCTCTCCGGGTAAA	990
Db	458	GlnLysSerLeuSerLeuSerProGlyLys	467
RESULT 9			
ADA47336			
XX	ID	ADA47336 standard; protein; 467 AA.	
AC	ADA47336;		
XX	20-NOV-2003	(first entry)	
DT	TRX1 heavy chain #SEQ ID 9.		
XX	Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;		
KW	graft rejection; autoimmune disease; humanised.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
PH	Peptide	1..19	
FT		/label= leader peptide	
FT	Region	50..54	
FT		/label= CDR	
FT	Region	69..85	
FT		/label= CDR	
FT	Region	118..126	
FT		/label= CDR	
XX	WO2002102853-A2.		
XX	27-DEC-2002.		
XX	14-JUN-2002; 2002WO-GB002796.		
XX	14-JUN-2001; 2001GB-00014517.		
PR	20-SEP-2001; 2001GB-00022724.		
PR	19-OCT-2001; 2001US-0345194P.		
PR	18-APR-2002; 2002US-0373470P.		
PR	18-APR-2002; 2002US-0373471P.		
XX	(ISIS-) ISIS INNOVATION LTD.		
PA			

PA	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
PA	(TOLLE-) TOLLERX INC.
XX	
PI	Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;
PI	Ringler D, Cobbold S, Winsor-Hines D;
XX	
DR	WPI; 2003-175228/17.
XX	
PT	Treating a primate to induce tolerance to at least one antigen, useful
PT	for inhibiting graft rejection or treating an autoimmune disease,
PT	comprises administering a TRX1 antibody to reduce the amount of CD4+
PT	CD25+ cells produced.
XX	
CC	Claim 27; Fig 1F; 131pp; English.
XX	
CC	The invention relates to a method for treating a primate to induce
CC	tolerance to at least one antigen. The method of the invention comprises
CC	administering at least one compound which when in a primary mixed
CC	lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells
CC	produced. The preferred compound is a humanised antibody or its fragment,
CC	that does not bind to the PC receptor, and includes CDRs that are free of
CC	a glycosylation site. The method of the invention is useful for inducing
CC	tolerance to at least one antigen, specifically for inhibiting,
CC	ameliorating or reducing an immune response to an antigen. The antibody
CC	is useful for manufacturing a medicament for inducing tolerance to an
CC	antigen (possibly in the form of a vaccine), for inhibiting an immune
CC	response, for inhibiting the rejection of a graft (such as an organ) in a
CC	human patient, and for treating an autoimmune disease. The current
CC	sequence represents the TRX1 heavy chain amino acid sequence.
XX	
SQ	Sequence 467 AA;
Alignment Scores:	
Pred No.:	6,24e-113 Length: 467
Score:	1765.00 Matches: 330
Percent Similarity:	Conservative: 0
Best Local Similarity:	Mismatches: 0
Query Match:	Indels: 0
DB:	Gaps: 0
US-10-733-563-111 (1-990) x ADA47336 (1-467)	
Qy	1 GCCTCCACCAAGGCCCATCGGTCTTCCCCTGGCACCCCTCCTCCAAGACGACCTCTTGCG 60
Db	138 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
Qy	61 GGACAGGGCCCTGGGCTGCCTGGTCAGAGACTACTTCCCGGAACCGGTGACGGTGTCG 120
Db	158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
Qy	121 TGGAATCTCAGCGCCCTGACCAGCGGGGTGCACACTTCCCGGTGTCTCTACAGTCCCTCA 180
Db	178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
Qy	181 GGACTCTACTCCCTCAGCAGCGGTGGTGACCGGTGCCCTCCAGCAGCTTGGGCAACCCAGACC 240
Db	198 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
Qy	241 TAGATCTGCAACGTGAATCACAGCCGACCAACCAAGGTGGACAGAAAGTTGAGCC 300
Db	218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237
Qy	301 AATATTGTGAAAAATCACACATGCCACCGTSCCCAGACACCTGAACTCCGCGGGGCA 360
Db	238 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 257
Qy	361 CCGTCACTTCTCTTCTTCCCCCAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCT 420
Db	258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277
Qy	421 GAGTCCATCGCGTGGTGGTAGCGCCACGNAGACCCCTGAGGTCNAGTTCAACTGG 480
Db	278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297

QY 481 TACGTGACGCGGTGGAGTGCATTAATGCCAAGCAAGCCGCGGAGGACGACTACAC 540  
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317  
QY 541 AGCAGGTACCGTGTGGTGCAGCGTCTCACCGTCTCGACACGAGGACTGGCTGAATGGCAAG 600  
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337  
QY 601 GAGTACAAAGTGAAGGTCTCCAAACAAGCCCTCCACGCCCCCATCGAGAAAACCATCTCC 660  
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357  
QY 661 AAGCCAAAGGCGAGCCGAGACACACAGGTGTACACCTCGCCCTCCCGGATGAG 720  
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377  
QY 721 CTGACCAAGAACACGAGTGCAGCTGACCTGCTCGTCAAAAGGCTTCTATCCACGCGACATC 780  
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397  
QY 781 GCCGTGAGTGGGAGACAATGGGAGCGCGAGAACCACTACAAGACACGCTCCCGTG 840  
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProVal 417  
QY 841 CTGACCTCCGACGGCTCTCTCTCTCTACAGCAAGCTCACCGTGGACAGCAGGTGG 900  
Db 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437  
QY 901 CAGCAGGGGAACTGCTTCTCATGCTCCGTGATGATGATGATGATGATGATGATGATGAT 960  
Db 438 GlnGlnGlnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 457  
QY 961 CAGAAGAGCTCTCCCTGCTCTCCGGGTAAA 990  
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467  
RESULT 10  
ADP88446  
ID ADP88446 standard; protein; 467 AA.  
XX AC ADP88446;  
XX DT 09-SEP-2004 (first entry)  
XX DE Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 23.  
XX KW immunosuppressive; transplamt rejection; antigen tolerance; antibody;  
XX OS TRX1.  
XX OS Unidentified.  
XX PN WO2004052398-A1.  
XX PD 24-JUN-2004.  
XX PF 09-DEC-2003; 2003WO-US039165.  
XX PR 09-DEC-2002; 2002US-0431839P.  
XX PA (TOLE-) TOLERRX INC.  
XX PI Windsor-Hines D, Rao P, Ringler DJ;  
XX WPI; 2004-468712/44.  
DR N-PSDB; ADP88444, ADP88445.  
XX  
PT Treating a primate to induce tolerance to at least one antigen comprises  
PT administering at least one anti-CD4 antibody or its fragment in an  
PT initial dose of at least 40 mg/kg and at least one compound that inhibits  
PT CD8+ T cells.  
XX PS Disclosure; SEQ ID NO 23; 113pp; English.

XX CC The present invention relates to a process of treating a primate to  
CC induce tolerance to at least one antigen, which comprises administering  
CC to the primate at least one anti-CD4 antibody or its fragment in an  
CC initial dose of at least 40 mg/kg and at least one compound that inhibits  
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
CC the primate when the antigen is present in the primate. The method is  
CC useful in treating a primate to induce tolerance to at least one foreign  
CC antigen to prevent transplant rejection. The present sequence is an  
CC antibody fragment used in the exemplification of the invention.  
XX  
SQ Sequence 467 AA;  
Alignment Scores: 6.24e-113 Length: 467  
Pred. No.: 1765.00 Matches: 330  
Score: 100.00% Conservativeness: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 98.22% Indels: 0  
Query Match: 8 Gaps: 0  
DB:  
US-10-733-563-111 (1-990) x ADP88446 (1-467)  
QY 1 GCCTCCACCAAGGCGCCCATCGCTCTCCCTCGCACCTCTCTCCAAAGAGCACCTCTGGG 60  
Db 138 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157  
QY 61 GGCACAGCGCCCTGGGCTGCTGGTCAAGGACTTACTTCCCGCAACCGGTGACGCTGCG 120  
Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177  
QY 121 TGGNACTCAGCGCCCTGACGAGCGGCTGCACACCTTCCCGGCTGCTCTACAGTCTCA 180  
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
QY 181 GGACTCTACTCTCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGCGCACCCAGACC 240  
Db 198 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 217  
QY 241 TACATCTGCAACGTGAATCAAGCCAGCAACCAAGGTGGACAAGAAGTTGAGCC 300  
Db 218 TyrlleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
QY 301 AATCTTGTGACAAACTCACACATGCCACCGTGCACACCTGACCTGACCTCGGGGGCA 360  
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
QY 361 CCCTGAGTCT 420  
Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277  
QY 421 GAGTCAATCGCTGGTGGAGCTGAGCCAGCAAGACCTGAGGTCAAGTTCACTGCG 480  
Db 278 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
QY 481 TAGCTGACGCGCTGGAGGTGCATATGCCAAGCAAGCCGCGGAGGAGGAGGAGGAGGAG 540  
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317  
QY 541 AGCAGGTACCGTGTGGTGCAGCTCTCACCGTCTCTGACACGAGGACTGGCTGAATGGCAAG 600  
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337  
QY 601 GAGTCAAGTGAAGGTCTCCAAACAAGCCCTCCACGCCCCCATCGAGAAAACCATCTCC 660  
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357  
QY 661 AAGCCAAAGGCGAGCCGCGAGACACAGGTGTACACCTCGCCCTCCCGGATGAG 720  
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377  
QY 721 CTGACCAAGAACACGAGTGCAGCTGACCTGCTCGTCAAAAGGCTTCTATCCACGCGACATC 780

Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 397  
QY 781 GCCGTGGAGTGGAGCAATGGCGAGCGGAGCAACTACAGACACGCTCCCGTG 840  
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyLysThrProVal 417  
QY 841 CTGAGCTCGAGCGGCTCTTCTCTCTACAGCAAGCTCAGGTGGACAGAGCGTGG 900  
Db 418 LeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArgTrp 437  
QY 901 CAGCAGGGGAAGCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACG 960  
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyThr 457  
QY 961 CAGAAGAGCCTCTCCCTCTCCGCGTAA 990  
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 11  
ADP88430  
ID ADP88430 standard; protein; 467 AA.  
XX AC  
XX ADP88430;  
XX DT 09-SEP-2004 (first entry)  
XX DE Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 7.  
XX KW immunosuppressive; transplant rejection; antigen tolerance; antibody;  
XX KW TRX1.  
XX OS Unidentified.  
XX PN WO2004052398-A1.  
XX PD 24-JUN-2004.  
XX PF 09-DEC-2003; 2003WO-US039165.  
XX PR 09-DEC-2002; 2002US-0431839P.  
XX PA (TOLE-) TOLERRX INC.  
XX PI Windsor-Hines D, Rao P, Ringler DJ;  
XX DR WPI; 2004-468712/44.  
XX DR N-PSDB; ADP88429, ADP88428.  
XX FT Treating a primate to induce tolerance to at least one antigen comprises  
PT administering at least one anti-CD4 antibody or its fragment in an  
PT initial dose of at least 40 mg/kg and at least one compound that inhibits  
PT CD8+ T cells.  
XX PS Disclosure; SEQ ID NO 7; 113pp; English.  
XX CC The present invention relates to a process of treating a primate to  
CC induce tolerance to at least one antigen, which comprises administering  
CC to the primate at least one anti-CD4 antibody or its fragment in an  
CC initial dose of at least 40 mg/kg and at least one compound that inhibits  
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
CC the primate when the antigen is present in the primate. The method is  
CC useful in treating a primate to induce tolerance to at least one foreign  
CC antigen to prevent transplant rejection. The present sequence is an  
CC antibody fragment used in the exemplification of the invention.  
XX SQ Sequence 467 AA;

Alignment Scores:  
Pred. No.: 6.24e-113 Length: 467  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0

RESULT 12

DB: 8 Gaps: 0  
US-10-733-563-111 (1-990) x ADP88430 (1-467)  
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCGACCCCTCTCCAGAGCACCTCTGGG 60  
Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157  
QY 61 GGCACAGCGGCGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGGTGTCG 120  
Db 158 GlyThrAlaLeuLeuGlyCysLeuValLysAspTyPheProGluProValThrValSer 177  
QY 121 TGGAACTCAGCGCGCCCTGACCCAGCGGCGTGACACCTTCCCGGTCTCTACAGTCTCA 180  
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
QY 181 GGACTCTACTCCCTCAGCAGCGGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 198 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217  
QY 241 TACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGGTGGACAAAGAAAGTTGAGCCC 300  
Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
QY 301 AAATCTTGTGACAAACTCAACATGCCACCGTCCCGCAGCACCTGAACTCGCGGGGCA 360  
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
QY 361 CCGTCAGTCTCTCTTCCCCCCCCCAAGCAGACACCTCATGATCTCCCGGACCCCT 420  
Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277  
QY 421 GAGGTACATGCTGCTGGTGGAGCTGAGCCACCAAGACCTCTAGGTCAAGTTCAACTGG 480  
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
QY 481 TACGTGACGCGCTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAA 540  
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyraen 317  
QY 541 AGCAGTACCGTGGTGGAGCTCTCAACAAAGCCCTCCAGCCCCCATCGAGAACCATCTCC 600  
Db 318 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337  
QY 601 GAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAACCATCTCC 660  
Db 338 GluTyLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrLysSer 357  
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTCTGCCCGCCCATCCCGGATGAG 720  
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSerArgAspGlu 377  
QY 721 CTGACCAAGAACAGGTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780  
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 397  
QY 781 GCCGTGGAGTGGAGCAATGGCGAGCAACTACAGACACGCTCCCGTG 840  
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyLysThrProVal 417  
QY 841 CTGAGCTCGAGCGGCTCTTCTCTCTACAGCAAGCTCAGGTGGACAGAGCGTGG 900  
Db 418 LeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArgTrp 437  
QY 901 CAGCAGGGGAAGCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACG 960  
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyThr 457  
QY 961 CAGAAGAGCCTCTCCCTCTCCGCGTAA 990  
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467

ADQ87966  
 ID ADQ87966 standard; protein; 467 AA.  
 AC ADQ87966;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Heavy chain of a humanised TRX1 antibody #1.  
 XX  
 KW Primate; tolerance; antigen; mixed lymphocyte reaction; MLR; CD4+; CD25+;  
 KW IL-2; IL-4; IL-12; immune response; graft rejection; immunosuppressive;  
 KW antirheumatic; antiarthritic; antidiabetic; neuroprotective;  
 KW antiinflammatory; antiallergic; antidiabetic; cytoprotective;  
 KW transplant; graft-versus-host disease; autoimmune disease; inflammation;  
 KW allergy; asthma; cancer; infection; humanised; TRX1; heavy.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Leader peptide  
 FT Region 20..49  
 FT /label= Framework region 1  
 FT Region 50..54  
 FT /label= Complementarity determining region 1  
 FT Region 55..68  
 FT /label= Framework region 2  
 FT Region 69..85  
 FT /label= Complementarity determining region 2  
 FT Region 86..117  
 FT /label= Framework region 3  
 FT Region 118..126  
 FT /label= Complementarity determining region 3  
 FT Region 127..137  
 FT /label= Framework region 4  
 FT Region 138..467  
 FT /label= Constant region  
 XX  
 PN WO2004067554-A2.  
 XX  
 PD 12-AUG-2004.  
 XX  
 PF 28-JAN-2004; 2004WO-US002643.  
 XX  
 PF 29-JAN-2003; 2003US-00353708.  
 XX  
 PR (TOLE-) TOLERRX INC.  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
 XX  
 PI Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;  
 PI Ringler D, Cobbold S, Winsor-Hines D;  
 XX  
 DR WPI; 2004-580970/56.  
 DR N-PSDB; ADQ87965.  
 XX  
 PT Inducing tolerance to an antigen comprises administering a CD4 antibody  
 PT alone or in combination with other compounds that induce tolerance  
 PT against one or more antigens.  
 XX  
 PS Claim 11; Fig 1D; 85pp; English.  
 XX  
 CC The invention relates to a novel method for treating a primate to induce  
 CC tolerance to at least one antigen. The method comprises administering a  
 CC compound, or a combination of compounds, that induces tolerance against  
 CC one or more antigens. The compound or the combination being in a primary  
 CC mixed lymphocyte reaction (MLR) in vitro, which reduces the amount of  
 CC CD4+ CD25+ cells produced in the mixed lymphocyte reaction and that  
 CC generates in the primary mixed lymphocyte reaction a cell population that  
 CC reduces at least one of the amount of CD4+ CD25+ cells produced in vitro  
 CC in at least one of a primary and secondary mixed lymphocyte reactions,  
 CC and the amount of at least one of IL-2, IL-4 and IL-12 in a secondary  
 CC mixed lymphocyte reaction. The compound or the combination being

CC administered in an amount and for a time so as to induce tolerance  
 CC against the antigen, the compound or the combination being present in the  
 CC primate when the antigen is present in the primate. The invention further  
 CC comprises: an antibody that binds to the same epitope as the humanised  
 CC antibody given in the specification; a composition comprising the  
 CC antibody and a pharmaceutical carrier; inducing tolerance to an antigen  
 CC in a patient; inhibiting an immune response in a patient or for  
 CC inhibiting the rejection of a graft in a human patient; and screening for  
 CC a compound, or a combination of at least two compounds for use in  
 CC inducing tolerance. The compositions of the invention have the following  
 CC activities: immunosuppressive, antirheumatic, antiarthritic,  
 CC antidiabetic, neuroprotective, antinflammatory, antiallergic,  
 CC antiasthmatic, cytoprotective, and antimicrobial. The composition and methods  
 CC are useful for inhibiting, preventing or ameliorating an immune response  
 CC against an antigen, such as in the inhibition or treatment of transpl  
 CC rejection, graft-versus-host disease, autoimmune diseases (e.g.  
 CC rheumatoid arthritis, diabetes or multiple sclerosis), inflammation,  
 CC allergy, asthma, cancer or infections. These may also be used for  
 CC identifying compounds or agents useful for inducing tolerance against  
 CC antigens. This sequence represents the protein of a humanised TRX1  
 CC antibody region of the invention.  
 XX  
 SQ Sequence 467 AA;

Alignment Scores:  
 Pred. No.: 6.24e-113 Length: 467  
 Score: 1765.00 Matches: 330  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.22% Indels: 0  
 DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADQ87966 (1-467)

Qy 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCCACAGACACCTCTGGG 60  
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 Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157  
 Qy 61 GGCACAGCGCCCTCGGCTGCTGCTCAAGGACTACTTCCCGAACCCGGTGAGGTGTCG 120  
 |||||  
 Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177  
 Qy 121 TGGAACTCAGCGCCCTCGACAGCGGCTGCACACCTTCCCGGTGCTCTACAGTCTCTCA 180  
 |||||  
 Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
 Qy 181 GGACTCTACTCTCCCTCAGCAGCGTGGTGACCGTCCCTCCACAGCAGCTTGGCAGCCAGACC 240  
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 Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217  
 Qy 241 TACATCTGCAACGTGAATCAAGCCCGACGACCAACAGGTGGACAGAAAGTTGAGCCCC 300  
 |||||  
 Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
 Qy 301 AAATCTTGTCACAAACTCACACATGCCACCTGCCAGCAGCTGAACCTCGCGGGGGCA 360  
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 Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
 Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420  
 |||||  
 Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277  
 Qy 421 GAGGTCAATCGGTGGTGGAGCGTGAGCCAGAGACCCCTGAGGTCAAGTTCACATGG 480  
 |||||  
 Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
 Qy 481 TAGCTGACCGCGCTGGAGGTCATATGCCAAGACAAAGCCGCGGAGGAGGAGTACACAC 540  
 |||||  
 Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317  
 Qy 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
 |||||  
 Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337





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Db      178 TrpAnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
Qy      181 GGACTTACTCCCTCAGCAGCGTGGTGACCGTCCAGCAGCTGGGACCCAGCAGC 240
Db      198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
Qy      241 TACATCTGCACGCGTGAATCACAAGCCCAAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300
Db      218 TyrIleCysAenValAenHisLysProSerAenThrLysValAspLysValGluPro 237
Qy      301 AAATCTTGTGTGACAAACTCACACATGCCACCGTCCAGCAGCAGCTGAACCTCGCGGGGCA 360
Db      238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
Qy      361 CCGTCAGTCTTCTCTTCCCCCCCCAAAACCAAGACACCCCTCATGATCTCCCGGACCCCT 420
Db      258 ProSerValPheLeuPheProProLysPheProLysAspThrLeuMetIleSerArgThrPro 277
Qy      421 GAGGTCAATCGTGGTGGTGGAGTGGAGTGGAGCCACGAGACCCCTGAGTTCAGTTCAGTGG 480
Db      278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenThr 297
Qy      481 TACGTGACGCGCGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGACGAGTACAAC 540
Db      298 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGluGlnTyrAsn 317
Qy      541 AGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db      318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTyrLeuAsnGlyLys 337
Qy      601 GAGTACAGTGCAGGTTCTCCAAAGACCCCTCCAGCCCCCATCGAGAAACCATCTCC 660
Db      338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357
Qy      661 AAAGCCAAAGGCGAGCCGAGACACACAGGTGTACACCCCTGCCCTCCATCCCGGATGAG 720
Db      358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
Qy      721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      378 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
Qy      781 GCCGTGAGTGGGAGACATGGCCGAGCCGAGACCAACTACAAGACCAAGCCCTCCGCTG 840
Db      398 AlaValGluTyrGluSerAsnGlyGlnProGluAenAenTyrLysThrThrProProVal 417
Qy      841 CTGACTCCGACGCGCTCTTCTCTCTTCTTACAGCAAGCTCACCGTGGCAAGCAGCAGTGG 900
Db      418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTyr 437
Qy      901 CAGCAGGGGAAACGCTTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db      438 GlnGlnGlyAenValPheSerCysSerValMetHisGluAlaLeuHisAenHisTyrThr 457
Qy      961 CAGBAGAGCTCTCCCTGCTCTCCGGTAAA 990
Db      458 GlnLysSerLeuSerLeuSerProGlyLys 467
```

## RESULT 14

ABG70743

ID ABG70743 standard; protein; 473 AA.

XX ABG70743;

AC ABG70743;

XX 02-DEC-2002 (first entry)

XX Mouse/human chimeric anti-MAG antibody heavy chain protein.

XX Stroke; neurological disease; neurodegeneration; brain injury;

KW spinal cord injury; chronic disease; Alzheimer's disease; tauopathy;

KW fronto-temporal dementia; peripheral neuropathy; Parkinson's disease;

KW Huntington's disease; multiple sclerosis; mouse; human; anti-MAG;

```
KW antibody; heavy chain.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX WO200262383-A2.
XX
XX 15-AUG-2002.
XX
XX 08-FEB-2002; 2002WO-GB000551.
XX
XX 08-FEB-2001; 2001GB-00003174.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Irving EA, Vinson M;
XX
XX WPI; 2002-698554/75.
XX
XX Treating or preventing stroke and neurological diseases, e.g. Alzheimer's
PT disease, multiple sclerosis or Parkinson's disease, comprises
PT administering a myelin-associated glycoprotein (MAG) antagonist or anti-
PT MAG antibody.
XX
XX Disclosure; Fig 5; 41pp; English.
XX
XX The present invention relates to a new method of treating or preventing
CC stroke and other neurological diseases in a human. The method involves
CC administering a myelin-associated glycoprotein (MAG) antagonist or anti-
CC MAG antibody, including altered antibodies or their functional fragments.
CC The MAG antagonist or anti-MAG antibody, including altered antibodies or
CC their functional fragments are useful in preparing a medicament for
CC treating or preventing stroke and other neurological diseases, or for
CC inhibiting neurodegeneration and/or promoting functional recovery in a
CC human patient suffering or at risk of developing stroke or other
CC neurological disease, such as stroke, traumatic brain injury and spinal
CC cord injury, chronic diseases including Alzheimer's disease, fronto-
CC temporal dementias (taupathies), peripheral neuropathy, Parkinson's
CC disease, Huntington's disease and multiple sclerosis. The present amino
CC acid sequence represents the mouse/human chimeric anti-MAG antibody heavy
CC chain protein
XX
SQ Sequence 473 AA;
```

## Alignment Scores:

```
Pred. No.: 6.25e-113 Length: 473
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 5 Gaps: 0
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US-10-733-563-111 (1-990) x ABG70743 (1-473)

```
Qy      1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCGGACCCCTCTCCAAAGACAGCACTCTGGG 60
Db      144 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 163
Qy      61 GGCACAGCGCCCTCGGCTCGCTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTCG 120
Db      164 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 183
Qy      121 TGGAACTCAGCGCCCTCGACAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCTCTCA 180
Db      184 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 203
Qy      181 GGACTTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGACCCAGCAGC 240
Db      204 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 223
Qy      241 TACATCTGCAACGTGAATCATCAAGCCGAGCAACCAAGGTGGACAAAGAAAGTTGAGCCC 300
```

```
Db 224 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 243
Qy 301 AAATCTTGAGCAAACTCACATGCGCCACCGTCCAGCAGCAGCTGAACTGCGGGGCA 360
Db 244 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuAlaGlyAla 263
Qy 361 CGGTGAGTCTTCTCTTCCCAAAACCAAGGACCCCTCATGATCTCCGGACCCCT 420
Db 264 ProSerValPheLeuPheProProlsProlsAspThrLeuMetIleSerArgThrPro 283
Qy 421 GAGTCCATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 284 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 303
Qy 481 TACGTGAGCGGTGGAGTGCATATGCAAGACAAAGCCGCGGAGCAGGACGATACAC 540
Db 304 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 323
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 324 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 343
Qy 601 GAGTCAAGTCAAGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCC 660
Db 344 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 363
Qy 661 AAAGCCAAAGGCGCCCGAGAACACAGGTGTACCCCTGCGCCCATCCCGGATCAG 720
Db 364 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 383
Qy 721 CTGACCAAGAACAGGTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCC 780
Db 384 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 403
Qy 781 GCCGTGGTGGAGAGCAATGGGAGCGCGGAGAGCAATGAGAGCAATGAGAGCAATGAGAG 840
Db 404 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 423
Qy 841 CTGGAATCCGAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 424 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 443
Qy 901 CAGCAGGGGAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 444 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 463
Qy 961 CAGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 464 GlnLysSerLeuSerLeuSerProGlyLys 473
```

## RESULT 15

ADL23051  
ID ADL23051 standard; protein; 475 AA.

XX AC ADL23051;

XX XX 20-MAY-2004 (first entry)

XX DE Mouse/human chimeric anti-MAG antibody heavy chain #1.

XX KW antibody; MAG; myelin associated glycoprotein; heavy chain; CDR; stroke;  
XX KW neurodegenerative disorder; gene therapy; vaccine; human; mouse.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Chimeric.

XX FN WO2004014953-A2.

XX XX 19-FEB-2004.

XX XX 05-AUG-2003; 2003WO-EP008749.

XX 06-AUG-2002; 2002GB-00018229.  
PR 06-AUG-2002; 2002GB-00018230.  
PR 06-AUG-2002; 2002GB-00018232.  
PR 06-AUG-2002; 2002GB-00018234.  
XX (GLAX ) GLAXO GROUP LTD.  
PA Ellis JH, Germaaschewski V;  
XX WPI; 2004-180641/17.

XX New altered antibody that binds to and neutralizes myelin associated  
PT glycoprotein (MAG), useful for preparing a composition for treating or  
PT preventing stroke or other neurodegenerative disorders e.g., Alzheimer's  
PT disease.

XX Example 2; Fig 1; 67pp; English.

XX The present invention relates to a new altered antibody or its functional  
CC fragment, which binds to and neutralizes myelin associated glycoprotein  
CC (MAG) and comprises a light chain variable domain (VL) comprising  
CC complementary determining region light 1 (CDRL1), CDRL2 or CDRL3 and/or a  
CC heavy chain variable domain (VH) comprising CDRH1, CDRH2 or CDRH3. The  
CC antibody is useful for preparing a composition for treating or preventing  
CC stroke or other neurodegenerative disorders in a human, e.g., traumatic  
CC brain injury, Alzheimer's disease, dementia, peripheral neuropathy,  
CC Parkinson's disease, Huntington's disease and multiple sclerosis. The  
CC present sequence is a human/mouse chimeric anti-MAG antibody heavy chain.

XX Sequence 475 AA;

## Alignment Scores:

Pred. No.: 5,26e-113 Length: 475  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADL23051 (1-475)

Qy 1 GCCTCCACAGGGCCCATCGGTCTTCCCTCCGACCCCTCTCTCCAGAGCACCTCTCTGGG 60  
Db 146 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 165  
Qy 61 GGCACAGCGCCCTCGGTGCTGCTGCTCAAGACTACTTCCCGAACCCGGTACGGGTGCG 120  
Db 166 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185  
Qy 121 TGGAACTCAGCGCCCTGACCCAGCGGGGTGCACACCTTCCCGGTGCTCTACAGTCTCA 180  
Db 186 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205  
Qy 181 GGACTTACTCTCTCAGCAGCGGTGCTGACCGTCCCTCCAGCAGCTTGGGACCCAGACCC 240  
Db 206 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225  
Qy 241 TACATCTGCAACGTGAATCAAGCCAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300  
Db 226 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 245  
Qy 301 AAATCTTGCAAAACTCCACATGCCCGCCCGGAGCCAGCAGCTGAACTCGCGGGGCA 360  
Db 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 265  
Qy 361 CCGTCAGTCTTCTCTTCT 420  
Db 266 ProSerValPheLeuPheProProlsProlsAspThrLeuMetIleSerArgThrPro 285  
Qy 421 GAGTCCATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
Db 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 305

QY 481 TACGTGGAGCGGTGGAGTGCATTAATCCCAAGACAAAGCCCGGGAGGACAGTACAAAC 540  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
306 TyrValAspGlyValGluValHisAsnAlaIysThrLysProArgGluGluGlnTyrAsn 325  
QY 541 AGCACGTACCGTGTGGTCTCAGCGTCTCACCGTCTGTGCACACAGGACTGGCTGAATGGCAAG 600  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
326 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 345  
QY 601 GAGTACAAGTCAAGGTCTCCAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCC 660  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
346 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 365  
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCTGCCGCCCATCCCGGATGAG 720  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
366 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 385  
QY 721 CTGACCAAGAACCAAGGTCTGACCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATC 780  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
386 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 405  
QY 781 GCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACCAACTACAAGACCACGCCCTCCCGTG 840  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
406 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 425  
QY 841 CTGACTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 900  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
426 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 445  
QY 901 CAGCAGGGGAACGTCTTCTCATGTCTCGTGATGATGAGGCTCTGCACAACCACTACACG 960  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
446 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 465  
QY 961 CAGAAGAGCCTCTCCCTGTCTCCGGTAAA 990  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
466 GlnLysSerLeuSerLeuSerProGlyLys 475

Search completed: January 28, 2006, 08:33:44  
Job time : 166.595 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:20:11 ; Search time 27.0045 Seconds  
(without alignments)  
7054.719 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797  
Sequence: 1 gctccaccaggcccatc.....tctccctgtctccgggtaaa 990

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 568832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO spool p/US10733563/runat\_27012006.180006.4797/app\_query.fasta\_1.2716  
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1.83 @runat\_27012006.180006.4797 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUEURY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1751	97.4	330	1	GHU	Ig gamma-1 chain C
2	1619.5	90.1	377	2	A23511	Ig gamma-3 chain C
3	1617.5	90.0	377	2	A60764	Ig gamma-3 chain C
4	1603	89.2	326	1	G2HU	Ig gamma-2 chain C
5	1579.5	87.9	327	1	G4HU	Ig gamma-4 chain C
6	1259	70.1	328	2	I47159	Ig gamma 2a chain
7	1256.5	69.9	374	2	S69339	Ig heavy chain v r
8	1253	69.7	328	2	I47160	Ig gamma 2b chain
9	1249	69.5	255	4	S31866	Ig gamma-1 chain C
10	1243	69.2	234	2	P70207	Ig gamma chain C r
11	1235	68.7	328	2	I47158	Ig gamma 1 chain c
12	1231	68.5	328	2	I47161	Ig gamma 1 chain c
13	1219.5	67.9	323	1	GHRB	Ig gamma chain C r
14	1201.5	66.9	329	1	G2GP	Ig gamma-2 chain C

15	1195.5	66.5	472	2	S31459	Ig gamma-1 chain -
16	1171.5	65.2	470	2	S22080	Ig heavy chain pre
17	1157.5	64.4	308	2	C30554	Ig heavy chain C r
18	1156	64.3	444	2	PC4436	monoclonal antibod
19	1149	63.9	326	2	PS0017	Ig gamma-1 chain C
20	1148.5	63.9	289	1	G3HUW1	Ig gamma-3 heavy c
21	1144	63.7	324	1	G1MS	Ig gamma-1 chain C
22	1139	63.4	393	1	G1MSM	Ig gamma-1 chain C
23	1135.5	63.2	333	2	PS0018	Ig gamma-2b chain
24	1130	62.9	329	1	G1MSC	Ig gamma-3 chain C
25	1119	62.3	398	1	G3MSM	Ig gamma-3 chain C
26	1115	62.0	469	2	S37483	Ig gamma-2a chain
27	1114.5	62.0	329	2	S00847	Ig gamma-2c chain
28	1112.5	61.9	335	1	G2MSAB	Ig gamma-2a chain
29	1110	61.8	330	1	G2MSA	Ig gamma-2a chain
30	1110	61.8	399	1	G2MSAM	Ig gamma-2a chain
31	1109	61.7	322	2	PS0019	Ig gamma-2a chain
32	1100	61.2	446	2	S40295	Ig gamma-2a chain
33	1092.5	60.8	327	2	S06611	Ig gamma-2 chain C
34	1078	60.0	405	1	G2MSBM	Ig gamma-2b chain
35	1063	59.2	475	2	S01321	Ig gamma-2b chain
36	1061	59.0	277	2	I47162	Ig gamma 4 chain c
37	1055.5	58.7	474	1	G2MS11	Ig gamma-2b chain
38	707	39.3	180	2	I46732	Ig gamma heavy cha
39	672.5	37.4	548	2	S38864	Ig epsilon chain C
40	577.5	32.1	249	2	S69340	Ig heavy chain VH
41	574.5	32.0	218	2	A36040	Ig heavy chain V-I
42	571	31.8	152	2	S14236	Ig gamma-1 chain C
43	560	31.2	549	2	S04845	Ig heavy chain pre
44	536	29.8	241	2	S69131	Ig heavy chain (DO
45	534	29.7	220	2	A49444	Ig gamma-1 heavy c

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A>Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, S.

A>Note: Lys-330 is removed after translation

R:Haris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI0000013C6FE; EMBL:Z17370

R:Kakahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a s

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113:235-330 <TAK>

A:Cross-references: UNIPARC:UPI0000017378B; UNIPARC:UPI0000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>  
A:Cross-references: UNIPARC:UPI000017378D  
A:Note: this sequence has the G1m(3) marker, 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence  
A:Reference number: A90564; MUID:71064025; PMID:5530842  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: protein  
A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,  
A:Cross-references: UNIPARC:UPI000017378E  
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
Igen Primärstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
A:Cross-references: UNIPARC:UPI000017378F  
A:Note: this sequence has the G1m(17) and G1m(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH  
A:Cross-references: UNIPARC:UPI0000173790  
A:Note: this sequence has the G1m(3) and G1m(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
  
Alignment Scores:  
Pred. No.: 9.74e-104 Length: 330  
Score: 1751.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.44% Indels: 0  
DB: 1 Gaps: 0  
  
US-10-733-563-111 (1-990) x GHU (1-330)  
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCGACCCCTCTCCAGAGCACCTCTGGG 60

Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20  
QY 61 GGCACAGCGGCGCTCGCTGGTCAAGACTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 21 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
QY 121 TGGAACTCAGGCGCTGACAGCGGGGTGCACACCTTCCCGGTCTCTACAGTCTCTCA 180  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 181 GGACTCTACTCCCTCAGCAGCGGTGCACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80  
QY 241 TACATCTGCACCGTAATCAAGCCAGCAACCAAGGTGGCAAGAAAGTTGAGCCC 300  
Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100  
QY 301 AAATCTTGTGACAAAATCTCACATGCCACCGTGCAGCACCTGAACTCGCGGGGCA 360  
Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 120  
QY 361 CCCTCAGTCTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
Db 121 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 140  
QY 421 GAGTCTCATCTCGTGGTGGAGCGTGGAGCACCAAGACCTGAGGTCAAGTTCAACTGG 480  
Db 141 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 160  
QY 481 TACGTGACCGCGTGGAGGTGCATATATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAC 540  
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180  
QY 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200  
QY 601 GAGTACAGTGCAGGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGCAAAACCATCTCC 660  
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrLysSer 220  
QY 661 AAGCCAAAGGCGAGCCCGGAGAACCAAGGTGACACCTTGCCTCCCTCCCTCCCTCCCT 720  
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240  
QY 721 CTGACCAAGAACCAAGGTGACCTGACCTGCTGGTCAAGGCTTCTATCCAGCGGACATC 780  
Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260  
QY 781 GCCGTGAGTGGGAGAGCAATAGGCGACCGGAGAACCAACTACAGACCAAGCCCTCCCTG 840  
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 280  
QY 841 CTGACTCCAGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 900  
Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300  
QY 901 CAGCAGGGGAGCGTCTTCTCATCTGCTGATGATGATGATGATGATGATGATGATGATGAT 960  
Db 301 GlnGlnGlnAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 320  
QY 961 CAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA 990  
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330  
RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA  
A:Reference number: A23511; MUID:86148507; PMID:3081877

A:Accession: A23511

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272

C:Genetics:

A:Gene: IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2,15e-95 Length: 377  
Score: 1619.50 Matches: 307  
Percent Similarity: 84.08% Conservative: 10  
Best Local Similarity: 81.43% Mismatches: 13  
Query Match: 90.12% Indels: 47  
DB: 2 Gaps: 1

US-10-733-563-111 (1-990) x A23511 (1-377)

Qy 1 GCCTCCACAAAGGGCCCATCGTCTTCCCTGGCACCTCTCTCCAAAGACACCTCTGGG 60  
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20  
Qy 61 GGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
Qy 121 TGGAACTCAGCGCCCTGACACAGCGGTGTGACACCTTCCCGGTGCTCTCAGTCTCA 180  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 80  
Qy 241 TACATCTGCAACGTGAATCACAAGCCCAACCAACACCAAGGTGGAGAAAGTT----- 294  
Db 81 TyrThrCysAsnValAsnHisLysProSerAsnThrLysValAspLysArgValGluLeu 100  
Qy 294 ----- 294  
Db 101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys 120  
Qy 294 ----- 294  
Db 121 AspThrProProProCysProArgCysProGluProLysSerCysAspThrProProPro 140  
Qy 295 -----GAGCCCAAAATCTGTGACAAAACCTCACATGCCCCACCGTGCCCA 339  
Db 141 CysProArgCysProGluProLysSerCysAspThrProProCysProArgCysPro 160  
Qy 340 GCACCTGAACCTCGGGGGGACCGTCACTCTTCTTCTTCCCTCCCAAAACCAAGACAC 399  
Db 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThr 180  
Qy 400 CTCATGATCTCCCGGACCCCTGAGTACATGCTGACCGGTGGAGTGGAGCCAGGAC 459  
Db 181 LeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp 200  
Qy 460 CCTGAGGTCAAGTTCAACTGTGACCGGTGGAGTGCATATGTCACCAAGACAAAG 519  
Db 201 ProGluValGlnPheLysTyrValAspGlyValGluValHisAsnAlaLysThrLys 220  
Qy 520 CCGCGGAGGAGACGATCAACAGCAGTACCGTGTGTCAGCTCTCCAGCAGCTTGGGAC 579

Db 221 ProArgGluGluGlnTyrAsnSerThrPheArgValValSerValLeuThrValLeuHis 240  
Qy 580 CAGGACTGGCTGAATGGCAAGAGTACAAAGTCAAGGTCTCAACAAAGCCCTCCAGCC 639  
Db 241 GlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAla 260  
Qy 640 CCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACC 699  
Db 261 ProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyrThr 280  
Qy 700 CTGCCCCCATCCCGGATGAGTACCAACCAAGACCAAGGTGTACAGCTGCTGCTGCTCAA 759  
Db 281 LeuProProSerArgGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys 300  
Qy 760 GGCTTCTATCCAGCAGCATCGCGTGGAGTGGAGAGCAATGGCAGCCGAGAACAC 819  
Db 301 GlyPheTyrProSerAspIleAlaValGluTrpGluSerSerGlyGlnProGluAsnAsn 320  
Qy 820 TACAAGACACGCTCCCGTCTGGACTCCGACCGCTCTTCTTCTTCTTCTTCTTCTTCT 879  
Db 321 TyrAsnThrThrProProMetLeuAspSerAspGlySerPhePheLeuTyrSerLysLeu 340  
Qy 880 ACCGTGCAACAGCAGGTGGCAGCGGGGAAACGTCTTCTCTCATGCTCCGTGATCATGAG 939  
Db 341 ThrValAspLysSerArgTrpGlnGlnGlyAsnIlePheSerCysSerValMetHisGlu 360  
Qy 940 GCTCTGCACCAACTACACGACAGAGCTCTCCCTGTCTCCGGGTAAA 990  
Db 361 AlaLeuHisAsnArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 377

RESULT 3

A60764

Ig gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert

A:Reference number: A60764; MUID:90007613; PMID:2571587

A:Accession: A60764

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

C:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI00000176F0B

C:Superfamily: immunoglobulin homology

C:Keywords: immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 2,88e-95 Length: 377

Score: 1617.50 Matches: 307

Percent Similarity: 84.08% Conservative: 10

Best Local Similarity: 81.43% Mismatches: 13

Query Match: 90.01% Indels: 47

DB: 2 Gaps: 1

US-10-733-563-111 (1-990) x A60764 (1-377)

Qy 1 GCCTCCACAAAGGGCCCATCGTCTTCCCTGGCACCTCTCTCCAAAGACACCTCTGGG 60  
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20  
Qy 61 GGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
Qy 121 TGGAACTCAGCGCCCTGACACAGCGGTGTGACACCTTCCCGGTGCTCTACAGTCTCTCA 180  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTGTGTCAGCTCTCCAGCAGCTTGGGAC 240

Db 61 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80  
Qy 241 TACATCTGCAACGTAATCATCAAGCCGACGAAACACCAAGGTGGACAGAAAGTT----- 294  
Db 81 TyrThrCysAsnValAsnHisLysProSerAsnThrLysValAspLysArgValGluLeu 100  
Qy 294 ----- 294  
Db 101 LysThrProLeuGlyAspThrHisThrCysProArgCysProGluProLysSerCys 120  
Qy 294 ----- 294  
Db 121 AspThrProProCysProArgCysProGluProLysSerCysAspThrProProPro 140  
Qy 295 -----GAGCCCAATCTGTGACAAAACCTCACATGCCACCGTGGCCCA 339  
Db 141 CysProArgCysProGluProLysSerCysAspThrProProCysProArgCysPro 160  
Qy 340 GCACCTGAACCTCGCGGGGACCGCTCAGTCTCTCTCCCCCAAAACCCCAAGGACAC 399  
Db 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThr 180  
Qy 400 CTCATGATCTCCCGGACCCCTGAGGTCCATGCGTGGTGGACGTGAGCCACGACGAC 459  
Db 181 LeuMetIleSerArgThrProGluValThrCysValValAspValSerHisGluAsp 200  
Qy 460 CCTGAGGTCAAGTTCAACTGTGAGTGGACCGGTGGAGGTGCATATATGCCAAGCAAG 519  
Db 201 ProGluValGlnPheLysTrpTyrValAspGlyValGluValHisAsnAlaLysThrLys 220  
Qy 520 CCGCGGAGGAGCAGTCAACAGCAGCTACCGTGGTTCAGCGTCCCTCACCGCTCCGAC 579  
Db 221 ProArgGluGluInTyraAsnSerThrPheArgValValSerValLeuThrValLeuHis 240  
Qy 580 CAGGACTGGCTGAATGGCAAGAGTCAAGGTCAAGGTCTCCAAACAAGCCCTCCAGCC 639  
Db 241 GlnAspTrpLeuAsnGlyLysGluTyrlsCysLysValSerAsnLysAlaLeuProAla 260  
Qy 640 CCCATCGAGAAACATCTCAAGCCAAAGGGACGCCCGGAGAACCCAGGTGTACACC 699  
Db 261 ProileGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyThr 280  
Qy 700 CTGCCCCCATCCCGGGATGACTCACCAAGAACCAAGTCCAGCTCGCTCGTCTCAA 759  
Db 281 LeuProSerArgGluLysThrLysGlnValSerLysValSerLysValLys 300  
Qy 760 GGCTTCTATCCAGCAGCATCCCGTGGAGTGGAGAGCAATGGCGACCGGAGAACAC 819  
Db 301 GlyPheTyProSerAspIleAlaValGluTrpGluSerSerGlyGlnProGluAsnAsn 320  
Qy 820 TACAAGACCGCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTTACAGCAAGCTC 879  
Db 321 TyrAsnThrThrProProValLeuAspSerAspGlySerPhePheLeuTySerArgLeu 340  
Qy 880 ACCGTGCAAGACAGGTGGCAGCAGCGGAGACGTCTCTCATCTCGTGCATGCATGAG 939  
Db 341 ThrValAspLysSerArgTrpGlnGluLysAsnValPheSerCysSerValMetHisGlu 360  
Qy 940 GCTCTGCACACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGGTAAA 990  
Db 361 AlaLeuHisAsnArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 377  
RESULT 4  
G2HU  
Ig gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906; MUID:82197621; PMID:6804948  
A:Accession: A93906

A:Molecule type: DNA  
A:Residues: 1-326 <ELL>  
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:932:  
A:Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Contents: myeloma protein T11  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19,'Q','21-57','Z','59','A','61-193','D',195-325 <WAN>  
A:Cross-references: UNIPARC:UPI0000173791  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a t  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24,'E','26-57','EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-;  
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793  
A:Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
A:Cross-references: UNIPARC:UPI0000173794  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatio  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4940472  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 2,42e-94 Length: 326  
Score: 1603.00 Matches: 302  
Percent Similarity: 95.15% Conservative: 12  
Best Local Similarity: 91.52% Mismatches: 12  
Query Match: 89.20% Indels: 4  
DB: 1 Gaps: 2



US-10-733-563-111 (1-990) x G2HU (1-326)

```
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCCTGGCACCTCTCTCCAGAGCACCTCTGGG 60
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20
QY 61 GGCACAGGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCAGGTGACGTGTG 120
Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGGCGCCTGACACAGCGGTGACACCTTCCCGGTCTCTCAGTCTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 60
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr 80
QY 241 TACATCTGCAAGCTGAATCACAAGCCCGAACAACAAGGTGGACAAGAAAGTTGAGCCC 300
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysThrValGluArg 100
QY 301 AAATCTCTGTGACAAACTCACACATGCCCGTCCCGTCCAGCAGCTTGGGACCCAGACC 360
Db 101 LysCysCysValGlu-----CysProProCysProAlaProProValAlaGly--- 116
QY 361 CGGTGAGTCTTCTCTCTCCCGCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 117 ProSerValPheLeuPheProProlLysProLysAspThrLeuMetIleSerArgThrPro 136
QY 421 GAGTTCACATGCTGCTGCTGAGTGAACGTCGACCAAGACCTGAGGTCAAGTTCACATGG 480
Db 137 GluValThrCysValValAlaAspValSerHisGluAspProGluValGlnPheAsnTrp 156
QY 481 TACGTGGAGCGGTGAGTGCATATCCAGACAAAGACCGCGGAGGACGAGTACAC 540
Db 157 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn 176
QY 541 AGCAGTACCGTGTGCTCAGCGTCTCTCCCGTCTGACACCGTCTGACACCGTCTGAATGGCAAG 600
Db 177 SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeuAsnGlyLys 196
QY 601 GAGTACAAAGTCAAGTCTTCCAAAGACCTTCCAGCGCCCATCGAGAAACCAATCTCC 660
Db 197 GluTyrLysCysLysValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSer 216
QY 661 AAAGCCAAAGGCGACCGGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGATCAG 720
Db 217 LysThrLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgGluGlu 236
QY 721 CTGACCAAGAACCCAGTCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 237 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 256
QY 781 GCCGTGGAGTGGAGCAATGGGACCGCGGAGAACCAACTCAAGACCAACCGCTCCCGTG 840
Db 257 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMet 276
QY 841 CTGGACTCCGACGGCTCTCTTCTCTTACAGCAGCTCACCGTGGACAAGAGCGAGTGG 900
Db 277 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 296
QY 901 CAGCAGGGGAAAGCTTCTCTGCTGCTGATGATGAGGTCTCTGACAAACCAACCTACACG 960
Db 297 GlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 316
QY 961 CAGAAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 317 GlnLysSerLeuSerLeuSerProGlyLys 326
```

RESULT 5

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C&gt;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 &lt;ELL&gt;

A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A:Note: The sequence was determined from the germline gene

P:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant r

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 &lt;PIN&gt;

A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology &lt;IM1&gt;

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology &lt;IM2&gt;

F:240-307/Domain: immunoglobulin homology &lt;IM3&gt;

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

Pred. No.: 7,49e-93 Length: 327

Score: 1579.50 Matches: 298

Percent Similarity: 93.94% Conservative: 12

Best Local Similarity: 90.30% Mismatches: 17

Query Match: 87.90% Indels: 3

DB: 1 Gaps: 1

US-10-733-563-111 (1-990) x G4HU (1-327)

```
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCCTGGCACCTCTCTCCAGAGCACCTCTGGG 60
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20
QY 61 GGCACAGGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCAGGTGACGTGTG 120
Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGGCGCCTGACACAGCGGTGACACCTTCCCGGTCTCTCAGTCTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 60
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrLysThr 80
QY 241 TACATCTGCAAGCTGAATCACAAGCCCGAACAACAAGGTGGACAAGAAAGTTGAGCCC 300
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysArgValGluSer 100
QY 301 AAATCTCTGTGACAAACTCACACATGCCCGTCCCGTCCAGCAGCTTGGGACCCAGACC 360
Db 101 Lys-----TyrGlyProProCysProSerCysProAlaProGluPheLeuGlyGly 117
QY 361 CGGTGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
```

```
Db 118 ProSerValPheLeuPheProProlysProLysAspThrLeuMetIleSerArgThrPro 137
Qy 421 GAGTCAATCGTGGTGGAGCGTGGAGCCACGACGAGACCCCTGAGGTCAAGTTCACATGG 480
Db 138 GluValThrCysValValAspValSerGlnGluAspProGluValGlnPheAsnTrp 157
Qy 481 TACGTGGACGGCGGTGCATATCCCAAGACAAAGACGCGCGGAGGAGCAGTACAAAC 540
Db 158 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn 177
Qy 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 178 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 197
Qy 601 GAGTCAAGTCAAGGTCTCAACAAAGCCCTCCAGCGCCCTCCAGCGCCCTCCAGCGCCCTCC 660
Db 198 GluTyrLysCysLysValSerAsnLysGlyLeuProSerSerIleGluLysThrIleSer 217
Qy 661 AAAGCCAAAGCGACCGCCGAGAACCAAGTGTACACCTGCGCCCTGCGCCCTGCGCGGATGAG 720
Db 218 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerGlnGluGlu 237
Qy 721 CTGACCAAGAACAGGTCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 780
Db 238 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 257
Qy 781 GCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAGCAACTACAGAACCAAGCCCTCCCGTG 840
Db 258 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 277
Qy 841 CTGACTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 278 LeuAspSerAspGlySerPheLeuTyrSerArgLeuThrValAspLysSerArgTrp 297
Qy 901 CAGCAGGGGAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 298 GlnGluGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 317
Qy 961 CAGAAGAGCCCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 318 GlnLysSerLeuSerLeuSerLeuGlyLys 327

RESULT 6
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3563-3573, 1994
A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:G433123; PIDN:AAAS2217.1; PI
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
P:133-202/Domain: immunoglobulin homology <IMM>
```

```
Alignment Scores:
Pred. No.: 1.65e-72 Length: 328
Score: 1259.00 Matches: 233
Percent Similarity: 82.83% Conservative: 42
Best Local Similarity: 70.18% Mismatches: 51
Query Match: 70.06% Indels: 6
DB: 2 Gaps: 3
```

US-10-733-563-111 (1-990) x I47159 (1-328)

```
Qy 1 GCCTCCACCAAGGCGCCCATCGGTCTTCCCTCCCTGGCACCCCTCCTCCAAAGACGACCTCTGGG 60
Db 1 AlaProLysThrAlaProSerValTyrProLeuAlaProCysSerArgThrSerGly 20
Qy 61 GGCACAGCGCGCGTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 21 ProAsnValAlaLeuLysGlyCysLeuAspSerSerTyrPheProGluProValThrValThr 40
Qy 121 TGSAACTCAGCGCGCCCTGACAGCGCGTGCACACCTTCCCGGTGCTCTACAGTCCTCA 180
Db 41 TrpAsnSerGlyAlaLeuSerSerGlyValHisThrPheProSerValLeuGlnProSer 60
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGCACCGTGCCTCCAGCAGCTTGGGACCCAGAC 240
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80
Qy 241 TACATCTGCAACGTAATCAAGCCCAAGCAACCAAGGTGGCAAGAAAGTGGAGGCC 300
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrThrLysValAspLysArgValGlyThr 100
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTGCACGACCTGAACCTGCGCGGGCA 360
Db 101 LysThr-----LysProProCysProIleCysProAlaCysGluSerProGly--- 116
Qy 361 CCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 117 ProSerValPheIlePheProLysProLysProLysProLysProLysProLysProLysPro 136
Qy 421 GAGTCACTACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 137 GlnValThrCysValValValAspValSerGlnGluAsnProGluValGlnPheSerTrp 156
Qy 481 TACGTGACGCGGTGGAGTGCATTAATGCCAAGCAAAAGCGCGGAGGAGCAGTACAAAC 540
Db 157 TyrValAspGlyValGluValHisThrAlaGlnThrArgProLysGluGlnPheAsn 176
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuAsnGlyLys 196
Qy 601 GAGTCAAGTGCAGGTCTCCAAAGCCCTCCAGCGCCCTCCAGCGCCCTCCAGCGCCCTCCAG 660
Db 197 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleThrArgIleIleSer 216
Qy 661 AAAGCCAAAGCGCAGCGCCGAGAACCAAGTGTACACCTGCTCCCTCCCTCCCTCCCTCCCTCC 720
Db 217 LysAlaLysGlyGlnThrArgGluProGlnValTyrThrLeuProProHisAlaGluGlu 236
Qy 721 CTGACCAAGAACGAGTGCAGCTGACCTGCTGGTGCAGAGGCTCTATCCAGCGGAGATC 780
Db 237 LeuSerArgSerLysValSerIleThrCysLeuValIleGlyPheTyrProProAspIle 256
Qy 781 GCCGTGAGTGGGAGAGCAATGGGCGAG-----CCGAGAGAACCAACTACAGACCCAGCCCT 834
Db 257 AspValGluTyrGlnArgAsnGlyGlnProGluProGluGlyAsnTyrArgThrThrPro 276
Qy 835 CCCGTGCTGAGTCCCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 894
Db 277 ProGlnGlnAspValAspGlyThrTyrPheLeuTyrSerLysPheSerValAspLysLys 296
Qy 895 AGGTGGCAGCAGGGGAGCGCTCTCTCATCTCCGTGATGATGATGATGATGATGATGATGATG 954
Db 297 SerTrpGlnGlyGlyIlePheGlnCysAlaValMetHisGluAlaLeuHisAsnHis 316
Qy 955 TACACGACGAGAGCGCTCTCCCTGCTCTCCCGGTAAA 990
Db 317 TyrThrGlnLysSerIleSerLysThrProGlyLys 328

RESULT 7
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
```

C:Accession: S69339; S72664  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95562687; PMID:7744049  
A:Accession: S69339  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: UNIPARC:UPI0000176P24; EMBL:X81695  
R:Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:Cross-references: UNIPARC:UPI0000176P25; EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Alignment Scores:  
Pred. No.: 2,36e-72 Length: 374  
Score: 1256.50 Matches: 258  
Percent Similarity: 75.14% Conservative: 14  
Best Local Similarity: 71.27% Mismatches: 48  
Query Match: 69.92% Indels: 42  
DB: 2 Gaps: 7

US-10-733-563-111 (1-990) x S69339 (1-374)

```
QY 30 CTGTCACCTCTCCAGAGACCTCTGCGGGGCAACAGCGCCCTGGGCTG-----CCT 83
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 14 ProSerTrpValLeuSerGlnIleThrLeuLysGluSerGlyProThrLeuValLysPro 33
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 84 GGTCAAGGACTA-----CTTCCCGCAACCGGTAC 113
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 34 ThrGlnThrLeuThrLeuThrCysThrPheSerGlyPheSerLeuSerLysSerGlyVal 53
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 114 GGTGTCTGTGGAACTCAGCGCCCT-----CTTCCCGCAACCGGTAC 137
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 54 GlyValGlyTrpIleArgGlnProProGlyGlnAlaLeuGluTrpLeuAlaLeuIlePhe 73
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 138 ---GACCAGCGGTGACACACTTCCCGGTCTCTACAGTCTCTCAGG-----182
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 74 TrpAspAspLysArgTrpSerProSerLeuArgThrArgLeuThrIleThrLysAsp 93
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 183 ACTCTACTCTCAGCAGCGGTGTGACCGTGCCTCC---AGCAGCTTGGGCACCCAGAC 239
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 94 ThrSerLysAsnGlnValValLeuThrMetThrAsnValAspProAlaAspThrAlaTh 113
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 240 CTACATCTGCAACGTGAAT-----CACAAAG---CC 266
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 113 rTyTrpCysGlyTrpSerValGluGlyTrpGlyGlnGlyTrpArgPheHisSerTrpGI 133
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 267 CAGCAACACCAAGGTGGAGAAAGTTGAGCCCAAAATCTTGTGACAAACTCACACATG 326
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 133 yGlnGlyThrLeuValThrValSerSerGluProLysSerCysAspLysThrHisTrpCy 153
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 327 CCCACGTCCTCCAGCACTGAACCTCGCGGGGCAACCGTCAGTCTCTCTCCCGCCAAA 386
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 153 sProProCysProAlaProGluLeuLeuGlyProSerValPheLeuPheProProLy 173
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 387 ACCCAAGGACACCTCATGATCTCCCGGACCCCTCAGGTGCATCGTGGTGGTGCAGT 446
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 173 sProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValAlaAspVa 193
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 447 GAGCCACCAAGACCTCAGGTCAAGTTCACTGTGACGTGGACGCGGTGGAGGTGCATAA 506
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 193 lSerHisGluAspProGluValLysPheAsnTrpTrpValAspGlyValGluValHisAs 213
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 507 TGCCAGACAAAGCCCGGGAGGACAGTACACAGCAGTACCGTGTGTGTGTCAGGTCTCT 566
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 213 nAlaLysThrLysProArgGluGlnTyrAsnSerThrTrpArgValValSerVal 233
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

## RESULT 8

I47160

Ig Gamma 2b chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C:Accession: I47160

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 &lt;KAC&gt;

A:Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:9433125; PIDN:AAAS2218.1; PII

C:Genetics:

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology &lt;IMW&gt;

## Alignment Scores:

Pred. No.:	3.97e-72	Length:	328
Score:	1253.00	Matches:	232
Percent Similarity:	82.23%	Conservative:	41
Best Local Similarity:	69.88%	Mismatches:	53
Query Match:	69.73%	Indels:	6
DB:	2	Gaps:	3

US-10-733-563-111 (1-990) x I47160 (1-328)

```
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACCCTCTCTCCAGAGACCTCTGGG 60
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 1 AlaProLysThrAlaProLeuValTyrProLeuAlaProCysGlyArgAspThrSerGly 20
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 61 GGCACAGCGGCCCTGGGCTGCTGTCAGGACTACTTCCCGCAACCGGTGACGCGTGTGCG 120
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrValThr 40
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 121 TGGAACTCAGCGCCCTTGACCGGGGTGCACACCTTCCCGGGTGTCTACAGTCTTCA 180
DB   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

Db 41 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProSerValLeuGlnProSer 60  
Qy 181 GGACTTACTCTCCAGCAGCGTGGTGAACCGTGCCTCCAGAGCTGGGGCACCAGACC 240  
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80  
Qy 241 TACATCTGCAACGCGTGAATCAACAAGCCAGCAACCAAGGTCGACAGAAAGTTGAGCCC 300  
Db 81 TyrThrCysAenValAenHisProAlaThrThrLysValAspLysArgValGlyThr 100  
Qy 301 AAATCTTGTGCAAAATCAACATGCCCCACCGTGCACCAAGACCCCTGAACTCCGCGGGCA 360  
Db 101 LysThr-----LysProCysProIleCysProAlaCysGluSerProGly--- 116  
Qy 361 CCGTCAGTCTTCTTCTCCCCCAAAACCAAGGACACCCCTCATGATCTCCGGACCCCT 420  
Db 117 ProSerValPheIlePheProLysProLysAspThrLeuMetIleSerArgThrPro 136  
Qy 421 GAGTTCATCGTGGTGGTGGAGCTGAGCCACCAAGACCCCTGAGGTCAAGTTCAACTGG 480  
Db 137 GlnValThrCysValValValAspValSerGlnGluAenProGluValGlnPheSerTrp 156  
Qy 481 TACGTGACGCGCGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGACAGTACAAC 540  
Db 157 TyrValAspGlyValGluValHisThrAlaGlnThrArgProLysGluGlnPheAen 176  
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuAenGlyLys 196  
Qy 601 GAGTACAAGTCAAGGTCCTCAACAAGACCCCTCCAGCCGCCATCGAGAAACCATCTCC 660  
Db 197 GluPheLysCysLysValAenAenLysAspLeuProAlaProIleThrArgIleLeuSer 216  
Qy 661 AAAGCCAAAGGCGCCCGGAGAACCAAGTGTACACCTCGCCCACTCCCGGAGTACG 720  
Db 217 LysAlaLysGlnThrArgLysGlnValThrLeuProProHisAlaGluGlu 236  
Qy 721 CTGACCAAGAACAGGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 237 LeuSerArgSerLysValSerIleThrCysLeuValIleGlyPheTyrProProAspIle 256  
Qy 781 GCCGTGAGTGGGAGAGCAATGGGCGAG-----CCGAGAACAACTACAAGACCAAGCCT 834  
Db 257 AspValGluTrpGlnArgAenGlnProGluProGluGlnValThrArgThrPro 276  
Qy 835 CCCGTGCTGGAACCGACCGCT 894  
Db 277 ProGlnGlnAspValAspGlyThrTyrPheLeuTyrSerLysPheSerValAspLysAla 296  
Qy 895 AGTGGCAGCAGGGAAGCTCTTCTCATGCTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 954  
Db 297 SerTrpGlnGlyGlyIlePheGlnCysAlaValMetHisGluAlaLeuHisAenHis 316  
Qy 955 TACACGCAAGAGACCT 990  
Db 317 TyrThrGlnLysSerIleSerLysThrProGlyLys 328  
RESULT 9  
S31866  
Ig gamma-1 chain C region - synthetic  
C/Species: synthetic  
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C/Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C/Accession: S31866  
R/Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A/Description: Screening method for protein-protein interactions of cloned gene products.  
A/Reference number: S31866  
A/Accession: S31866  
A/Molecule type: mRNA  
A/Residues: 1-255 <F1>  
A/Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PID:CAA49866.1; PID

C/Keywords: immunoglobulin  
F;1-22/Region: Escherichia coli outer membrane protein A precursor  
F;23-255/Region: human Ig gamma-1 chain C region

Alignment Scores:  
Pred. No.: 7,22e-72 Length: 255  
Score: 1249.00 Matches: 231  
Percent Similarity: 96.65% Conservative: 0  
Best Local Similarity: 96.65% Mismatches: 8  
Query Match: 69.50% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x S31866 (1-255)

Qy 274 ACCAAGTGGACAAAGAAAGTTGAGCCCAATTTGTGCAAAAACTCACATGCCACCG 333  
Db 17 ThrValAlaGlnAlaAspValGluSerLysSerCysAspLysThrHisThrCysProPro 36  
Qy 334 TGCCACGACCTGAACTCGCGGGGACACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 393  
Db 37 CysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLys 56  
Qy 394 GACACCTCATGATCTCCCGACCCCTGAGTGCATGCGTGGTGGTGGTGGTGGTGGTGG 453  
Db 57 AspThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHis 76  
Qy 454 GAAGACCTGAGGTCAAAGTTCAACTGTCGTGACCGCGTGGAGTGCATTAATGCCAAG 513  
Db 77 GluAspProGluValLysPheAenTrpTyrValAspGlyValGluValHisAenAlaLys 96  
Qy 514 ACAAGCCGCGGGAGGAGCAGTACAACAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 573  
Db 97 ThrLysProArgGluGluGlnTyrAenSerThrTyrArgValValSerValLeuThrVal 116  
Qy 574 CTGACACGAGCTGCTGTAATGGCAAGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTC 633  
Db 117 LeuHisGlnAspTrpLeuAenGlyLysGluTyrLysCysLysValSerAenLysAlaLeu 136  
Qy 634 CCAGCCCTCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGCCAGAACCAAGGT 693  
Db 137 ProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnVal 156  
Qy 694 TACACCTGCTGCCCATCCCGGAGTACCTACCAAGAACCAAGTGCAGCTGACCTGCTGCT 753  
Db 157 TyrThrLeuProProSerArgAspGluLeuThrLysAenGlnValSerLeuThrCysLeu 176  
Qy 754 GTCAAGGCTTCTATCCAGCAGCATCCCGTGGAGTGGGAGAGCAATGGCAGCCGAG 813  
Db 177 ValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerAenGlyGlnProGlu 196  
Qy 814 AACCACTACAGACACGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873  
Db 197 AsnAenTyrLysThrThrProProValLeuAspSerAspGlySerPhePheLeuTyrSer 216  
Qy 874 AAGCTCACCTGAGCAGAGCAGTGGCAGCGGGAACCTCTCTCTCATGCTCCGCTGATG 933  
Db 217 LysLeuThrValAspLysSerArgTrpGlnGlnGlyAenValPheSerCysSerValMet 236  
Qy 934 CATGAGGCTCTGCACACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGGTAAA 990  
Db 237 HisGluAlaLeuHisAenHisThrThrGlnLysSerLeuSerLeuSerProGlyLys 255

RESULT 10  
PT0207

Ig gamma chain C region - chimpanzee  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C/Accession: PT0207  
R/Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A/Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A/Reference number: PT0207; MUID:91287716; PMID:2062315  
A/Accession: PT0207

A:Molecule type: mRNA  
A:Residues: 1-234 <EHR>  
A:Cross-references: UNIPARC:UPI0000176F05  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:48-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1,74e-71 Length: 234  
Score: 1243.00 Matches: 229  
Percent Similarity: 98.29% Conservative: 1  
Best Local Similarity: 97.86% Mismatches: 4  
Query Match: 69.17% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x PT0207 (1-234)

```
QY 268 AGCACACCAAGGTGGACAGAAAGTTGAGCCCAATCTTGTGACAAACTCAGACATGC 327
Db 1 SerAsnThrLysValAspLysLysValGluProLysSerCysAspThrThrHisThrCys 20
QY 328 CCACCGTCCCGACACCTGAACTCCGGGGGCACCGTCACTCTCTCTCCGCCCAAAA 387
Db 21 ProProCysAlaAlaProGluLeuLeuGlyProSerValPheLeuPheProLys 40
QY 388 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTCACTGCGTGGTGGACGTG 447
Db 41 ProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValAspVal 60
QY 448 AGCCAGGAAGCCCTGAGGTCAAGTTCACTGGTACGTGGAGCGGTGGAGTGCATAT 507
Db 61 SerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsn 80
QY 508 GCCAAGACAAAGCCGGGAGGAGCAGTACACACGATACCGTACCGTGTGTGAGCTCC 567
Db 81 AlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValValSerValLeu 100
QY 568 ACCGTCCTGCACAGGACTGGTGAATGCAAGGAGGTACAAGTCAAGGTCTTCCAAACA 627
Db 101 ThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys 120
QY 628 GCCCTCCAGCCCCCATGAGAAACCATCTTCCAAAGCCAAAGGGGAGCCCCGAGAACCA 687
Db 121 AlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluPro 140
QY 688 CAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGACCAAGCGTACGCTGACC 747
Db 141 GlnValTyrThrLeuProSerArgAspGluLeuThrLysAsnGlnValSerLeuThr 160
QY 748 TGCCTGGTCAAGGCTTCTATCCAGCGACATCGCGGTGGAGTGGGAGAGCAATGGGCAG 807
Db 161 CysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerSerGlyGln 180
QY 808 CCGGAGAACAACTACAAGACACGCTCCCGTGTGACTCCGAGCGGTCTTCTTCTCCTC 867
Db 181 ProGluAsnAsnTyrLysThrThrProValLeuAspSerAspGlySerPhePheLeu 200
QY 868 TACACAGACTCACCGTGGACAGAGCAGGTGGGAGGAGGAAAGTCTTCTCATGCTCC 927
Db 201 TyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSer 220
QY 928 GTGATGCATGAGGCTCTGCACAAACACTACACGCAAGAGAGC 969
Db 221 ValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSer 234
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RESULT 11

Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: I47158, MUID:95015845; PMID:7930579  
A:Accession: I47158  
A:Status: Preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:9433121; PIDN:AAAS2216.1; PII  
C:Genetics:  
A:Gene: IgG1  
A:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 5,51e-71 Length: 328  
Score: 1235.00 Matches: 231  
Percent Similarity: 81.33% Conservative: 39  
Best Local Similarity: 69.58% Mismatches: 56  
Query Match: 68.73% Indels: 6  
DB: 2 Gaps: 3

US-10-733-563-111 (1-990) x I47158 (1-328)

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QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACCCCTCTCCAGAGACCTCTCTGGG 60
Db 1 AlaProLysThrAlaProSerValTyrProLeuAlaProCysGlyArgAspValSerGly 20
QY 61 GGCACAGCGGCCCTGGGTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTGC 120
Db 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrValThr 40
QY 121 TGGAACTCAGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTACAGCTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProSerValLeuGlnProSer 60
QY 181 GGACTCTACTCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerLysSer 80
QY 241 TACATCTCAACGTGAATCAACAAGCCAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrLysValAspLysArgVal----- 98
QY 301 AAATCTTGTGACAAACTCACACATGCCCGTCCAGCACCTGAACTCCCGGGGCA 360
Db 99 --GlyIleHisGlnProGlnThrCysProIleCysProGlyCysGluValAlaGly--- 116
QY 361 CGCTCAGTCTTCTCTTCCCGCCAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 117 ProSerValPheIlePheProLysProLysAspThrLeuMetIleSerGlnThrPro 136
QY 421 GAGGTACATCGGTGGTGGAGTGCATTAATGCCAAGCAAAAGCCCGGAGGAGCAGTACAC 480
Db 137 GluValThrCysValValValAspValSerLysGluHisAlaGluValGlnPheSerTrp 156
QY 481 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGCAAAAGCCCGGAGGAGCAGTACAC 540
Db 157 TyrValAspGlyValGluValHisThrAlaGluThrArgProLysGluGluGlnPheAsn 176
QY 541 AGCAGTACCGTGTGGTCAAGCTCTCACCGTCTCGACACGAGGACTGGCTGAATGGCAAG 600
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuLysGlyLys 196
QY 601 GAGTACAGTGCAGAGTCTCCCAAGACCCCTCCCGACCCCATCGAGAAACCATCTCC 660
Db 197 GluPheLysCysLysValAsnAsnValAspLeuProAlaProIleThrArgThrIleSer 216
QY 661 AAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCTGCGCCCATCTCCCGGATGAG 720
Db 217 LysAlaIleGlyGlnSerArgGluProGlnValTyrThrLeuProProAlaGluGlu 236
QY 721 CTGACCAAGAACCGAGTCAAGCTGACCTGCTGTGTCGTCGCAAGGCTTCTATCCAGCAGCATC 780
Db 237 LeuSerArgSerLysValThrLeuThrCysLeuValIleGlyPheTyrProProAspIle 256
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QY 781 GCCGTGGAGTGGGAGCAATGGGCGAG-----CCGGAGAACAACTACAAAGACCCAGCCT 834
Db 257 HisValGluTrpLysSerAsnGlyGlnProGluProGluValAsnThrTyrArgThrThrPro 276
QY 835 CCCGTGCTGGACTCCGACGGCTCTCTTCCTCTACACAAAGCTCACCGTGGACAAAGAGC 894
Db 277 ProGlnGlnAspValAspGlyThrPhePheLeuTyrSerLysLeuAlaValAspLysAla 296
QY 895 AGGTGGCAGCAGGGAACGCTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAAACAC 954
Db 297 ArgTrpAepHisGlyAspLysPheGluCysAlaValMetHisGluAlaLeuHisAsnHis 316
QY 955 TACACGACAGAGCCTCTCCCTGCTCTCCGGGTAAA 990
Db 317 TyrThrGlnLysSerIleSerLysThrGlnGlyLys 328

RESULT 12
147161
Ig gamma 3 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: 147161
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: 147158; MUID:95015845; PMID:7930579
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:g433127; PIDN:AAAS2219.1; PI
C:Genetics:
A:Gene: IG3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMW>

Alignment Scores:
Pred. No.: 9.89e-71 Length: 328
Score: 1231.00 Matches: 230
Percent Similarity: 81.33% Conservative: 40
Best Local Similarity: 69.28% Mismatches: 56
Query Match: 68.50% Indels: 6
DB: 2 Gaps: 3

US-10-733-563-111 (1-990) x 147161 (1-328)

QY 1 GCCTCCCAAGAGGCCATCGTCTTCCCTGGCACCCTCTCTCCAAAGCAGCACCTCTGGG 60
Db 1 AlaProLysThrAlaProSerValTyrProLeuAlaProCysGlyArgAspThrSerGly 20
QY 61 GGCACAGCGGCTGGGTGCTGTCTCAAGGACTACTTCCCGAACCGGTGACCGTGTGCG 120
Db 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrMetThr 40
QY 121 TGGAACTCAGCGGCTGACAGCGGCTGCACACCTTCCCGGTGCTCTCAGTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProSerValLeuGlnProSer 60
QY 181 GGACTCTACTCTCCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTCCGACCCAGCAGCC 240
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80
QY 241 TACATCTGCAACGTGAATCAAGCCAGCAACCAAGGTGGAGCAAGAAATGTGAGCCC 300
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrThrLysValAspLysArgValGlyThr 100
QY 301 AAATCTGTGCAAAACTCACATGCCACCGTCCAGCACCTGAACCTGCGGGGCA 360
Db 101 LysThr-----LysProProCysProLysProGlyCysGluValAlaGly--- 116
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
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Db 117 ProSerValPheIlePheProProLysProLysAspThrLeuMetIleSerGlnThrPro 136
QY 421 GAGTTCACATCGTGTGGTGGACGTGAGCCACGACGACCTGAGGTCAAGTTCAACTGG 480
Db 137 GluValThrCysValValValAspValSerLysGluHisAlaGluValGlnPheSerTrp 156
QY 481 TACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGACGACTACAC 540
Db 157 TyrValAspGlyValGluValHisThrAlaGluThrArgProLysGluGlnPheAsn 176
QY 541 AGCAGTACCGTGTGGTGCAGCGTCTCACCGCTCTGCACACGAGGACTGGCTGAATGGCAAG 600
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuLysGlyLys 196
QY 601 GAGTACAAGTGCAGGTCTCCAAAGCCCTCCAGCCCGCCATCGAGAAAAACCATCTCC 660
Db 197 GluPheLysCysLysValAsnAsnValAspLeuProAlaProIleThrArgThrIleSer 216
QY 661 AAAGCCAAAGGGCAGCCCGACACACAGGTGTACACCTGCCCTCCCGGATGAG 720
Db 217 LysAlaIleGlyGlnSerArgGluProGlnValTyrThrLeuProProAlaGluGlu 236
QY 721 CTGACCAAGAACACAGGTGACCTGCTGTGTCAAGGCTTCTATCCAGCGACATC 780
Db 237 LeuSerArgSerLysValThrValThrCysLeuValIleGlyPheTyrProProAspIle 256
QY 781 GCCGTGAGTGGGAGAGCAATGGGCGAG-----CCGGAGAACAACTACAAAGCAGCCCT 834
Db 257 HisValGluTrpLysSerAsnGlyGlnProGluProGluGlyAsnTyrArgThrThrPro 276
QY 835 CCCGTGCTGACTCCGACGGCTCTCTCTCTTCTTCTTACAGCAGCTCACCGTGGACAGAGC 894
Db 277 ProGlnGlnAspValAspGlyThrPhePheLeuTyrSerLysLeuAlaValAspLysAla 296
QY 895 AGGTGGCAGCAGGGGAAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACAC 954
Db 297 ArgTrpAepHisGlyGluThrPheGluCysAlaValMetHisGluAlaLeuHisAsnHis 316
QY 955 TACACGACAGAGCCTCTCCCTGCTCTCCGGGTAAA 990
Db 317 TyrThrGlnLysSerIleSerLysThrGlnGlyLys 328

RESULT 13
GHRB
Ig gamma chain C region - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype
A:Reference number: A91749; MUID:84030930; PMID:6313520
A:Accession: A91749
A:Molecule type: mRNA
A:Residues: 1-323 <BER>
A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012837D
A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R:Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin
A:Reference number: A90290; MUID:76135469; PMID:1243651
A:Accession: A90290
A:Molecule type: protein
A:Residues: 1-47, 'E', '49-71', 'PV', 72-128 <PRA>
A:Cross-references: UNIPARC:UPI00001737AB
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A:Reference number: A93928; MUID:83299917; PMID:6193512
A:Accession: A93928
A:Molecule type: mRNA
A:Residues: 88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A:Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g
```

A>Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker  
 R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
 Biochem. J. 116, 249-259, 1970

A>Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin  
 A;Reference number: A90245; MUID:70110015; PMID:5461106

A;Accession: A90245  
 A;Molecule type: protein  
 A;Residues: 132-143, 'E', 145-161 <FRU>

A;Cross-references: UNIPARC:UPI00001737AC  
 R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
 in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almquist and Wiksell,

A;Reference number: A94416  
 A;Accession: A94416  
 A;Molecule type: protein

A;Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',  
 A;Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE

A>Note: this has the e15 allotypic marker, 185-Ala  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-82/Domain: immunoglobulin homology <IM1>  
 F;130-199/Domain: immunoglobulin homology <IM2>  
 F;236-303/Domain: immunoglobulin homology <IM3>

F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred. No.: 5,32e-70 Length: 323  
 Score: 1219.50 Matches: 327  
 Percent Similarity: 79.82% Conservative: 34  
 Best Local Similarity: 69.42% Mismatches: 59  
 Query Match: 67.86% Indels: 7  
 DB: 1 Gaps: 2

US-10-733-563-111 (1-990) x GHRB (1-323)

Qy 10 AAGGCCCATCGTCTTCCCTCGCACCTCTCCACAGAGACCTCTCGGGGCGACAGC 69

Db 4 LysAlaProSerValPheProLeuAlaProCysGlyAspThrProSerSerThrVal 23

Qy 70 GCCCTGGCTCGCTGGTCAAGACTACTTCCCGAACCGGTGACGGTGTCTGGGAACCTCA 129

Db 24 ThrLeuGlyCysLeuValGlyGlyTyrLeuProGluProValThrValThrTrpAsnSer 43

Qy 130 GCGCGCTTCAGCAGCGGGTGCACACCTTCCCGGTCTCTACAGTCTCTCAGGACTCTAC 189

Db 44 GlyThrLeuThrAsnGlyValArgThrPheProSerValArgGlnSerSerGlyLeuTyr 63

Qy 190 TCCCTCAGCAGCGTGGTACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTTACATCTGC 249

Db 64 SerLeuSerSerValValSerValThrSerSerSer-----GlnProValThrCys 80

Qy 250 AACGTGATCACAAGCCAGCCAGCACCAAGTGGAGCAAGAAGTTGAGCCCAATCTTGT 309

Db 81 AsnValAlaHisProAlaThrAsnThrLysValAspLysThrValAlaProSerThrCys 100

Qy 310 GACAAACTACACATGCCACCGTCCAGCACCTGAACTCGCGGGCGCACCGTCACTC 369

Db 101 SerLys-----ProThrCysProProGluLeuLeuGlyGlyProSerVal 116

Qy 370 TTCCTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 429

Db 117 PheIlePheProProLysPheProLysAspThrLeuMetIleSerArgThrProGluValThr 136

Qy 430 TCGCTGGTGGTGGAGCTGAGCCACCAAGACCTGAGTCAAGTTCACTGTGACTGGAC 489

Db 137 CysValValValAspValSerGlnAspAspProGluValGlnPheThrTrpTyrIleAsn 156

Qy 490 GCGGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGGAGGACGACTACACAGCAGCTAC 549

Db 157 AsnGluInValArgThrAlaArgProProLeuArgGluGlnInPheAsnSerThrIle 176

Qy 550 CGTGTGGTCAGCGTCTCACCCTCTGCACCCAGGACTGGCTGAATGGCAAGGAGTACAAG 609

Db 177 ArgValValSerThrLeuProIleThrHisGlnAspTrpLeuArgGlyLysGluPheLys 196

Qy 610 TGCAGGTCTCCACAAAGCCCTCCACGCCCTCCAGCCCTCGAGAAACCATCTCCAAAGCCAAA 669

Db 197 CysLysValHisAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaArg 216

Qy 670 GCGAGCCCGGAGAACACAGGTGTACACCTCTGCCCTCCATCCCGGATGAGCTGACCAAG 729

Db 217 GlyGlnProLeuGluProLysValTyrThrMetGlyProProArgGluLeuSerSer 236

Qy 730 AACAGGTGAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGGACATCCCGCTGGAG 789

Db 237 ArgSerValSerLeuThrCysMetIleAsnGlyPheTyrProSerAspIleSerValGlu 256

Qy 790 TGGGAGACCAATGGCAGCGGAGAACCACTACAGACCAAGCGCTCCCGTGTGAGCTCC 849

Db 257 TrpGluLysAsnGlyLysAlaGluAspAsnTyrLysThrProAlaValLeuAspSer 276

Qy 850 GACGCTCTTCTCTCTCAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 909

Db 277 AspGlySerTyrPheLeuTyrAsnLysLeuSerValProThrSerGluTyrGlnArgGly 296

Qy 910 AACGTCTTCTCATGCTCCGTGATGATGAGCTCTTGCAACACCATACACGAGAGAGC 969

Db 297 AspValPheThrCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSer 316

Qy 970 CTCTCCCTGCTCTCCGGTAAA 990

Db 317 IleSerArgSerProGlyLys 323

#### RESULT 14

G2GP

Ig gamma-2 chain C region - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004

C;Accession: A94553; A90352; A90359; A90384; A90385; A02151

R;Trischmann, T.M.

submitted to the Atlas, April 1975

A;Reference number: A94553

A;Accession: A94553

A;Molecule type: protein

A;Residues: 1-3 <TRI>

A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E

R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.

Biochemistry 10, 18-25, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Ami

A;Reference number: A90352; MUID:71058471; PMID:5538606

A;Accession: A90352

A;Molecule type: protein

A;Residues: 4-68 <BIR>

A;Cross-references: UNIPARC:UPI000017379F

R;Turner, K.J.; Cebra, J.J.

Biochemistry 10, 9-17, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir

A;Reference number: A90359; MUID:71058486; PMID:5538616

A;Accession: A90359

A;Molecule type: protein

A;Residues: 69-133;312-329 <TUR>

A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1

R;Tracey, D.E.; Cebra, J.J.

Biochemistry 13, 4796-4803, 1974

A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90384; MUID:75036072; PMID:4429665

A;Accession: A90384

A;Molecule type: protein

A;Residues: 134-226 <TRA>

A;Cross-references: UNIPARC:UPI00001737A2

R;Trischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974

A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90385; MUID:75036073; PMID:4609467

A;Accession: A90385







[illegible]

Search completed: January 28, 2006, 08:46:04  
Job time : 34.0045 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 ; Search time 151.869 Seconds  
(without alignments)  
9198.340 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797  
Sequence: 1 gctccaccagggcccatc.....tctccctgtctccgggtaaa 990

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool.p/US10733563/runat.27012006.180005.4782/app.query.fasta.1.2716  
-DB=uniprot -QFWT=fastan -SUPPIX=n2p.rup -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CGN 1 1 632 @runat.27012006.180005.4782 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 05.80.\*

1: uniprot.spot.\*

2: uniprot.trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1756	97.7	465	2 Q6GMX6 HUMAN	Q6gmxf4 homo sapien
2	1756	97.7	469	2 Q569F4 HUMAN	Q569f4 homo sapien
3	1756	97.7	469	2 Q727P5 HUMAN	Q727p5 homo sapien
4	1756	97.7	475	2 Q5EF85 HUMAN	Q5ef85 homo sapien
5	1756	97.7	475	2 Q6GMW7 HUMAN	Q6gmw7 homo sapien
6	1756	97.7	476	2 Q6GMX1 HUMAN	Q6gmxf1 homo sapien
7	1753	97.6	472	2 Q5N089 HUMAN	Q5n089 homo sapien
8	1752	97.5	473	2 Q6P055 HUMAN	Q6p055 homo sapien
9	1752	97.5	475	2 Q6MZQ6 HUMAN	Q6mzq6 homo sapien
10	1752	97.5	480	2 Q6N094 HUMAN	Q6n094 homo sapien
11	1752	97.5	481	2 Q6N097 HUMAN	Q6n097 homo sapien
12	1751	97.4	330	1 IGHG1 HUMAN	P01857 homo sapien
13	1751	97.4	470	2 Q725W1 HUMAN	Q725w1 homo sapien
14	1751	97.4	470	2 Q6PJ44 HUMAN	Q6pj44 homo sapien
15	1748	97.3	466	2 Q6IN78 HUMAN	Q6in78 homo sapien
16	1747	97.2	348	2 Q6PYX1 HUMAN	Q6pyx1 homo sapien

#### ALIGNMENTS

RESULT 1

Q6GMX6 HUMAN  
 ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.  
 AC Q6GMX6;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;

17 1747 97.2 480 2 Q6PJF1 HUMAN Q6pjf1 homo sapien  
 18 1747 97.2 482 2 Q72351 HUMAN Q72351 homo sapien  
 19 1745 97.1 475 2 Q6N095 HUMAN Q6n095 homo sapien  
 20 1745 97.1 544 2 Q6PJ95 HUMAN Q6pj95 homo sapien  
 21 1744 97.1 466 2 Q6N096 HUMAN Q6n096 homo sapien  
 22 1742 96.9 478 2 Q6P181 HUMAN Q6p181 homo sapien  
 23 1737 96.7 473 2 Q6MZV7 HUMAN Q6mzv7 homo sapien  
 24 1687 93.9 475 2 Q5RE17 PONPY Q5rez17 pongo pygma  
 25 1619.5 90.1 519 2 Q5EBM2 HUMAN Q5ebm2 homo sapien  
 26 1615.5 89.9 521 2 Q8N4Y9 HUMAN Q8n4y9 homo sapien  
 27 1614.5 89.8 518 2 Q6N030 HUMAN Q6n030 homo sapien  
 28 1608 89.5 517 2 Q6N093 HUMAN Q6n093 homo sapien  
 29 1604.5 89.3 509 2 Q6NF17 HUMAN Q6nf17 homo sapien  
 30 1603 89.2 326 1 IGHG2 HUMAN P01859 homo sapien  
 31 1603 89.2 465 2 Q6P6C4 HUMAN Q6p6c4 homo sapien  
 32 1593 88.6 464 2 Q6MZU6 HUMAN Q6mzu6 homo sapien  
 33 1589 88.4 470 2 Q68CN4 HUMAN Q68cn4 homo sapien  
 34 1579.5 87.9 327 1 IGHG4 HUMAN P01861 homo sapien  
 35 1579.5 87.9 473 2 Q6TC63 HUMAN Q6tc63 homo sapien  
 36 1570.5 87.4 476 2 Q6MZX7 HUMAN Q6mzx7 homo sapien  
 37 1508.5 83.9 354 2 Q86TT2 HUMAN Q86tt2 homo sapien  
 38 1255.5 69.9 337 2 Q95M34 HORSE Q95m34 equus caball  
 39 1253 69.7 679 2 Q6P08 HUMAN Q6p08 homo sapien  
 40 1237.5 68.9 487 2 Q85ZL2 9MURI Q85zl2 mus sp. fv/  
 41 1219.5 67.9 323 1 GC RABIT P01870 oryctolagus  
 42 1201.5 66.9 329 1 IGHG2 CAVPO P01862 cavia porce  
 43 1157 64.4 463 2 Q99LC4 MOUSE Q99lc4 mus musculu  
 44 1154 64.2 465 2 Q510J0 RAT Q510j0 rattus norv  
 45 1154 64.2 467 2 Q4VBH1 RAT Q4vbh1 rattus norv

RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766.1; -, mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00407; IGV; 3.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

## Alignment Scores:

Pred. No.: 9,45e-110 Length: 465  
 Score: 1756.00 Matches: 328  
 Percent Similarity: 99.39% Conservative: 0  
 Best Local Similarity: 99.39% Mismatches: 2  
 Query Match: 97.72% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x Q6GMK6\_HUMAN (1-465)

Qy 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCTCTCTCAAGAGCACCTCTGGG 60  
 Db 136 AlaserThryLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 155  
 Qy 61 GGCACAGCGCGCTGGGTGCTGTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTG 120  
 Db 156 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 175  
 Qy 121 TGGAACTCAGCGCGCTGACAGCGGGGTGCACACCTTCCCGGTGCTCAGTCACTCA 180  
 Db 176 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 195  
 Qy 181 GGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240  
 Db 196 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 215  
 Qy 241 TACATCTGCAACGTGAATCACAGCCCGACCAACCAAGGTGGAGCAAGAAAGTTGAGCCC 300  
 Db 216 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 235  
 Qy 301 AAATCTGTGTGACAAACTCACACATGCCCGTCCCGCCAGCAGCTGAACCTCGCGGGGCA 360  
 Db 236 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 255  
 Qy 361 CCGTCAGTCTTCTCTCTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420  
 Db 256 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 275  
 Qy 421 GAGTGCATCATCGTGTGGTGGAGCTGAGCCACGACCAAGACCTGAGGTCAAGTTCACTGG 480  
 Db 276 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 295  
 Qy 481 TACGTGACGCGGTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540  
 Db 296 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 315  
 Qy 541 AGCAGCTACCGTGTGGTGGAGTCTCTCCCGTCTCGACCCAGGAGTGGCTGAATGGCAAG 600  
 Db 316 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 335  
 Qy 601 GAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCC 660  
 Db 336 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 355  
 Qy 661 AAAGCCAAAGGGGCGCCCGGAGAACCAACAGGTGTGTACACCTGTGCCCCCATCTCCGGGATGAG 720

Db 356 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 375  
 Qy 721 CTGACCAAGAACCAAGGTGAGCTGACCTGACCTGCTCAAGGCTTCTATCCAGCGACATC 780  
 Db 376 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 395  
 Qy 781 GCCGTGAGTGGGAGAGCAATGGCCAGCGGAGAGAACTACAGACCAACGCTCCCGTG 840  
 Db 396 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProVal 415  
 Qy 841 CTGACTCCGACGCGCTCTCTCTCTTACAGCAAGCTCACCGTGGCAAGCAGAGGTGG 900  
 Db 416 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 435  
 Qy 901 CAGCAGGGGAACTGCTTCTCATGCTCGTATGATGATGAGGTCTGCACCAACTACACG 960  
 Db 436 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 455  
 Qy 961 CAGAAGAGCCT 990  
 Db 456 GlnLysSerLeuSerLeuSerProGlyLys 465  
 RESULT 2  
 Q569F4\_HUMAN  
 ID Q569F4\_HUMAN PRELIMINARY; PRT; 469 AA.  
 AC Q569F4;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE IGHG1 protein.  
 GN Name=IGHG1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klaubner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.B.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph;  
 RG NIH MGC Project;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC092518; AAH92518.1; -, mRNA.  
 SQ SEQUENCE 469 AA; 51254 MW; AC13448B3047784F CRC64;

Alignment Scores:  
 Pred. No.: 9,46e-110 Length: 469  
 Score: 1756.00 Matches: 328  
 Percent Similarity: 99.39% Conservative: 0

Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x Q569P4\_HUMAN (1-469)

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QY 1 GCCTCCACAGGGCCCATCGTCTTCCCTGGGACCTCTCTCCAGAGACCTCTCTGGG 60
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Db 140 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSergly 159
   |||

QY 61 GGCACAGCGGCGCTCGCTGCTCAAGGACTACTTCCCGACCGGTGACGGTGTGCG 120
   |||
Db 160 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 179
   |||

QY 121 TGGAACTCAGGCGCCTTGACACAGCGCGCTGCACACCTTCCCGGCTGTCTACAGTCTCA 180
   |||
Db 180 TrpAsnSerGlyAlaLeuThrSerglyValHisThrPheProAlaValLeuGlnSerSer 199
   |||

QY 181 GGACTCTACTCCTCAGCAGGTGTGTGACGTCCTCCCTCCAGCAGCTTGGGACCCAGACC 240
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Db 200 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 219
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QY 241 TACATCTCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGGCAAGAAAGTTGAGGCC 300
   |||
Db 220 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 239
   |||

QY 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCCGACGACCTGAACCTCGCGGGGCA 360
   |||
Db 240 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 259
   |||

QY 361 CCGTCAGTCTTCTTCTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
   |||
Db 260 ProSerValPheLeuPheProProlsProLysAspThrLeuMetIleSerArgThrPro 279
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QY 421 GAGTTCATCGTGGTGGAGCTGACGACGACGACGACGACGACGACGACGACGACGACG 480
   |||
Db 280 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 299
   |||

QY 481 TACGTGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540
   |||
Db 300 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 319
   |||

QY 541 AGCAGTACCGTGGTGGAGCTCTCACCGTCTCTGACACGAGGAGTGGCTGAATGGCAAG 600
   |||
Db 320 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 339
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QY 601 GAGTACAGTCCAGGCTCTCCACAAAGCCCTCCCGACGCCCCCATCGAGAAACCATCTCC 660
   |||
Db 340 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 359
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QY 661 AAAGCCAAAGCGCAGCCCGGAGAACACACAGGTGTACACCTGCGCCCATCCCGGATCAG 720
   |||
Db 360 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 379
   |||

QY 721 CTGACCAAGAACCGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
   |||
Db 380 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 399
   |||

QY 781 GCGTGGAGTGGGAGCAATGGCGGCGGAGACCACTACAGACCAACGACCTCCCGTGG 840
   |||
Db 400 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 419
   |||

QY 841 CTGGAAGTCCGAGCGGCTCTCTTCTCTCTACAGAGCTCACGCTGACAGCAGGAGTGG 900
   |||
Db 420 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 439
   |||

QY 901 CAGCAGGGGAACGCTTCTCTCATGCTTCCGTGATGATGAGGCTCTGACACCACTACACG 960
   |||
Db 440 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 459
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QY 961 CAGAAGAGCCTCTCCCTGCTCCCGGTAAA 990
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Db 460 GlnLysSerLeuSerLeuSerProGlyLys 469
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## RESULT 3

Q727P5\_HUMAN PRELIMINARY; PRT; 469 AA.

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AC Q727P5;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHL1 protein.
GN Name=IGHL1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettner M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
EN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAHS1328.1; -, mRNA.
DR HSSP; P01857; 1LZH.
DR SMR; Q727P5; 20-469.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
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## Alignment Scores:

Pred. No.:	9.46e-110	Length:	469
Score:	1756.00	Matches:	328
Percent Similarity:	99.39%	Conservative:	0
Best Local Similarity:	99.39%	Mismatches:	2
Query Match:	97.72%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-111 (1-990) x Q727P5\_HUMAN (1-469)

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QY 1 GCCTCCACAGGGCCCATCGTCTTCCCTGGGACCTCTCTCCAGAGACCTCTCTGGG 60
   |||
Db 140 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSergly 159
   |||

QY 61 GGCACAGCGGCGCTCGCTGCTCAAGGACTACTTCCCGACCGGTGACGGTGTGCG 120
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Db 160 GlyThrAlaAlaLeuGlyCysLeuVallyAspTyrPheProGluProValThrValSer 179  
Qy 121 TGSAACTCAGCGCGCTTCCAGCAGCGCGTGCACACCTTCCCGCTGTCTTACAGTCTCA 180  
Db 180 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 199  
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 200 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 219  
Qy 241 TACATCTGCAACGTAATCAACAAGCCCAAGCCCAAGTGGCAACAAGAAAGTTGAGCCC 300  
Db 220 TyrIleCysAenValAenHisLysProSerAenThrLysValAspLysValGluPro 239  
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCAGCTGAACTCGCGGGGCA 360  
Db 240 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 259  
Qy 361 CCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420  
Db 260 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 279  
Qy 421 GAGTTCACATCGTGTGTGAGTGCAGTGCAGCAGCAGCAGTGCAGTCAAGTTCACATGG 480  
Db 280 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 299  
Qy 481 TACGTGAGCGCGTGGAGTGCATAATGCCAAGCAAAAGCCCGGAGGAGCAGTACAAAC 540  
Db 300 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGlnTyrAen 319  
Qy 541 AGCAGTACCGTGTGTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 600  
Db 320 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAenGlyLys 339  
Qy 601 GAGTACAAAGTCAAGTCTCAACAAGCCCTCCAGCAGCCCGTCCAGCAGCAGCAGCAGTCC 660  
Db 340 GluTyrLysCysLysValSerAenLysAlaLeuProAlaProLleGluLysThrIleSer 359  
Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGTGTACACCTTCCCGCCATCCCGGATGAG 720  
Db 360 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 379  
Qy 721 CTGACCAAGAACCGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 780  
Db 380 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspile 399  
Qy 781 GCCGTGAGTGGGAGCAATGGGCGAGCGGAGCAACTACAAGACCACCGCTCCCGTG 840  
Db 400 AlaValGluTrpGluSerAenGlyGlnProGluAenAenTyrLysThrProProVal 419  
Qy 841 CTGACTCCGAGCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
Db 420 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 439  
Qy 901 CAGCAGGGGAACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960  
Db 440 GlnGlnGlyAenValPheSerCysSerValMetHisGluAlaLeuHisAenHisTyrThr 459  
Qy 961 CAGAAGAGCCCTCTCCCTGTCTCCGGTAAA 990  
Db 460 GlnLysSerLeuSerLeuSerProGlyLys 469

## RESULT 4

QSEFE5\_HUMAN  
ID QSEFE5\_HUMAN PRELIMINARY; PRT; 475 AA.  
AC QSEFE5;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE Anti-RHD monoclonal T125 gamma1 heavy chain precursor.  
OS Homo sapiens (Human).  
QC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Gaucher C., Klein P., Belliard R.;  
RT "Sequence determination of the recombinant human anti-RHD monoclonal  
antibody T125.";  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY894992; AAW82028.1; -, mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Signal.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 475 anti-RHD monoclonal T125 gamma1 heavy  
FT chain.  
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;  
Alignment Scores:  
Pred. No.: 9,48e-110 Length: 475  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-111 (1-990) x QSEFE5\_HUMAN (1-475)

Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCCCTGCGACCTCTCTCAAGAGACCTCTGGG 60  
Db 146 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 165  
Qy 61 GGCACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
Db 166 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185  
Qy 121 TGGAACTCAGCGCGCTGACAGCGCGGTGCACACCTTCCCGCTGTCTTACAGTCTCTCA 180  
Db 186 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205  
Qy 181 GGACTCTACTCTCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 206 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225  
Qy 241 TACATCTGCAACGTAATCAACAAGCCCAAGCCCAAGTGGCAACAAGAAAGTTGAGCCC 300  
Db 226 TyrIleCysAenValAenHisLysProSerAenThrLysValAspLysValGluPro 245  
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCAGCTGAACTCGCGGGGCA 360  
Db 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 265  
Qy 361 CCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420  
Db 266 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 285  
Qy 421 GAGTTCACATCGTGTGTGAGTGCAGTGCAGCAGCAGCAGTGCAGTCAAGTTCACATGG 480  
Db 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 305  
Qy 481 TACGTGAGCGCGTGGAGTGCATAATGCCAAGCAAAAGCCCGGAGGAGCAGTACAAAC 540  
Db 306 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGlnTyrAen 325







Qy	841	CTGAGACTCCGACGGCTCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG	900
Db	427	LeuAepSerAepGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp	446
Qy	901	CAGCAGGGGAAAGCTCTTCTCATGCTCCGCTGATGTCATGAGGCTCTGCACAAACCACTACACG	960
Db	447	GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisGlnHisTyrThr	466
Qy	961	CAGAAGAGCCTCTCCCTCTCTCCGGGTAAA	990
Db	467	GlnLysSerLeuSerLeuSerProGlyLys	476
RESULT 7			
Q6N089_HUMAN			
ID	Q6N089	HUMAN PRELIMINARY;	PRT; 472 AA.
AC	Q6N089;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Hypothetical protein DKFP686F15220.		
GN	Name=DKFP686F15220;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Rectum tumor;		
RG	The German cDNA Consortium;		
RA	Wamburt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,		
RA	Fobo G., Han M., Wiemann S.;		
RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX640627; CAE45781.1; -; mRNA.		
DR	HSSP; P01861; 1ADQ.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG_CL.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF07654; C1-set; 3.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGc1; 3.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS08835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;		
Alignment Scores:			
Pred. No.:		1.51e-109	Length: 472
Score:		1753.00	Matches: 327
Percent Similarity:		99.39%	Conservative: 1
Best Local Similarity:		99.09%	Mismatches: 2
Query Match:		97.55%	Indels: 0
DB:		2	Gaps: 0
US-10-733-563-111 (1-990) x Q6N089_HUMAN (1-472)			
Qy	1	GCCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCCCTCTCTCCAGAGCACCTCTGGG	60
Db	143	AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly	162
Qy	61	GGCACAGCGGCCCTGGGGCTGGCTGGTGTCAAGACTACTTCCCGCAACCGGTGACGGTGTG	120
Db	163	GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer	182
Qy	121	TGGAACTCAGCGCCCTGCACAGCGCGGTGCACACCTTCCCGGCTGTCTCAGTCCCTCA	180
Db	183	TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer	202
Qy	181	GGACTCTACTCCCTCAGCAGCGGTGGTGTGACCGGTGCCCTCCAGCAGCTTGGGCACCCAGACC	240

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E.,  
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Marra M.A.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2].  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RA Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC065820; AAH65820.1; -, mRNA.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PP07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

## Alignment Scores:

Pred. No.: 1.76e-109 Length: 473  
 Score: 1752.00 Matches: 327  
 Percent Similarity: 99.09% Conservatives: 0  
 Best Local Similarity: 99.09% Mismatches: 3  
 Query Match: 97.50% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x Q6P055\_HUMAN (1-473)

Qy 1 GCCTCCACCAAGGGCCGTCGGTCTTCCCTGGCACCTCTCCAGAGCACCTCTGGG 60  
 Db 144 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 163  
 Qy 61 GGCACAGCGCCCTGGGCTGCTGTCAGAGCACTTCCCGGACCGGTGACGGTGTGCG 120  
 Db 164 GlyThrAlaAlaLeuGlyCysLeuValLysAspThrPheProGluProValThrValSer 183  
 Qy 121 TGGAACTCAGCGCCCTGACAGCGGCGTGCACACCTTCCCGGCTGCTCAGTCTCTCA 180  
 Db 184 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 203  
 Qy 181 GGACTCTACTCTCAGCAGCGTGTGACCGTGGCTCCAGAGCTTGGGACCCAGACC 240  
 Db 204 GlyLeuThrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 223  
 Qy 241 TACATCTGCAACGTGAATCACAGCCAGCACACCGAGGTGGACAGAAAGTTGAGCCC 300  
 Db 224 TyrIleCysAsnValAsnHisGlyProSerAsnThrLysValAspLysValGluPro 243  
 Qy 301 AAATCTTTGTGACAAACTCACACATGCCACCGTCCAGACCTGAACTCGCGGGGCA 360  
 Db 244 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 263

Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCAGAGCACCTCTATGATCTCCCGGACCCCT 420  
 Db 264 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 283  
 Qy 421 GAGGTCACTGCGTGGTGGAGCTGAGCCACCAAGACCTCGAGGTCAAGTTCACATGG 480  
 Db 284 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 303  
 Qy 481 TACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA 540  
 Db 304 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 323  
 Qy 541 AGCAGTACCGTGTGGTTCAGGTCTCTCCGTCTCGACACGAGTGGTGTGAATGGCAG 600  
 Db 324 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 343  
 Qy 601 GAGTACAGTGCAGAGGTCTCCAAACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCC 660  
 Db 344 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 363  
 Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTTCCCGCCCTCCCGGATGAG 720  
 Db 364 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 383  
 Qy 721 CTGACCAAGAACAGGTTCAGCTGACCTGCTGGTCAAGAGCTTCTATCCAGGACATC 780  
 Db 384 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 403  
 Qy 781 GCCGTGAGTGGGAGAGCAATGGGACGCGAGAACAACTACAGACCCAGCCCTCCCGTG 840  
 Db 404 AlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProProVal 423  
 Qy 841 CTGACTCTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 900  
 Db 424 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 443  
 Qy 901 CAGCAGGGGAACTCTTCTCATGCTCCGTGATGATGAGGTCTGCGACACCATACACG 960  
 Db 444 GlnGlnGlyAsnValPheSerCysSerValMetHisGluGlyLeuHisAsnHisTyrThr 463  
 Qy 961 CAGAAGAGCTCTCCCTGTCTCCGGGTAAA 990  
 Db 464 GlnLysSerLeuSerLeuSerProGlyLys 473  
 RESULT 9  
 Q6MZQ6 HUMAN  
 ID Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.  
 AC Q6MZQ6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFP686G11190.  
 GN Name=DKFP686G11190;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Esophagus tumor;  
 RA The German cDNA Consortium;  
 RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
 RA Han M., Wiemann S.;  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640947; CAE45972.1; -, mRNA.  
 DR HSSP; P01861; IADQ.  
 DR SMR; Q6MZQ6; 20-475.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.

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DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52043 MW; B7BAE255A26F4B8E CRC64;  
  
Alignment Scores:  
Pred. No.: 1.76e-109 Length: 475  
Score: 1752.00 Matches: 327  
Percent Similarity: 99.09% Conservative: 0  
Best Local Similarity: 99.09% Mismatches: 3  
Query Match: 97.50% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-733-563-111 (1-990) x Q6MZQ6_HUMAN (1-475)  
  
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DB 146 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 165  
  
QY 61 GGCACAGCGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGTGCG 120  
DB 166 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185  
  
QY 121 TGGAACTCAGGCGCCTGACACAGCGGCTGCACACCTTCCCGGCTGCTCAGTCTCTCA 180  
DB 186 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205  
  
QY 181 GGACTCTACTCCCTCAGCAGCGTGTGTGACCGTCCCTCAGCAGCTTCGGCACCAGACC 240  
DB 206 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225  
  
QY 241 TACATCTCAACGTGAATCACAAAGCCCAAGCAACCAAGGTGGACAAAGAAATTTGAGCCC 300  
DB 226 TyrIleCysAsnValAsnHisLysProSerAenThrLysValAspLysValGluPro 245  
  
QY 301 AAATCTGTGCAAAACTCACATGCCCGGTCGCCAGCACCTGAACCTCGCGGGGCA 360  
DB 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly 265  
  
QY 361 CCCTCAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
DB 266 ProSerValPheLeuPheProProlsProLysAspThrLeuMetIleSerArgThrPro 285  
  
QY 421 GAGTTCACATCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGG 480  
DB 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 305  
  
QY 481 TACGTGAGCGGTGGAGGTGCATATCCAAAGACAAAGCCGCGGGAGGACAGTACAAAC 540  
DB 306 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 325  
  
QY 541 AGCAGTACCGTGGTGGTGGTCTCTCCCGTCCCTGACACGAGGACTGCTCAATGGCAAG 600  
DB 326 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 345  
  
QY 601 GAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCGCCCGCATCGAGAAACCATCTCC 660  
DB 346 GluTyrLysCysValValSerAsnLysAlaLeuProAlaProLleGluYThrIleSer 365  
  
QY 661 AAAGCCAAAGGCGCCCGGAGAACCAAGGTGTACACCTTGGCCCCCGCATCCCGGATGAG 720  
DB 366 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 385  
  
QY 721 CTGACCAAGAACCGAGTTCAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780  
DB 386 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 405  
  
QY 781 CCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACAACTACAAGACCCAGCCCTCCCGTG 840  
  
Db 406 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAenTyrLysThrProProVal 425  
QY 841 CTGGACTCCGAGCGGCTCTTCTCTCTTACAGCAAGCTCACCCTGGACAGCGAGGTGG 900  
Db 426 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 445  
QY 901 CAGCAGGGGAACGTCTTCTCATGTCCGTGATGATGAGGTCTGCACACCAACCACTACACG 960  
Db 446 GlnGlnGlyAsnValPheSerCysSerValMetHisGluGlyLeuHisAsnHisTyrThr 465  
QY 961 CAGAAGAGCCTCTCCCTGCTCCCGGTAAA 990  
Db 466 GlnLysSerLeuSerLeuSerProGlyLys 475  
  
RESULT 10  
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ID Q6N094_HUMAN PRELIMINARY; PRT; 480 AA.  
AC Q6N094;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFP686001196.  
GN Name=DKFP686001196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RG The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640622; CAB45776.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.CI.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig.V.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.76e-109 Length: 480  
Score: 1752.00 Matches: 327  
Percent Similarity: 99.09% Conservative: 0  
Best Local Similarity: 99.09% Mismatches: 3  
Query Match: 97.50% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-733-563-111 (1-990) x Q6N094_HUMAN (1-480)  
  
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACCCTCTCTCCAAAGACACCTCTGGG 60  
Db 151 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 170  
  
QY 61 GGCACAGCGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGTGCG 120  
Db 171 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 190  
  
QY 121 TGGAACTCAGGCGCCTGACACAGCGGCTGCACACCTTCCCGGCTGCTCAGTCTCTCA 180  
Db 191 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 210
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Qy	181	GGACTCTACTCTCCTCCAGCAGCGTGGTGGACCGTGCCCTCCAGCAGCTTGGGACCCAGACC	240
Db	211	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	230
Qy	241	TACATCTCAACGCTGAATCAACAAGCCAGCAGCAACCAAGGTGGACAAGAAAGTTCGAGCCC	300
Db	231	TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro	250
Qy	301	AAATCTTGTCAGAAATCTACACATGCCACCGTGCCAGACACTGAACCTCCGGGGGCA	360
Db	251	LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly	270
Qy	361	CCGTCAAGTCTCTCTCTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT	420
Db	271	ProSerValPheLeuPheProProlysProlysAspThrLeuMetIleSerArgThrPro	290
Qy	421	GAGTTCACATCGCTGGTGGACGTGAGCCACGAAAGACCTTGAGGTCAAGTTCAACTGG	480
Db	291	GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp	310
Qy	481	TACGTGGAGCGCTGGAGGTGCATAATCCAAAGACAAAGCCGCGGAGGAGCAGGTACAAAC	540
Db	311	TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn	330
Qy	541	AGCAGTACCGTGGTGGTCCAGCGTCTCTCACCGTCTCGCACAGGACTGGCTGAATGGCAAG	600
Db	331	SerThrTyrArgValValIserValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	350
Qy	601	GAGTACAGTCCAGGCTCTCAACAAGCCCTCCAGCGCCCTCATCGAAGAACCACTCC	660
Db	351	GluTyrLysCysLysValIserAsnLysAlaLeuProAlaProIleGluLysThrIleSer	370
Qy	661	AAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAG	720
Db	371	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu	390
Qy	721	CTGACCAAGAACCGAGTCCAGCTGACCTGCTGGTCAAAAGGTTCTATCCAGCGACATC	780
Db	391	LeuThrLysAsnGlnValIserLeuThrCysLeuValLysGlyPheTyrProSerAspIle	410
Qy	781	GCCGTGGAGTGGGAGAGCAATGGGAGCGGAGAGAACAACTACAAGACACAGCTCCCGTG	840
Db	411	AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal	430
Qy	841	CTGACTCCGAGCGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGG	900
Db	431	LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp	450
Qy	901	CAGCAGGGGAACGCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACACG	960
Db	451	GlnGlnGlyAsnValPheSerCysSerValMetHisGluGlyLeuHisAsnHisTyrThr	470
Qy	961	CAGAAGAGCCTCTCCCTCTCTCCCGGGTAAA	990
Db	471	GlnLysSerLeuSerLeuSerProGlyLys	480

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DT	03-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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OS	Homo sapiens (Human).
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OC	Homo.
OX	NCBII_TaxID=9606;
OX	(1)
RN	NUCLEOTIDE SEQUENCE.
RP	

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RC      TISSUE=Esophagus tumor;
RA      The German cDNA Consortium;
RG      Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA      Fobo G., Han M., Wiemann S.;
RL      Submitted (JAN-2005) to the EMBL/GenBank/DBDJ databases.
DR      EMBL; BX640619; CAE45773.1; -, mRNA.
DR      HSSP; P01861; IADQ.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG_c1.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF07654; C1-set; 3.
DR      SMART; SM00409; IG; 2.
DR      SMART; SM00407; IGc1; 3.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS00835; IG LIKE; 4.
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KW      Hypothetical protein_KW
SQ      SEQUENCE      481 AA; 52759 MW; 47220D9B64BDF98B CRC64;

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US-10-733-563-111 (1-990) x Q6N097 HUMAN (1-481)

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Qy	61	G	S	C	A	G	C	G	G	C	C	T	G	G	T	G	C	T	G	T	C	G	T	C	C	A	A	G	A	C	G	G	T	G	A	C	G	G	T	G	C	G	G	T	G	C	G	120							
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Qy	241	T	A	C	A	T	C	G	A	C	G	T	G	A	A	T	C	A	C	A	A	C	C	C	C	A	C	A	C	C	A	C	C	A	C	A	C	A	C	A	C	A	A	A	A	T	T	G	A	C	C	300			
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Db 392 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 411  
QY 781 GCCGTGGAGTGGAGCAATCGGCAGCGCGAGAGCACTACAGCACCGCCTCCCGTG 840  
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DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
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GN Name=IGHG1;  
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
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RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP PROTEIN SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino  
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Fomstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic  
RT peptides of the H-chain, alignment of the tryptic peptides and  
RT discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1504 (1976).  
RN [5]  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.

RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary  
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein NIE), I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -I- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
CC GIM(1) marker, 239-D and 241-L. KOL and EU sequences have the  
CC GIM(3) marker and the GIM (non-1) markers.  
CC -I- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -I- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -I- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
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DR PDB; 1D5I; X-ray; H=1-101.  
DR PDB; 1D6V; X-ray; H=1-101.  
DR PDB; 1DN2; X-ray; A/B=120-326.  
DR PDB; 1E4K; X-ray; A/B=106-330.  
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DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
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Pfam; PF07654; CI-set; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
3D-structure; Direct protein sequencing; Glycoprotein;
Immunoglobulin C region; Immunoglobulin domain.
REGION 1 98
REGION 99 110
REGION 111 223
REGION 224 330
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HELIIX 130 134
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QY 301 AAATCTTGTGACAAAACCTCACATGCCACCCACCGTGCAGCAGCTGAAGCTGCGGGGCGCA 360
Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 120
QY 361 CCGTCAGTCTCTCTCTTCCCGCCCAAAACCAAGACACACCTCATGATCTCCCGACCCCT 420
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Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180
QY 541 AGCAGGTACCGTGGTGGTCCAGCGTCCCTCAGCAGCTGTCACCGAGGACTGGCTGAATGGCAAG 600
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Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220
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Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260
QY 781 GCCGTGGAGTGGAGAGCAATGGGCAGCCGAGAGCAACCACTACAGACCAAGCCCTCCCGTG 840
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 280
QY 841 CTGACTCCGACCGGCTCTCTCTCTTCTCTTACAGCAAGCTCACCGTGGAGCAGAGCAGGTGG 900
Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC NUCLEOTIDE SEQUENCE.
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAHS3984.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
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 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
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 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Bartholomew J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH MGC Project;  
 RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018747; AAH18747.1; -, mRNA.  
 DR HSP; P01861; IADQ.  
 DR SMR; Q6PUA4; 20-470.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGc1; 3.  
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 Best Local Similarity: 99.39% Mismatches: 2  
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 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGHG1 protein.  
 GN Name=IGHG1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]



RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heltón E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green G.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2].

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC072419; AAH72419.1; -, mRNA.  
 DR HSPF; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig C1.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
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US-10-733-563-111 (1-990) x Q6IN78\_HUMAN (1-466)

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TOPOLOGY: linear  
US-08-457-918-7

Alignment Scores:

Pred. No.: 2,58-134 Length: 371  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-08-457-918-7 (1-371)

Qy 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACCCCTCTCTCCACGAGCACCTCTGGG 60  
Db 42 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 61  
Qy 61 GGCACAGGGCCCTGGGTCTGTCTCAAGACTACTTCCCGGACCGGTGACGGTGTGC 120  
Db 62 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 81  
Qy 121 TGGAACTCAGCGCCCTCACCAGGGCGTGCACACTTCCCGGTCTCTACAGTCCTCA 180  
Db 82 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 101  
Qy 181 GGACTCTACTCTCCAGCAGCGTGTGTGACCGTGGCCCTCCAGCAGCTTGGGCACCCAGC 240  
Db 102 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 121  
Qy 241 TACATCTGCAACGGTGAATCAGACGCCGAGCAACCAAGGTGGAGCAAGAAAGTTGAGCC 300  
Db 122 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 141  
Qy 301 AAATCTGTGACAAACTCAGACATGCCACCGTCCAGCACCTGAACCTCGCGGGCA 360  
Db 142 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 161  
Qy 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCAAGACACCTCATGATCTCCCGGACCCCT 420  
Db 162 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 181  
Qy 421 GAGTCAATCGTGGTGGAGCTGAGCCAGCAAGACCTCGAGGTCAAGTCAACTGG 480  
Db 182 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 201  
Qy 481 TACGTGACGGCGTGGAGTGCATAATGCCAGCAAGCCGCGGAGGACGACTACAC 540  
Db 202 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 221  
Qy 541 AGCAGTACCGTGTGGTCCAGCGTCTCACCCTCTGCACACGAGTGGCTGAATGGCAAG 600  
Db 222 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 241  
Qy 601 GAGTCAAGTCAAGGTCTCAACAAAGCCCTCCAGCCCGCCATCGAGAAAACCATCTCC 660  
Db 242 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 261  
Qy 661 AAAGCCAAAGGGCCCGGAGACCCAGCTGTACACCTGCCCTGCCCATCCCGGGATGAG 720  
Db 262 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 281  
Qy 721 CTGACCAAGAACCAAGTCCAGCTGACCTGCTGCTCAAGGCTTCTATCCCGAGGCATC 780  
Db 282 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 301  
Qy 781 GCCTGGAGTGGGAGCAATGGGAGCGGAGCAACAACTACAAGACCAACCGCTCCCGTG 840  
Db 302 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 321  
Qy 841 CTGCACTCCGAGCGGTCTCTTCTTCTTACAGCAAGCTCACCGTGGAGCAAGAGGTGG 900  
Db 322 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 341

Qy 901 CAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGATGAGGTCTGCACCAACCATACAG 960  
Db 342 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 361  
Qy 961 CAGAAGAGCTCTCTCCCTGTCTCCGGGTAAA 990  
Db 362 GlnLysSerLeuSerLeuSerProGlyLys 371  
RESULT 3  
US-10-157-408-7  
; Sequence 7, Application US/10157408  
; Patent No. 6710169  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/157,408  
; FILING DATE: 28-May-2002  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,918  
; FILING DATE: 1-JUN-1995  
; APPLICATION NUMBER: 08/236311  
; FILING DATE: 02-MAY-1994  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0444P1C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8228  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-157-408-7

Alignment Scores:  
Pred. No.: 2,58-134 Length: 371  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-10-157-408-7 (1-371)

Qy 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACCCCTCTCTCCAGAGCACCTCTGGG 60

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Db 42 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 61
Qy 61 GGCACAGGGCCCTGGCTGCTGGTCAAGAGCTACTTCCCGCAACCGGTGACGGTGTGCG 120
Db 62 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 81
Qy 121 TGGAACTCAGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTTACAGTCTCTCA 180
Db 82 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 101
Qy 181 GGACTCTACTCCCTCAGCAGCGTGGTACCGCTGCGCTCCAGCAGCTGGGCACCCAGACC 240
Db 102 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 121
Qy 241 TACATCTGCAACGTGAATCAACAGCCCAAGCAACCAAGGTGGAGCAAGAAAGTTGAGCCC 300
Db 122 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 141
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCTGACCTGCGGGGCA 360
Db 142 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 161
Qy 361 CCGTCAGTCTTCTCTTCCCGCAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 162 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 181
Qy 421 GAGTCACTGCGTGGTGGAGCTGAGCAGCAGCAGCTGAGTCAAGTCAAGTCACTGG 480
Db 182 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 201
Qy 481 TACGTGACCGCGTGGAGGTGCATAAGTCCAGACAAAGCCGCGGAGGAGCAGTACAC 540
Db 202 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTrpAsn 221
Qy 541 AGCAGTACCGTGTGGTGCAGCTGCTCACCGTCTCGCAGCAGGACTGGCTGAATGGCAAG 600
Db 222 SerThrThrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 241
Qy 601 GAGTCAAGTCAAGGTCTCCAAAGACCTCCCGCCCGCCATCGAGAAACCATCTCC 660
Db 242 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 261
Qy 661 AAGCCAAAGGAGCGCCGAGACCAAGTGTACACCTGCGCCCGCCATCCCGGATGAG 720
Db 262 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 281
Qy 721 CTGACCAAGAACCAAGTGCAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780
Db 282 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 301
Qy 781 GCGTGTGAGTGGGAGAGCAATGGCAGCGGAGAACCACTACAAGACACGCTCCCGTG 840
Db 302 AlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProProVal 321
Qy 841 CTGAGCTCCGACGCTCTCTTCTCTTCTACAGCAGCTCACCGTGGACAGAGAGTGG 900
Db 322 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 341
Qy 901 CAGCAGGGGAACGTCTTCTCATGTCCGTGATGATGAGGCTCTGCAACACCATACACG 960
Db 342 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 361
Qy 961 CAGAGAGCTCTCCCTGTCTCCGGGTAAA 990
Db 362 GlnLysSerLeuSerLeuSerProGlyLys 371
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## RESULT 4

US-08-458-516-13

; Sequence 13, Application US/08458516

; Patent No. 577085

; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung

```
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13
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## Alignment Scores:

Pred. No.:	2,646-134	Length:	449
Score:	1756.00	Matches:	328
Percent Similarity:	99.39%	Conservative:	0
Best Local Similarity:	99.39%	Mismatches:	2
Query Match:	97.72%	Indels:	0
DB:	1	Gaps:	0

US-10-733-563-111 (1-990) x US-08-458-516-13 (1-449)

Qy	1	GCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCTCTCCAGAGCAGCCTCTGGG	60
Db	120	AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly	139
Qy	61	GGCACAGCGCCCTGGGCTCGCTGGTCAAGCACTACTTCCCGCAACCGGTGACGGTGTGCG	120
Db	140	GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer	159
Qy	121	TGGAATCTCAGCGCCCTGACAGCGCGGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA	180
Db	160	TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer	179
Qy	181	GGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCCAGCAGCTTGGGCACCCAGACC	240
Db	180	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	199
Qy	241	TACATCTGCAACGTGAATCAACAGCCAGCAACCAAGGTGGACAAAGAAAGTTGAGCCC	300
Db	200	TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro	219
Qy	301	AAATCTTGTGACAAACTCACATGCCACCGTCCAGCAGCTGACCTGCGGGGCA	360
Db	220	LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly	239

QY 361 CGGTGAGTCTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCTCC 420  
DB 240 ProSerValPheLeuPheProProlysProLysAspThrLeuMetIleSerArgThrPro 259  
QY 421 GAGGTCAATGCTGCTGCTGAGTGCACGACGAGACCTGAGTCAAGTTCACCTGG 480  
DB 260 GluValThrCysValValValValValValValValValValValValValValVal 279  
QY 481 TACGTGGACGGCTGAGGTGCTAATGTCACAGACAAAGCCGCGGAGGAGCAGTACAC 540  
DB 280 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 299  
QY 541 AGCAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 300 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 319  
QY 601 GAGTCAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCTCC 660  
DB 320 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 339  
QY 661 AAAGCCAAAGGCGACGCCCGGAGAACACAGGTGTACACCTGCTGCTGCTGCTGCTGCT 720  
DB 340 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 359  
QY 721 CTGACCAAGAACAGGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
DB 360 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 379  
QY 781 GCCGTGGAGTGGAGCAATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
DB 380 AlaValGluTyrPglUserAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 399  
QY 841 CTGGAACCTCCGAGCT 900  
DB 400 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 419  
QY 901 CAGCAGGGAAGCT 960  
DB 420 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 439  
QY 961 CAGAGAGCT 990  
DB 440 GlnLysSerLeuSerLeuSerProGlyLys 449

## RESULT 5

US-08-030-175-41

; Sequence 41, Application US/08030175

; Patent No. 6767996

; GENERAL INFORMATION:

; APPLICANT: Gorman, Scott D.

; APPLICANT: Clark, Michael R.

; APPLICANT: Cobbold, Stephen P.

; APPLICANT: Waldmann, Herman

; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESS: Rothwell, Figg, Ernst &amp; Kurz, P. C.

; STREET: 555 13TH ST., NW Suite 701 East

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage

; COMPUTER: IBM AT compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2

; SOFTWARE: WordPerfect 5.0 (Dos Text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/030,175

; FILING DATE: 17-MAY-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB91/01578

; FILING DATE: 13-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ernst, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1768-113  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-030-175-41

Alignment Scores:  
Pred. No.: 2,68e-134 Length: 467  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-08-030-175-41 (1-467)

QY 1 GCCTCCACAAAGGGCCCATCGTCTTCCCTGGCACCTCTCTCCAAAGAGCACCTCTGGG 60  
DB 138 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157  
QY 61 GGCACAGCGCGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCCGGTGCAGGTGTCG 120  
DB 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177  
QY 121 TGGAACTCAGCGCGCTGACACAGCGGCGTGCACACCTTCCCGGCTGTCTCAGTCTCA 180  
DB 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
QY 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACCC 240  
DB 198 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 217  
QY 241 TACATCTGCAACGTGAATCACAAAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
DB 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 237  
QY 301 AAATCTGTGACAAACTCACACATGCCCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
DB 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 257  
QY 361 CCGTCAGTCTTCTCTCTTCCCTCCCAAAACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
DB 258 ProSerValPheLeuPheProProlysProLysAspThrLeuMetIleSerArgThrPro 277  
QY 421 GAGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 278 GluValThrCysValValValValValValValValValValValValValValVal 297  
QY 481 TACGTGGACGGCTGGAGGTGCATATGCCCAAGCAAAAGCCGCGGAGGAGGAGGAGTACAC 540  
DB 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317  
QY 541 AGCAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 318 SerThrTyrArgValValValValValValValValValValValValValValVal 337  
QY 601 GAGTCAAGTCAAGGTCTCCAAACAAAGCCCTCCAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
DB 338 GluTyrLysCysLysValValValValValValValValValValValValValVal 357  
QY 661 AAAGCCAAAGGCGACGCCCGGAGAACACAGGTGTACACCTTGGCCCCCCTCCCGGATGAG 720  
DB 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377





Sequence 10, Application US/08378939  
Patent No. 5876961

## GENERAL INFORMATION:

APPLICANT: CROME, JAMES SCOTT  
APPLICANT: LEWIS, ALAN PETER  
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESS: ROTHWELL, FIGG, ERNST & KURZ  
STREET: 555 THIRTEENTH ST. N.W.  
CITY: WASHINGTON  
STATE: D. C.  
COUNTRY: U.S.  
ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,939  
FILING DATE:

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 476 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-378-939-10

## Alignment Scores:

Pred. No.: 2,69e-134 Length: 476  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 1 Gaps: 0

US-10-733-563-111 (1-990) x US-08-378-939-10 (1-476)

Qy 1 GCCTCCACCAAGGCGCCATCGTCTTCCCTGGCACCCTCTCCACAGCAGCCTCTGGG 60  
Db 147 AlaserThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 166  
Qy 61 GGCACAGCGCCCTGGGCTGGTGTCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTG 120  
Db 167 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 186  
Qy 121 TGGAACTCAGGCGCCCTGACACAGCGGCGGTGACACCTTCCCGGCTGTCTCAGTCTCA 180  
Db 187 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 206  
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTGGGACCCAGACC 240  
Db 207 GlyLeuThrSerLeuSerValValThrValProSerSerLeuGlyThrGlnThr 226  
Qy 241 TACATCTGCAACGTGAATCACAAAGCCCAAGCAGCAGGTTGGACAGCAAGAAAGTTGAGCC 300  
Db 227 TyrIleCysAsnValAsnHisLysProSerAnThrLysValAspLysValGluPro 246  
Qy 301 AAATCTTGACAAAACTCACACATGCCCGGCGCCAGCAGCTGAACCTCGCGGGGCA 360  
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Db 247 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 266  
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCAGCAGCACCCTCATGATCTCCCGGACCCCT 420  
Db 267 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 286  
Qy 421 GAGTTCACATCGGTGGTGGTGGAGCGTGGACCCAGCAGCAGCCTGAGGTCAAGTTCACCTGG 480  
Db 287 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 306  
Qy 481 TACGTGGACGGCGTGGAGTGCATATGCCAAGCAACAGCCGCGGAGAGCAGTACAC 540  
Db 307 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 326  
Qy 541 AGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
Db 327 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 346  
Qy 601 GAGTACAGTCAAGGTCTCCAAACAAAGCCCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660  
Db 347 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 366  
Qy 661 AAGCCAAAGGCGCAGCCCGAGAACCCAGCAGTGTACACCTCCCTCCCTCCCTCCCTCCCTCC 720  
Db 367 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 386  
Qy 721 CTGACCAAGAACCCAGGTCCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 780  
Db 387 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 406  
Qy 781 GCCTGGAGTGGGAGAGCAATGGCAGCGCGGAGAACAACTACAGACACACACCTCCCTCCCTG 840  
Db 407 AlaValGluTyrGluSerAsnGlyGlnProGluAsnValTyrLysThrThrProProVal 426  
Qy 841 CTGACTCCCGACCGCTCTTCTCTCTATGCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
Db 427 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 446  
Qy 901 CAGCAGGGGAGACGTCTTCTCTATGCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960  
Db 447 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 466  
Qy 961 CAGAAGAGCCTCTCTCTGTCTCTCCCGGTAAA 990  
Db 467 GlnLysSerLeuSerLeuSerProGlyLys 476

## RESULT 8

US-09-746-359A-54  
Sequence 54, Application US/09746359A  
Patent No. 6610286

## GENERAL INFORMATION:

APPLICANT: Thompson, Penny  
APPLICANT: Foster, Donald C.  
APPLICANT: Xu, Wenfeng  
APPLICANT: Madden, Karen L.  
APPLICANT: Kelly, James D.  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Blumberg, Hal  
APPLICANT: Egan, Maribeth A.  
APPLICANT: Jaspers, Stephen R.  
APPLICANT: Chandrasekhar, Yashin A.  
APPLICANT: No. 6610286a, Julia E.  
TITLE OF INVENTION: Method for Treating Inflammation  
FILE REFERENCE: 99-108  
CURRENT APPLICATION NUMBER: US/09/746,359A  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/171,969  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/213,341  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54

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; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

Alignment Scores:
Pred. No.: 2.8e-134 Length: 547
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-09-746-359A-54 (1-547)

Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTGGCACCCCTCTCCAGAGCACCTCTGGG 60
Db 218 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 237
Qy 61 GGCACAGGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTACGGTGTG 120
Db 238 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 257
Qy 121 TGGAACTCAGCGCCCTGACAGGCGGTGCACACCTTCCCGGCTGCTCTACAGTCTCA 180
Db 258 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 277
Qy 181 GGACTCTACTCCCTCAGCAGCGTGGTGAACCTGCGCTCCAGCAGCTGGGCAACCCAG 240
Db 278 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 297
Qy 241 TACATCTGCACCTGAATCAACAGCCCGACGACACCAAGGTGGACAGAAAGTTGAGCC 300
Db 298 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 317
Qy 301 AAATCTTGTGACAAATCAACATGCCACCGTCCAGCAGCTGAACCTGCGCGGGCA 360
Db 318 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 337
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
Db 338 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 357
Qy 421 GAGCTCACATCGTGGTGGTGGAGCTGAGCCAGCAGACCTGAGGTCAAGTTCACCTGG 480
Db 358 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 377
Qy 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAA 540
Db 378 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 397
Qy 541 AGCAGCTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 398 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 417
Qy 601 GAGTACAGTGCAGGTCTCAACAAAGCCCTCCCGCCCGCCATCGAGAAACCATCTCC 660
Db 418 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 437
Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCGCCCGCCATCCCGGATG 720
Db 438 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 457
Qy 721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATC 780
Db 458 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 477
Qy 781 GCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACACTACAGACCAACCCCTCCCGTG 840
Db 478 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 497
Qy 841 CTGACCTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
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Db 498 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 517
Qy 901 CAGCAGGGGAACGCTTCTCATGCTCGGTGATGATGAGGCTCTGCACAACCATACACG 960
Db 518 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 537
Qy 961 CAGAAGAGCCTCTCCCTGCTCCGGGTAAA 990
Db 538 GlnLysSerLeuSerLeuSerProGlyLys 547

RESULT 9
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalpahal1r/IgGgamma1 polypeptide
US-09-825-561A-16

Alignment Scores:
Pred. No.: 2.83e-134 Length: 567
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-09-825-561A-16 (1-567)

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Db 238 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 257
Qy 61 GGCACAGGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTACGGTGTG 120
Db 258 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 277
Qy 121 TGGAACTCAGCGCCCTGACAGGCGGTGCACACCTTCCCGGCTGCTCTACAGTCTCA 180
Db 278 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 297
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGGTGAACCTGCGCTCCAGCAGCTGGGCAACCCAG 240
Db 298 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 317
Qy 241 TACATCTGCACCTGAATCAACAGCCCGACGACACCAAGGTGGACAGAAAGTTGAGCC 300
Db 318 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 337
Qy 301 AAATCTTGTGACAAATCAACATGCCACCGTCCAGCAGCTGAACCTGCGCGGGCA 360
Db 338 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 377
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
Db 338 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 357
Qy 421 GAGCTCACATCGTGGTGGTGGAGCTGAGCCAGCAGACCTGAGGTCAAGTTCACCTGG 480
Db 358 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 377
Qy 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAA 540
Db 378 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 397
Qy 541 AGCAGCTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 398 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 417
Qy 601 GAGTACAGTGCAGGTCTCAACAAAGCCCTCCCGCCCGCCATCGAGAAACCATCTCC 660
Db 418 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 437
Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCGCCCGCCATCCCGGATG 720
Db 438 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 457
Qy 721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATC 780
Db 458 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 477
Qy 781 GCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACACTACAGACCAACCCCTCCCGTG 840
Db 478 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 497
Qy 841 CTGACCTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
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QY 361 CCGTCAGCTCTTCTCTTCCCTCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCT 420
Db 358 ProSerValPheLeuPheProProLysAspThrLeuMetIleSerArgThrPro 377
QY 421 GAGGTCAATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGG 480
Db 378 GluValThrCysValValValAspValSerHisGluAspProGluValValPheAsnTrp 397
QY 481 TACGTGGACGGCGTGGAGTGCATTAATCCAAAGACAAAGCCCGGGAGGAGCAGTACAA 540
Db 398 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 417
QY 541 AGCAGTACCGTGGTGGTGGAGCTCTCCCTGACAGGACCCCTGACAGGACCTGCTGAATGGCA 600
Db 418 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 437
QY 601 GAGTACAAAGTCAAGGCTCTCAACAAAGCCCTCCAGCAGCCCTCCAGAGAAACCATCTCC 660
Db 438 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaPheIleGluLysThrIleSer 457
QY 661 AAAGCCAAAGGCGACCCCGAGAACACACAGGTGTACACCCCTGCCCCCATCCCGGGATGAG 720
Db 458 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 477
QY 721 CTGACCAAGACCGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 478 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 497
QY 781 GCCGTGGAGTGGAGCAATGGGCGAGCGGAGCAACTACAGACCAACCGCTCCCGTGG 840
Db 498 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 517
QY 841 CTGAGCTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 900
Db 518 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 537
QY 901 CAGCAGGGGAAGCTTCTCATGTCTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 538 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 557
QY 961 CAGAAGACCTCTCCCTGCTCTCCGGTAAA 990
Db 558 GlnLysSerLeuSerLeuSerProGlyLys 567
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## RESULT 10

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US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: RastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
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## ; ORGANISM: Homo sapiens

US-09-746-359A-53

## Alignment Scores:

Pred. No.:	2,84e-134	Length:	571
Score:	1756.00	Matches:	328
Percent Similarity:	99.39%	Conservative:	0
Best Local Similarity:	99.39%	Mismatches:	2
Query Match:	97.72%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-111 (1-990) x US-09-746-359A-53 (1-571)

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QY 1 GCCTCCAAAGGCCCCATCGGTCTTCCCTTGGCACCTCTCTCAAGAGCACCTCTCTGGG 60
Db 242 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 261
QY 61 GGCACAGGCGCCCTGGGCTGCTGCTCAAGACTACTTCCCGGAAACCGGTGACGTGTGG 120
Db 262 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 281
QY 121 TGGAACTCAGCGCCCTGACACGCGGTGCACACCTTCCCGGTCTCTACAGTCCCTCA 180
Db 282 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 301
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGCTGCGCTCCAGCAGCTTGGGCACCCAG 240
Db 302 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 321
QY 241 TACATCTGCAACGTGAATATCAAGCCCAAGCAACCAAGGTGGACAAAGATTGAGCCC 300
Db 322 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 341
QY 301 AAATCTGTGACAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCGCGGGGCA 360
Db 342 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 361
QY 361 CCGTCAGTCTTCTCTTCTCCCTCCCAAGACACCTCATGATCTCCCGGACCCCT 420
Db 362 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 381
QY 421 GAGTCAATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGG 480
Db 382 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 401
QY 481 TACGTGGACGGTGGAGTGCATAATGCCAAAGCAAGCCCGGAGGACGAGTACAAAC 540
Db 402 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 421
QY 541 AGCAGTACCGTGGTGGTGGAGCTCTCCCTGACAGGACCCCTGACAGGACCTGCTGAATGG 600
Db 422 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 441
QY 601 GAGTCAATGCGTGGTGGTGGAGCTCCAAACAAAGCCCTCCAGCCCTCCAGAGAAACCAT 660
Db 442 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 461
QY 661 AAAGCCAAAGGCGACCCCGAGAACCAAGGTGTACACCTTCCCGGTCTCCCGGATGAG 720
Db 462 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 481
QY 721 CTGACCAAGACCGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 482 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 501
QY 781 GCCGTGGAGTGGAGAGCAATGGGCGAGCGGAGAACCAACTCAAGACCAACCGCTCCCG 840
Db 502 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 521
QY 841 CTGAGCTCCGAGCGGTCTCTTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 522 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 541
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QY 61 GGCACAGCGGCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGAGGTGCG 120
Db 642 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 661
QY 121 TGGAACTCAGGCGCTGACACGCGCGTGACACCTTCCCGGCTGCTCAAGTCTCA 180
Db 662 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 681
QY 181 GGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
Db 682 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 701
QY 241 TACATCTCAAGCTGAATCAGACGCGCCAGCAACACCAAGGTGGACAGAAAGTTGAGCCC 300
Db 702 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 721
QY 301 AAATCTGTGACAAACTCACACATGCCCGTCCAGCAGCTGAACTCGCGGGGCA 360
Db 722 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuGlyGly 741
QY 361 CGGTCAAGTCTTCTCTTCCCGCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCT 420
Db 742 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 761
QY 421 GAGTCAATGCGTGGTGTGACGTGACGCGTCCAGCAGCCAGCAGCTGAGGTCAAGTCACTGG 480
Db 762 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 781
QY 481 TACGTGACGCGTGGAGTGCATATGCTCAATGCAAGACAAAGCCGCGGAGGACGATACAC 540
Db 782 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 801
QY 541 AGCAGTACCGTGTGCTGAGCGTCTCCAGCTCTGACACGAGTGTGCTGAAAGTGGCAAG 600
Db 802 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 821
QY 601 GAGTCAAGTCAAGGTCTCCAGAACCCCTCCAGCCCTCCAGCCCGCCATCGAGAAACCATCTCC 660
Db 822 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrIleSer 841
QY 661 AAAGCAAAGCGAGCCGCGAGAACCCAGGTGTACACCTGCCCTCCCGGAGTGGAGTGG 720
Db 842 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 861
QY 721 CTGACCAAGAACCAAGCTCAGCTCAGCTGCTGCTGCTCAAGGCTTCTATCCAGCGCACATC 780
Db 862 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 881
QY 781 GCCGTGGAGTGGAGAGCAATGGGCGAGCGGAGAACAACTACAGACCAACGCTCCCGTGG 840
Db 882 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 901
QY 841 CTGGAATCCGAGCGCTCTTCTTCTTCTACAGCAGCTCACCGTGGACAGGAGGAGTGG 900
Db 902 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 921
QY 901 CAGCAGGGGAAGCTCTTCTCATGCTCCGTGATGATGAGGTCTGTCACAAACCACTACACG 960
Db 922 GlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 941
QY 961 CAGAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 942 GlnLysSerLeuSerLeuSerProGlyLys 951
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## RESULT 13

US-09-740-002-27

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; Sequence 27, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
```

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; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-27
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Alignment Scores:
Pred. No.: 5,68e-134 Length: 475
Score: 1752.00 Matches: 327
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 3
Query Match: 97.50% Indels: 0
DB: 2 Gaps: 0
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US-10-733-563-111 (1-990) x US-09-740-002-27 (1-475)

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QY 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCTCTCTCCAGAGCACCTCTCGG 60
Db 146 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 165
QY 61 GGCAAGCGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGG 120
Db 166 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185
QY 121 TGGAACTCAGGCGCGCTGACCGCGGTGACACCTTCCCGGCTGCTCAAGTCTCA 180
Db 186 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 205
QY 181 GGACTTACTCTCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
Db 206 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225
QY 241 TACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGGAGAAAGTTGAGCCC 300
Db 226 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysAlaGluPro 245
QY 301 AAATCTGTGACAAACTCACACATGCCCGTCCAGCAGCTGAACTCGCGGGGCA 360
Db 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly 265
QY 361 CGGTCAAGTCTTCTCTTCCCGCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
Db 266 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 285
QY 421 GAGTCAATGCGTGGTGTGACGTGAGCCAGCAACCAAGGACCCCTGAGGTCAAGTTCAC 480
Db 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 305
QY 481 TACGTGACGCGTGGAGTGCATATGCTCAAGCAACAAAGCCGCGGAGGACGATACAC 540
Db 306 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 325
QY 541 AGCAGTACCGTGTGCTCAGCGTCTCACCGTCTCGACACGAGGACTGGCTCAAGTGGCAAG 600
Db 326 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 345
QY 601 GAGTCAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCCGCCATCGAGAAACCATCTCC 660
Db 346 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysLeuThrIleSer 365
QY 661 AAAGCAAAGCGAGCCCGGAGAACCCAGGTGTACACCTTGGCCCGCCCATCTCCGGGATGAG 720
Db 366 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 385
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APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,550  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids

TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-487-550-12

Alignment Scores:  
Pred. No.: 5,68e-134 Length: 476  
Score: 1752.00 Matches: 327  
Percent Similarity: 99.09% Conservative: 0  
Best Local Similarity: 99.09% Mismatches: 3  
Query Match: 97.50% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-08-487-550-12 (1-476)

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Qy	61	GGCAGCGCGCCCTGGCTGGTCAAGCACTACTTCCCGAACCGGTGACGGTGTG	120
Db	167	GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer	186
Qy	121	TGGAACCTCAGCGCCCTCACCAGCGCGGTGACACCTTCCCGGCTGTCTACAGTCCTCA	180
Db	187	TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer	206
Qy	181	GGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCAGCAGCTTGGGCACCCAGACC	240
Db	207	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	226
Qy	241	TACATCTGCACGTCGATCAACAGCCGACACACACAGGTGGACAGAAAGTTGAGCCC	300
Db	227	TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysAlaGluPro	246
Qy	301	AAATCTGTGACAAACTCACACATGCCACCGTCCCGACACCTGAACTCGCGGGGCA	360
Db	247	LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly	266
Qy	361	CCGTGAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT	420

Db	267	ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro	286
Qy	421	GAGGTCAATCGGTGGTGGAGCTGAGCCACGAGACCTGTAGGTCAAGTTCAACTGG	480
Db	287	GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp	306
Qy	481	TACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGACGATACAC	540
Db	307	TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn	326
Qy	541	AGCAGTACCGTGTGGTCCAGCTCTCACCGTCTCTGACACAGGACTGGCTGAATGGCAAG	600
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Qy	601	GAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCCTCATCGAGAAACCATCTCC	660
Db	347	GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer	366
Qy	661	AAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTGCCCCCATCCCGGATGAG	720
Db	367	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu	386
Qy	721	CTGACCAAGAACACAGGTCCAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATC	780
Db	387	LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle	406
Qy	781	GCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAGACCCACCGCTCCCGTG	840
Db	407	AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal	426
Qy	841	CTGACTCCGACGGCTCCTTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG	900
Db	427	LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp	446
Qy	901	CAGCAGGGGAAACGTCTTCTCATGCTCCGTGTATGATGAGGCTCTGCAACACCATACAG	960
Db	447	GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr	466
Qy	961	CAGAAGAGCCCTCTCCCTGCTCTCCGGGTAAA	990
Db	467	GlnLysSerLeuSerLeuSerProGlyLys	476

Search completed: January 28, 2006, 08:48:58

Job time : 51.1441 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:44:22 ; Search time 120.901 Seconds  
(without alignments)  
6842.811 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA Main:  
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5: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	98.2	333	4	US-10-272-899A-10
2	1765	98.2	333	4	US-10-733-563-114
3	1765	98.2	356	4	US-10-272-899A-70
4	1765	98.2	448	4	US-10-171-452A-42
5	1765	98.2	448	4	US-10-171-452A-54
6	1765	98.2	448	4	US-10-353-708-42
7	1765	98.2	448	4	US-10-353-708-54
8	1765	98.2	448	4	US-10-731-984-8
9	1765	98.2	448	4	US-10-731-984-24
10	1765	98.2	467	4	US-10-171-452A-53
11	1765	98.2	467	4	US-10-353-708-53

12	1765	98.2	467	4	US-10-731-984-7	Sequence 7, Appl
13	1765	98.2	467	4	US-10-731-984-23	Sequence 23, Appl
14	1760	97.9	330	4	US-10-733-563-110	Sequence 110, Appl
15	1759	97.9	473	4	US-10-467-253-13	Sequence 13, Appl
16	1758	97.8	469	4	US-10-404-724-72	Sequence 72, Appl
17	1756	97.7	332	3	US-09-990-586-98	Sequence 98, Appl
18	1756	97.7	332	4	US-10-310-113-167	Sequence 167, Appl
19	1756	97.7	332	4	US-10-230-880-98	Sequence 98, Appl
20	1756	97.7	333	4	US-10-272-899A-8	Sequence 8, Appl
21	1756	97.7	356	4	US-10-272-899A-72	Sequence 72, Appl
22	1756	97.7	371	4	US-10-157-408-7	Sequence 7, Appl
23	1756	97.7	371	4	US-10-097-044A-7	Sequence 7, Appl
24	1756	97.7	371	4	US-10-769-247-7	Sequence 7, Appl
25	1756	97.7	444	4	US-10-150-475A-6	Sequence 6, Appl
26	1756	97.7	444	4	US-10-704-522-6	Sequence 6, Appl
27	1756	97.7	444	4	US-10-645-215-6	Sequence 6, Appl
28	1756	97.7	444	6	US-11-136-538-7	Sequence 7, Appl
29	1756	97.7	445	4	US-10-320-231A-79	Sequence 79, Appl
30	1756	97.7	445	4	US-10-408-901-34	Sequence 34, Appl
31	1756	97.7	445	4	US-10-408-901-42	Sequence 42, Appl
32	1756	97.7	445	5	US-10-867-506-79	Sequence 79, Appl
33	1756	97.7	445	5	US-10-937-596-3	Sequence 3, Appl
34	1756	97.7	447	3	US-03-256-156-1	Sequence 1, Appl
35	1756	97.7	447	5	US-10-684-957-17	Sequence 17, Appl
36	1756	97.7	447	5	US-10-684-957-19	Sequence 19, Appl
37	1756	97.7	447	5	US-10-684-957-21	Sequence 21, Appl
38	1756	97.7	447	5	US-10-684-957-32	Sequence 32, Appl
39	1756	97.7	447	6	US-11-010-797-2	Sequence 2, Appl
40	1756	97.7	448	4	US-10-378-567-2	Sequence 2, Appl
41	1756	97.7	448	5	US-10-985-584-18	Sequence 18, Appl
42	1756	97.7	449	5	US-10-635-908-16	Sequence 16, Appl
43	1756	97.7	449	5	US-10-635-908-18	Sequence 18, Appl
44	1756	97.7	449	5	US-10-476-265-12	Sequence 12, Appl
45	1756	97.7	449	5	US-10-985-584-10	Sequence 10, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-272-899A-10  
; Sequence 10, Application US/10272899A  
; Publication No. US20040033561A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa L.  
; APPLICANT: Healy, Judith Jacques  
; APPLICANT: Newman, Walter  
; APPLICANT: Ponath, Paul  
; APPLICANT: Bruce Keyt  
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,  
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF  
; TITLE OF INVENTION: USE THEREFOR  
; FILE REFERENCE: MP101-244P2RM  
; CURRENT APPLICATION NUMBER: US/10/272.899A  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human IgG1-FcRmut protein  
US-10-272-899A-10

Alignment Scores:  
Pred. No.: 7.05e-113 Length: 333  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-111 (1-990) x US-10-272-899A-10 (1-333)
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Db 4 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23
Qy 61 GGCAAGGGCCCTGGGTGCTGCTCAAGACTACTTCCCGGAAACCGGTGACGGTGTGCG 120
Db 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43
Qy 121 TGGAACTCAGGCGCCCTGACCAGGGGTGCACACCTTCCCGGTCTCTACAGTCTCA 180
Db 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 63
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
Db 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThr 83
Qy 241 TACATCTGCAACGTGAATCAACGCCAGCCAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300
Db 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 103
Qy 301 AAATCTTTGTGACAAACTCACACATGCCACCGTCCCGGCAGCACCTGAACTCGCGGGGCA 360
Db 104 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 123
Qy 361 CCCTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 124 ProSerValPheLeuPheProProLysPheProLysAspThrLeuMetIleSerArgThrPro 143
Qy 421 GAGTCCATCGCTGGTGGAGCTGAGCCACGAGACCTGAGGTCAAGTTCACATGG 480
Db 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 163
Qy 481 TACGTGACGCGCGGGAGGTGCATAATGCCAAGACCAAGCGCGGGAGGACGCTACAC 540
Db 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 183
Qy 541 AGCAGTACCGTGTGGTGCAGCGTCTCACCGCTCTGCACACGAGGACTGGCTGAATGGCAAG 600
Db 184 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 203
Qy 601 GAGTACAGTGCAGGCTCTCAACAAAGCCCTCCAGCCCTCCAGCCCTCGAGAAACCATCTCC 660
Db 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 223
Qy 661 AAAGCCAAAGGCGAGCCCGAGAACCCAGGTGTACACCTGCCCTGCCCTCCATCCCGGATGAG 720
Db 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 243
Qy 721 CTGACCAAGAACCAAGTGCAGCTGACCTCGCTCAAGGCTTCTATCCAGCGACATC 780
Db 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263
Qy 781 GCCGTGAGTGGGAGAGCAATGGGCGAGCGAGAACCACTACAGACACCGCTCCCGTG 840
Db 264 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 283
Qy 841 CTGGACTCCGACGGCTCTTCTCTCTTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 900
Db 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303
Qy 901 CAGCAGGGGAACTCTTCTCATGTCTCGTGTATGATGAGGTCTGCGCAACCACTACACG 960
Db 304 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 323
Qy 961 CAGAAAGCCTCTCCCTGTCTCCGGGTAAA 990
Db 324 GlnLysSerLeuSerLeuSerProGlyLys 333
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## RESULT 2

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US-10-733-563-114
; Sequence 114, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-PCRmut protein
US-10-733-563-114
Alignment Scores:
Pred. No.: 7,05e-113 Length: 333
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservatative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-111 (1-990) x US-10-733-563-114 (1-333)
Qy 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCCCTCTCTCCAGAGACACCTCTGGG 60
Db 4 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23
Qy 61 GGCAAGGGCCCTGGGTGCTGCTCAAGACTACTTCCCGGAAACCGGTGACGGTGTGCG 120
Db 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43
Qy 121 TGGAACTCAGGCGCCCTGACCAGGGGTGCACACCTTCCCGGTCTCTACAGTCTCA 180
Db 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 63
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
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Qy 361 CCCTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 124 ProSerValPheLeuPheProProLysPheProLysAspThrLeuMetIleSerArgThrPro 143
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Qy 481 TACGTGACGCGCGGGAGGTGCATAATGCCAAGACCAAGCGCGGGAGGACGCTACAC 540
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Qy 541 AGCAGTACCGTGTGGTGCAGCGTCTCACCGCTCTGCACACGAGGACTGGCTGAATGGCAAG 600
Db 184 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 203
Qy 601 GAGTACAGTGCAGGCTCTCAACAAAGCCCTCCAGCCCTCCAGCCCTCGAGAAACCATCTCC 660
Db 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 223
Qy 661 AAAGCCAAAGGCGAGCCCGAGAACCCAGGTGTACACCTGCCCTGCCCTCCATCCCGGATGAG 720
Db 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 243
Qy 721 CTGACCAAGAACCAAGTGCAGCTGACCTCGCTCAAGGCTTCTATCCAGCGACATC 780
Db 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263
Qy 781 GCCGTGAGTGGGAGAGCAATGGGCGAGCGAGAACCACTACAGACACCGCTCCCGTG 840
Db 264 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 283
Qy 841 CTGGACTCCGACGGCTCTTCTCTCTTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 900
Db 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303
Qy 901 CAGCAGGGGAACTCTTCTCATGTCTCGTGTATGATGAGGTCTGCGCAACCACTACACG 960
Db 304 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 323
Qy 961 CAGAAAGCCTCTCCCTGTCTCCGGGTAAA 990
Db 324 GlnLysSerLeuSerLeuSerProGlyLys 333
```



GENERAL INFORMATION:  
; APPLICANT: Frewin, Mark  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Gorman, Scott  
; APPLICANT: Hale, Geoff  
; APPLICANT: Rao, Patricia  
; APPLICANT: Kornaga, Tadeusz  
; APPLICANT: Ringler, Douglas  
; APPLICANT: Cobbold, Stephen  
; APPLICANT: Winsor-Hines, Dawn  
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor  
; FILE REFERENCE: 695458-59  
; CURRENT APPLICATION NUMBER: US/10/171,452A  
; CURRENT FILING DATE: 2003-02-10  
; PRIOR APPLICATION NUMBER: US60/373,471  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/373,470  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: GB0122724.8  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB0114517.6  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 60  
; SEQ ID NO 42  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Heavy chain of humanized antibody  
US-10-171-452A-42

Alignment Scores:  
Pred. No.: 7,31e-113 Length: 448  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-171-452A-42 (1-448)

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Qy 1 GCCTCCACGAGGCGCCATCGTCTCCCTCCGACCCCTCCACAGACGACCTCTGGG 60
Db 119 AlAserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138
Qy 61 GGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTGACCGGTGTCG 120
Db 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
Qy 121 TGGAACTCAGCGCCCTGACACAGCGGCGGTGACACCTTCCCGGTGCTCTACGTCTCA 180
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGTCGCTGCTCCCTCCAGCAGCTTGGGACCCAGACC 240
Db 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198
Qy 241 TACATCTGCAACGTGAATCAACAGCCCAAGCAACCAAGGTGGAGCAAGAAAGTTGAGCCC 300
Db 199 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
Qy 301 AAATCTTGTGACAAACTCACAATGCCACCGTCCAGCACTGAACCTCGCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238
Qy 361 CCGTCAGTCTCTCTTCCCTCCCAACCAAGCAACCTCATGATCTCCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 258
Qy 421 GAGGTCACTGCTGCTGGTGGAGCTGAGCCACCAAGACCCCTGAGGTCAAGTTCACCTGG 480
```

```
Db 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
Qy 481 TACGTGACCGCGGTGGAGGTGCATAATGCCAAGCAAAAGCGCGGAGGAGCAGTACAAC 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 298
Qy 541 AGCAGGTACCGTGTGGTCAGCGTCTCCACCGTCTCTGACCGAGGACTGGCTGAATGGCAAG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
Qy 601 GAGTACAAGTGCAGGTCTCCAAACAAAGCCCTCCACAGCCCTCCATCGAGAAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 338
Qy 661 AAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCTCCGGGATGAG 720
Db 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
Qy 721 CTGACCAAGAACCAAGGTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
Qy 781 GCCGTGAGGTGGAGAGCAATGGGCGAGCCGAGAACCAACTACAGACCAAGCAGGAGTGG 840
Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398
Qy 841 CTGACTCCGACGGCTCTCTCTCTCTACAGCAAGCTCACCGTGGGACAGAGCAGGTGG 900
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
Qy 901 CAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACACCACTACACG 960
Db 419 GlnGlnLysValPheSerCysSerValMechHisGluAlaLeuHisAsnHisTyrThr 438
Qy 961 CAGAAGAGCCCTCTCCCTGCTCTCCGGGTAAA 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448
RESULT 5
US-10-171-452A-54
; Sequence 54, Application US/10171452A
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 54
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
```

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US-10-171-452A-54
Alignment Scores:
Pred. No.: 7,31e-113 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-171-452A-54 (1-448)
QY 1 GCCTCCACAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCTCCAGAGCACCTCTGGG 60
DB 119 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138
QY 61 GGCACAGCGCCCTGGCTGCTGCTCAAGGACTTCTCCCGACCGGTGACGGTGTGCG 120
DB 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
QY 121 TGGAACTCAGCGCCCTGACAGCGCGCTGCACACTTCCCGGCTGTCTTACAGTCTCA 180
DB 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
QY 181 GGACTCTACTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACC 240
DB 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThr 198
QY 241 TACATCTGCAACGTAATCACAAGCCCAAGCCACACACCAAGGTGGACAGAAAGTTGAGCCC 300
DB 199 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
QY 301 AAATCTTGTCACAAACTCACACATGCCACCGTCCCGTCCAGCACCTGAACTCGCGGGGCA 360
DB 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238
QY 361 CCGTCAGTCTTCTCTTCCCCCCCCAAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
DB 239 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 258
QY 421 GAGTCCATCGGTGGTGGTGGACGTGAGCCACGACGACCTGAGTCAAGTTCACCTGG 480
DB 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
QY 481 TACGTGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGCAGGTACAAAC 540
DB 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 298
QY 541 AGCAGTACCTGTGGTGCAGGTCTCTACCGTCTCTGCAACCGAGGACTGGCTGAATGGCAAG 600
DB 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
QY 601 GAGTACAGTGCAGGTCTCCACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAAACCTCTCC 660
DB 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 338
QY 661 AAAGCCAAAGCGACCCCGAGAACCCACAGGTGTACACCTGCCCTCCCGCATCCCGGATGAG 720
DB 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
QY 721 CTGACCAAGAACCGAGTGCAGCTGTACCTGCTCCCTGGTCAAAGGCTTCTATCCAGGCGACATC 780
DB 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
QY 781 GCCGTGGAGTGGAGAGCAATGGGAGCGCGAGAGAACAACTACAGACCAACGCTCCCGTGG 840
DB 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 398
QY 841 CTGAGCTCCGAGCGCTCTCTTCTCTCTACAGCAGCTCACCGTGGACAGAGGAGGTGG 900
DB 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
QY 901 CAGCAGGGGAAACGTCTTCTCTGCTCCGTGATGATGAGGCTCTGTCACAAACCACTTACACG 960

US-10-353-708-42
; Sequence 42, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobboid, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 42
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-42
Alignment Scores:
Pred. No.: 7,31e-113 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-353-708-42 (1-448)
QY 1 GCCTCCACAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCTCCAGAGCACCTCTGGG 60
DB 119 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138
QY 61 GGCACAGCGCCCTGGCTGCTGCTCAAGGACTTCTCCCGACCGGTGACGGTGTGCG 120
DB 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
QY 121 TGGAACTCAGCGCCCTGACAGCGCGCTGCACACTTCCCGGCTGTCTTACAGTCTCA 180
DB 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
QY 181 GGACTCTACTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACC 240
DB 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThr 198
QY 241 TACATCTGCAACGTAATCACAAGCCCAAGCCACACCAAGGTGGACAGAAAGTTGAGCCC 300
```

```
Db 199 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
Qy 301 AAATCTTGACAAACTCAGACATGCCCGTCCAGACACTGAATCGCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238
Qy 361 CCGTCAGTCTTCTTCCCTCCCAAAACCCAGGACACCTCATGATCTCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 258
Qy 421 GAGGTCAATCGTGGTGGAGCTGAGCCAGACACCTCAGGTCAAGTTCAACTGG 480
Db 259 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
Qy 481 TACGTGACGGCGGTGAGGTGCATAATGCCAAGACAAAGCCCGGAGGAGCAGGTACAA 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 298
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
Qy 601 GAGTACAGTGCAGGTCTCCAAACAAAGCCCTCCAGGCCCTCCAGACACCTCGAGAAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 338
Qy 661 AAAGCCAAAGGGAGCCCGGAGAACCAAGGTGTACACCTGCGCCCTCCAGGCTTCTATCCAGGACATC 720
Db 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
Qy 721 CTGACCAAGACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
Qy 781 GCCGTGAGTGGGAGAGCAATGGGAGCGGAGGAGCAACTCAAGACCAAGCCCTCCCGTG 840
Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnThrLysThrProProVal 398
Qy 841 CTGACCTCCGAGCGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
Qy 901 CAGCAGGGGACGCTTCTCTCATGCTCCGTGATGATGATGATGATGATGATGATGATGAT 960
Db 419 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438
Qy 961 CAGAGAGCCCTCTCCCTGCTCCCGGTAAA 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448
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## RESULT 7

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US-10-353-708-54
; Sequence 54, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
```

```
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 54
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-54
Alignment Scores:
Pred. No.: 7,31e-113 Length: 448
Score: 1785.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-111 (1-990) x US-10-353-708-54 (1-448)
Qy 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCGACCTCTCTCCAAAGACACCTCTGGG 60
Db 119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 138
Qy 61 GGACACGGCCCTGGGCTGCTGGTCAAGACTACTTCCCGAACCGGTGACGGTGTG 120
Db 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
Qy 121 TGGAACTCAGCGCCCTGACAGCGGTGTCACACCTTCCCGGTGTCTTACAGTCTCTCA 180
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
Qy 181 GGACTCTACTCTCTTCCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACCCAGAC 240
Db 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198
Qy 241 TAGATCTGCAACGTGAATCAGACCCAGCAACACCAAGGTGGAGCAAGAAAGTTGAGCCC 300
Db 199 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
Qy 301 AAATCTTGTGACAAACTCAGACATGCCCGTCCAGCACCTGAACCTCGCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238
Qy 361 CCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
Db 239 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 258
Qy 421 GAGGTCAATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 259 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
Qy 481 TACGTGACGGCGGTGAGGTGCATAATGCCAAGACAAAGCCCGGAGGAGCAGGTACAA 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 298
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
Qy 601 GAGTACAGTGCAGGTCTCCAAACAAAGCCCTCCAGGCCCTCCAGACACCTCGAGAAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 338
Qy 661 AAAGCCAAAGGGAGCCCGGAGAACCAAGGTGTACACCTGCGCCCTCCAGGCTTCTATCCAGGACATC 720
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```

Db      339  LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
Qy      721  CTGACCAAGAACACGAGTCAGCTCCCTCGTCAAAAGGCTTCTATCCACGACATC 780
Db      359  LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
Qy      781  GCCGTGGAGTGGAGACGATGGGAGCGGAGCAACTACAGACCAACGCTCCCGTG 840
Db      379  AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398
Qy      841  CTGGAACCTCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db      399  LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
Qy      901  CAGCAGGGAACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db      419  GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438
Qy      961  CAGAGAGCCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db      439  GlnLysSerLeuSerLeuSerProGlyLys 448

RESULT 8
; Sequence 8, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-731-984-8

Alignment Scores:
Pred. No.: 7,31e-113 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-731-984-8 (1-448)
Qy      1  GCCTCCACCAAGGGCCCATCGGTCTTCCCTCGCACCTCTCTCAAGAGCACCTCTGGG 60
Db      119  AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138
Qy      61  GGCACAGGGCCCTGGGTGCTGTGTCAGGACTACTTCCCGCAACCGGTGACGGTGTG 120
Db      139  GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
Qy      121  TGGAACTCAGCGCCCTGACGAGCGGTGACACCTTCCCGGTGCTCTCTCTCTCTCT 180
Db      159  TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
Qy      181  GGACTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db      179  GlyLeuTyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThr 198
Qy      241  TACATCTGCAACGTGAATCAACAGCCCAAGCAACCAAGGTGGACAAGAAAGTTGAGCCC 300

```

```

Db      199  TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 218
Qy      301  AAATCTTGTCACAAACTCACACATGCCCGCGTCCCGACACCTGAAGTCCGGGGGCA 360
Db      219  LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 238
Qy      361  CCGTCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db      239  ProSerValPheLeuPheProLysProLysPheProLysPheProLysPheProLys 258
Qy      421  GAGTTCACATCGTGTGGTGGAGCTGAGCCACGAGACCTCTGAGGTCAAGTTCAGTGG 480
Db      259  GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
Qy      481  TACGTGGAGCGCGTGGAGTCAATAATGCCAAGACCAAGCCGCGGAGGAGCAGGTACAC 540
Db      279  TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 298
Qy      541  AGCAGTACCGTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db      299  SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
Qy      601  GAGTACAAAGTCTCAACAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db      319  GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrLysThrLys 338
Qy      661  AAAGCAAGGCGCGCGGAGACCAAGTGGAGTGTACACCTCTCTCTCTCTCTCTCTCTCT 720
Db      339  LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
Qy      721  CTGACCAAGAACACGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db      359  LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
Qy      781  GCCGTGGAGTGGAGAGCAATGGCAGCGGAGCAACTACAGACCAACGCTCCCGTG 840
Db      379  AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398
Qy      841  CTGCACTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db      399  LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
Qy      901  CAGCAGGGGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db      419  GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438
Qy      961  CAGAAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db      439  GlnLysSerLeuSerLeuSerProGlyLys 448

RESULT 9
; Sequence 24, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence

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US-10-731-984-24

Alignment Scores:  
Pred. No.: 7,31e-113 Length: 448  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-731-984-24 (1-448)

QY 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTGGCACCTCTCTCCAGAGCACCTCTGGG 60  
DB 119 AlaSerThrIysGlyProSerValPheProLeuAlaProSerSerIysSerThrSerGly 138  
QY 61 GGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTGTG 120  
DB 139 GlyThrAlaAlaLeuGlyCysLeuValIysAspTyrPheProGluProValThrValSer 158  
QY 121 TGGNACTCAGCGCCCTGACACCGCGGTGCACACCTTCCCGCTGTCTTACAGTCCCTCA 180  
DB 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178  
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGCTGCCCTCCAGCAGCTTGGGACCCAGACC 240  
DB 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198  
QY 241 TACATCTGCAACGTGAATCAAGCCCGACGACCAACACCAAGGTGGACAGAAAGTTGAGCCC 300  
DB 199 TyrIleCysAsnValAsnHisIlysProSerAsnThrLysValAspIlysIysValGluPro 218  
QY 301 AAATCTTGTCACAAAACCTCACACATGCCACCGTCCAGCAGCCCTGAACCTCCGCGGGGCA 360  
DB 219 LysSerCysAspIysThrHisThrCysProCysProAlaProGlnLeuAlaGlyAla 238  
QY 361 CCCTCAGTCTTCTCTTCCCCCAAAACCAAGCACACCTCTCATGATCTCCCGGACCCCT 420  
DB 239 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 258  
QY 421 GAGGTACATGCTGCTGTGGAGCTGAGCCAGAACGACCTGAGGTCAAGTTCACTGG 480  
DB 259 GluValThrCysValValAspValSerHisGluAspProGluValIysPheAsnTrp 278  
QY 481 TAGCTGACGCGCTGAGGTGCATAATGCAAGACAAAGCCGCGGAGGACGAGTACAAC 540  
DB 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGlnGlnTyrAsn 298  
QY 541 AGCAGTACCGTGTGCTGACGCTCTCACCGTCTGTCCACGAGGACTGGCTGAATGGCAAG 600  
DB 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyIys 318  
QY 601 GAGTACAGTGAAGGTCTCCAAAGCCCTCCAGCCCCCATGTGAGAAACCATCTCC 660  
DB 319 GluTyrIysCysIysValSerAsnLysAlaLeuProAlaProIleGluIysThrIleSer 338  
QY 661 AAAGCCAAAGGGGAGCCCGAGAACCAAGGTGTACACCTGCCCTCCCGGATGAG 720  
DB 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358  
QY 721 CTGACCAAGAACAGGTGACCTGACCTGCTGCTGCTCAAGGGCTTCTATCCAGCACATC 780  
DB 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValIysGlyPheTyrProSerAspIle 378  
QY 781 GCGGTGAGTGGAGAGCAATGGGACGCGGAGAACAACTACAAGACCAAGCTCCCGTG 840  
DB 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProVal 398  
QY 841 CTGAGCTCCAGCGCTCTTCTTCTCTCAGCAAGCTCACCGTGGACAAGAGGAGTGG 900  
DB 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspIysSerArgTrp 418  
QY 901 CAGCAGGGGAACGTCTTCTCATGCTCCGCTGATGCATGAGGCTCTGCACCAACCATCACAG 960



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QY 301 AAATCTTGACAAACTCACAATGCGCCACCGTCCCGAGCACCTGAACTCCGCGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CGGTCAAGTCTTCTCTCCCGCCAAACCCCAAGGACCCCTCATGATCTCCCGGACCCCT 420
Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGTTCACATGCGTGGTGGTGGACGTGAGCCACCAAGACCCCTGAGGTCAAGTTCACATGG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGGACGGCTGGAGGTGATATCCCAAGACAAAGCCCGGAGGAGGACGTACAAAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTrpAsn 317
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAAGTGGCAAGGTCTCCAAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 357
QY 661 AAAGCCAAAGGCGACCGCCGAGAACCCAGTGTACACCTTCCCGCCCATCCCGGATGAG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
QY 721 CTGACCAAGACCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCCGTGGAGTGGGAGCAATGGGAGCGGAGCAACTCAAGACCAACCGCTCCCGGTG 840
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 417
QY 841 CTGACCTCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGACAGCAGCGTGG 900
Db 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGACGCTTCTTCATGCTCCCGTGGATGATGAGGTCTGCGACCAACCATACAG 960
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457
QY 961 CAGAAGAGCTCTCCCTGCTCCCGGTAAA 990
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 11
US-10-353-708-53
; Sequence 53, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
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; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-53

Alignment Scores:
Pred. No.: 7,34e-113 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0
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QY 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTCCCGCACCCTCTCTCCCAAGACACCTCTCTGGG 60
Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCACAGCGGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGGCGCCTGACGAGCGGCGTGCACACCTTCCCGGTGTCTTACAGTCCCTCA 180
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAACGTGAATCACAAGCCCGACCAACCAACCAAGGTGGACAGAAAGTTGAGCCC 300
Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 237
QY 301 AAATCTTGACAAACTCACAATGCGCCACCGTCCCGAGCACCTGAACTCCGCGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CGGTCAAGTCTTCTCTCCCGCCAAACCCCAAGGACCCCTCATGATCTCCCGGACCCCT 420
Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGTTCACATGCGTGGTGGTGGACGTGAGCCACCAAGACCCCTGAGGTCAAGTTCACATGG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGGACGGCTGGAGGTGATATCCCAAGACAAAGCCCGGAGGAGGACGTACAAAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTrpAsn 317
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAAGTGGCAAGGTCTCCAAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 357
QY 661 AAAGCCAAAGGCGACCGCCGAGAACCCAGTGTACACCTTCCCGCCCATCCCGGATGAG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
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Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160  
QY 481 TACGTGGAGCGCGTGGAGTGCATATCCCAAGACAAGACCGCGGAGAGCAGGTACAAAC 540  
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180  
QY 541 AGCAGTACCGTGTGGTCCAGCGTCTCACCGTCCCTGCACACAGGACTGGCTCAATGGCAAG 600  
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200  
QY 601 GAGTACAGTCAAGGTCTCCAAACAAGCCCTCCAGAGCCGCCATCGAGAAAACCATCTCC 660  
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 220  
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCTGGCCGCCATCCCGGGATGAG 720  
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240  
QY 721 CTGACCAAGAACCGGTGAGCTGACCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATC 780  
Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260  
QY 781 GCCGTGAGTGGGAGCAATGGGCGAGCGGAGAACAACTACAAGACCAACCGCTCCCGGTG 840  
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 280  
QY 841 CTGAGCTCCGAGCGGTCTCTTCTTCTTACAGCAAGTCAACGTGGGACAAGAGCAGGTGG 900  
Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300  
QY 901 CAGCAGGGGAACGCTTCTCTCATGCTCCGTGATGATGAGGCTTGCACAACCACTACACG 960  
Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320  
QY 961 CAGAAGAGCTCTCCCTGCTCCGGGTAAA 990  
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330

## RESULT 15

US-10-467-253-13  
; Sequence 13, Application US/10467253  
; Publication No. US20040170627A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham plc  
; APPLICANT: Irving, Elaine A  
; TITLE OF INVENTION: Novel  
; FILE REFERENCE: SAL/P32763  
; CURRENT APPLICATION NUMBER: US/10/467,253  
; CURRENT FILING DATE: 2003-08-05  
; PRIOR APPLICATION NUMBER: GB 01031174.9  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: mouse/human  
; OTHER INFORMATION: chimeric anti-MAG antibody heavy chain  
US-10-467-253-13

Alignment Scores:  
Pred. No.: 1,9e-112 Length: 473  
Score: 1759.00 Matches: 329  
Percent Similarity: 99.70% Conservative: 0  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 97.89% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-467-253-13 (1-473)

QY 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCCAAAGACGACACCTCTGGG 60  
Db 144 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 163  
QY 61 GGCAACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACCGGTGCG 120  
Db 164 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 183  
QY 121 TGGAACTCAGGCGGCCCTGACAGCGGCGTGACACCTTCCCGGTGCTCTACAGTCTCTCA 180  
Db 184 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 203  
QY 181 GGACTCTACTCCCTCAGCAGCGGTGTGACCGTGGCTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 204 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 223  
QY 241 TACATCTGCAACGTGAATCAAGCCAGCAACCAACCAAGGTGGACAAGAAGTTGAGCCC 300  
Db 224 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 243  
QY 301 AAATCTTTGTGACAAACTCACACATGCCACCGTGGCCCGACCTGAACCTGCGGGGGCA 360  
Db 244 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 263  
QY 361 CCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 420  
Db 264 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 283  
QY 421 GAGGTCACTGCGTGGTGGAGCGTGCAGCCACCAAGACCTGTGAGGTCAAGTTCAACTGG 480  
Db 284 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 303  
QY 481 TACGTGACCGCGTGGAGTGCATTAATGCCAAGACAAGCGCGGAGGAGCAGTACAAC 540  
Db 304 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 323  
QY 541 AGCAGGTACCGTGGTGGTCCAGGTCTTCCCGTCTGACACCGACTGGCTGAATGGCAAG 600  
Db 324 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 343  
QY 601 GAGTACAAGTGAAGGTCTCAACAAGCCCTCCAGCCGCCCATCGAGAAAACCATCTCC 660  
Db 344 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 363  
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCTGGCCGCCATCCCGGGATGAG 720  
Db 364 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 383  
QY 721 CTGACCAAGAACCGGTGAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATC 780  
Db 384 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 403  
QY 781 GCCGTGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAAGACCAACCGCTCCCGGTG 840  
Db 404 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 423  
QY 841 CTGAGCTCCAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 900  
Db 424 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuIleValAspLysSerArgTrp 443  
QY 901 CAGCAGGGGAACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960  
Db 444 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 463  
QY 961 CAGAAGAGCTCTCCCTGCTCCGGGTAAA 990  
Db 464 GlnLysSerLeuSerLeuSerProGlyLys 473

Search completed: January 28, 2006, 09:31:22  
Job time : 131.901 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:46:13 ; Search time 12.6351 Seconds  
(without alignments)  
1696.980 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797

Sequence: 1 gctccaccagggcccatc.....tctccctgtctccgggtaaa 990

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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-MAXLEN=2000000000 -USER=US10733563 @CNC 1.1.1 @runat 27012006\_180008\_4917  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA New:  
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7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	1765	98.2	448	7	US-11-158-505-8	Sequence 8, Appli
2	1765	98.2	448	7	US-11-158-505-24	Sequence 24, Appli
3	1765	98.2	467	7	US-11-158-505-5	Sequence 5, Appli
4	1765	98.2	467	7	US-11-158-505-7	Sequence 7, Appli
5	1765	98.2	467	7	US-11-158-505-21	Sequence 21, Appli
6	1765	98.2	467	7	US-11-158-505-23	Sequence 23, Appli
7	1756	97.7	335	7	US-11-024-251-35	Sequence 35, Appli
8	1756	97.7	444	7	US-11-172-320-6	Sequence 6, Appli
9	1756	97.7	444	7	US-11-173-969-6	Sequence 6, Appli
10	1756	97.7	451	7	US-11-158-505-33	Sequence 33, Appli

11	1756	97.7	551	7	US-11-022-289-7	Sequence 7, Appli
12	1756	97.7	551	7	US-11-022-289-8	Sequence 8, Appli
13	1756	97.7	557	7	US-11-022-289-4	Sequence 4, Appli
14	1756	97.7	557	7	US-11-022-289-5	Sequence 5, Appli
15	1756	97.7	557	7	US-11-022-289-6	Sequence 6, Appli
16	1754	97.6	592	6	US-10-016-686-4	Sequence 4, Appli
17	1753	97.6	447	7	US-11-102-621-132	Sequence 132, App
18	1752	97.5	476	7	US-11-139-499-4	Sequence 4, Appli
19	1752	97.5	476	7	US-11-139-499-12	Sequence 12, Appli
20	1751	97.4	330	6	US-10-886-383-6	Sequence 6, Appli
21	1751	97.4	330	6	US-10-493-909-20	Sequence 20, Appli
22	1751	97.4	330	7	US-11-022-289-11	Sequence 11, Appli
23	1751	97.4	330	7	US-11-075-351-1	Sequence 1, Appli
24	1751	97.4	330	7	US-11-165-141-15	Sequence 15, Appli
25	1751	97.4	330	7	US-11-102-621-3	Sequence 3, Appli
26	1751	97.4	330	7	US-11-102-621-7	Sequence 7, Appli
27	1750	97.4	447	7	US-11-102-621-130	Sequence 130, App
28	1750	97.4	447	7	US-11-102-621-131	Sequence 131, App
29	1750	97.4	449	7	US-11-154-337-17	Sequence 17, Appli
30	1750	97.4	451	6	US-10-923-327-7	Sequence 7, Appli
31	1750	97.4	451	6	US-10-923-327-9	Sequence 9, Appli
32	1750	97.4	451	6	US-10-923-327-11	Sequence 11, Appli
33	1750	97.4	452	7	US-11-120-338-14	Sequence 14, Appli
34	1750	97.4	452	7	US-11-107-028-32	Sequence 32, Appli
35	1750	97.4	452	7	US-11-106-820-26	Sequence 26, Appli
36	1750	97.4	471	7	US-11-106-820-25	Sequence 25, Appli
37	1750	97.4	548	7	US-11-022-289-3	Sequence 3, Appli
38	1750	97.4	557	7	US-11-022-289-2	Sequence 2, Appli
39	1750	97.4	564	7	US-11-022-289-10	Sequence 10, Appli
40	1750	97.4	667	7	US-11-096-046-25	Sequence 25, Appli
41	1750	97.4	692	6	US-10-981-356A-26	Sequence 26, Appli
42	1750	97.4	695	7	US-11-096-046-26	Sequence 26, Appli
43	1749	97.3	449	7	US-11-080-587-6	Sequence 6, Appli
44	1748	97.3	330	7	US-11-102-621-71	Sequence 71, Appli
45	1748	97.3	446	7	US-11-102-621-121	Sequence 121, App

#### ALIGNMENTS

RESULT 1  
US-11-158-505-8  
; Sequence 8, Application US/11158505  
; Publication No. US20060002921A1  
; GENERAL INFORMATION:  
; APPLICANT: WINSOR-HINES, DAWN  
; APPLICANT: RAO, PATRICIA  
; APPLICANT: RINGLER, DOUGLAS J  
; APPLICANT: PONATH, PAUL  
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE  
; FILE REFERENCE: TLN-031  
; CURRENT APPLICATION NUMBER: US/11/158,505  
; PRIOR FILING DATE: 2005-06-21  
; PRIOR APPLICATION NUMBER: 60/582,181  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 8  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1  
; OTHER INFORMATION: antibody heavy chain construct  
US-11-158-505-8

#### Alignment Scores:

Pred. No.:	3.3e-115	Length:	448
Score:	1765.00	Matches:	330
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.22%	Indels:	0
DB:	7	Gaps:	0

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US-10-733-563-111 (1-990) x US-11-158-505-8 (1-448)
; Sequence 24, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: POWATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-24
Alignment Scores:
Pred. No.: 3,3e-115 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-111 (1-990) x US-11-158-505-24 (1-448)
QY 1 GCCTCCCAAGGGCCCATCGGTCTTCCCTCCGACCCCTCTCCAGAGCACCTCTGGG 60
Db 119 AlaserThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 138
QY 61 GGCAACAGCGCCCTCGGTGCTGCTCAAGGACTTCTCCCGAACCGGTGACGGTGTG 120
Db 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
QY 121 TGGAACTCAGCGCCCTGACAGCGGGGTGCACACCTTCCGGTGTCTCAGTCCCTCA 180
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 178
QY 181 GGACTCTACTCCCTCAGCAGCGGTGTCACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240
Db 179 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 198
QY 241 TACATCTGCAACGTGAATCATCAAGCCCGACCAACCAAGGTGGACAAGAAAGTTGAGCCC 300
Db 199 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
QY 301 AAATCTTGTCANAACATCACAATGCCACCGTCCCGTCCAGCACCTGAACTCCCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 238
QY 361 CCCTCAGTCTTCTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProProLysProLysAspThrLeuMetLleSerArgThrPro 258
QY 421 GAGTCTCATCGTGTGGTGGAGCGTGCAGCCACGACCAAGACCTTGAGGTCAAGTTCACATGG 480
Db 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
QY 481 TACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAAC 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysValAspLysValGluPro 298
QY 541 AGCAGTACCTGTGGTGTGAGTGTCTCACCCTGTGTCACAGGACTGTGCTGAATGGCAAG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
QY 601 GAGTACAGTGCAGGCTCTCAACAAAGCCCTCCAGCCGCCATCGAGAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 338
QY 661 AAAGCCAAAGGCGCAGCCCGAGAACCAACAGGTGTACACCTCGCCCGCATCGAGAAACCATCTCC 720
Db 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
QY 721 CTGACCAAGAACCAAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
QY 781 GCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAACACTACAGACCCAGCCCTCCCGT 840
Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398
QY 841 CTGACCTCCGAGCGGTCTCTTCTTCTTCTTACAGCAGCTCACCGTGGACAAGAGGAGGTGG 900
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
QY 901 CAGCAGGGGAACGTCTTCTCATGTCTCGTGTATGATGATGATGATGATGATGATGATGATGATG 960
Db 419 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438
QY 961 CAGAAGAGCCTCTCCCTGTCTCTCCGGTAAA 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448
RESULT 2
US-11-158-505-24
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Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
QY 601 GAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGAGCCCTCCATCGAGAAACCAATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 338
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCTCGCCCTCCCGGATGAG 720
Db 339 LysAlaLysGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
QY 721 CTGACCAAGAACCCAGTGCAGCTGACCTGCTCCCTGCTCAAGAGTCTATCCAGCGACATC 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
QY 781 GCCGTGAGTGGGAGAGCAATGGGAGCGGAGAGAACAACTCAAGACCAACGCTCCCGTG 840
Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398
QY 841 CTGGACTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
QY 901 CAGCAGGGGAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 419 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438
QY 961 CAGAAGAGCCCTCTCCCTCTCTCCGGGTAAA 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448

RESULT 3
US-11-158-505-5
; Sequence 5, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLM-031
; CURRENT APPLICATION NUMBER: US/11/158.505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in ver. 3.3
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-5

Alignment Scores:
Pred. No.: 3.29e-115 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-158-505-5 (1-467)
QY 1 GCCTCCACAAAGGCGCCATCGTCTTCCCTCCCTGGCACCTCTCTCAAGAGCACTCTGGG 60
Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCAAGCGGCGCTGGTGTCTGCTCAAGACTACTCTCCGGAACCGGTGACGGTGTGCG 120
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Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGGCGCTCGACAGCGGCTGCACACCTTCCGCGTCTCTCAGTCCCTCA 180
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCTCCAGCAGCTTGGGACCCAGACC 240
Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTCAGCAAGTGAATCAACAGCCCGAGCAACCAAGGTGGGACAGAAAGTTGAGCCC 300
Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 237
QY 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCCGAGCACCTGAACTCGCGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CCGTCAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 CAGGTCAATCGTGGTGGTGGAGCTGAGCCACGAGACCTGAGGTCAAGTTCAACTGCG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGAGCGGCTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTrpAsn 317
QY 541 AGCAGTACCGTGTGTGTCAGCGTCTCTCACCGTCTCTGCAACCAAGGACTGGCTGAATGGCAAG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGAGCCCTCCATCGAGAAACCAATCTCC 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCTCCCGCCATCCCGGATGAG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
QY 721 CTGACCAAGAACCCAGTGCAGCTGACCTGCTCGCTGTGTCAAGGCTCTTATCCAGCGACATC 780
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCCGTGAGTGGGAGAGCAATGGGAGCGGAGAACCAACTACAGACCCAGCTCCCGTGG 840
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 417
QY 841 CTGGACTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457
QY 961 CAGAAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 4
US-11-158-505-7
; Sequence 7, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
```

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; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-7

Alignment Scores:
Pred. No.: 3,29e-115 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-158-505-7 (1-467)

QY 1 GCCTCCACCAAGGGCCCATCGGCTTCCCTCGGACCCCTCTCTCCAGAGCACTCTGGG 60
DB 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCAAGCGGCGCTCGGCTCGTCAAGGACTTCCCGGACCGGTGACGGTGCG 120
DB 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCGCTCGACAGCGGGGTGCACACCTTCCCGGCTGTCTACAGTCTCTCA 180
DB 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCCCTCAGCAGGTGGTGACCGTGCCTCCAGCAGTGGGGACCCAGACC 240
DB 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAACGTGAATCAACAGCCAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300
DB 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237
QY 301 AAATCTTTGTGCAAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
DB 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CCGTCAGTCTTCTTCTTCCCCCAGCAAGCAACCAAGGACCCCTCATGATCTCCCGGACCCCT 420
DB 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGGTCAATCGCGTGGTGGAGTGCAGCCAGCACCGCTGAGTCAAGTCAAGTCACTGG 480
DB 278 GluValThrCysValValValAspValSerHisGluAspProGluValValPheAsnTrp 297
QY 481 TACGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAC 540
DB 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 317
QY 541 AGCAGTACCGTGGTGGTGGTCTCATCGTCTCTGACACAGGACTGGCTGAATGGCAAG 600
DB 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAGTCAAGGCTCTCAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCC 660
DB 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357
QY 661 AAAGCCAAAGGGCGCCCGGAGAACCAACAGGTGTACACCTTCGCCCCCTCCCGGGATGAG 720
DB 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
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QY 721 CTGACCAAGAACAGGTGACGCTGACCTGCTGCTCAAGGCTTCTATCCAGGACATC 780
DB 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCCGTGGAGTGGGAGAGCAATGGSCAGCGGAGAACAACTACAGAACCCAGCCCTCCCGTG 840
DB 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 417
QY 841 CTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGG 900
DB 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGAAAGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACCAACCATACACG 960
DB 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457
QY 961 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
DB 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 5
US-11-158-505-21
; Sequence 21, Application US/11/158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-21

Alignment Scores:
Pred. No.: 3,29e-115 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-158-505-21 (1-467)

QY 1 GCCTCCACCAAGGGCCCATCGGCTTCCCTCGGACCCCTCTCCAGAGCACTCTGGG 60
DB 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCAAGCGGCGCTCGGCTCGTCAAGGACTTCCCGGACCGGTGACGGTGCG 120
DB 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCGCTCGACAGCGGGGTGCACACCTTCCCGGCTGTCTACAGTCTCTCA 180
DB 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCCCTCAGCAGGTGGTGACCGTGCCTCCAGCAGTGGGGACCCAGACC 240
DB 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
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QY 241 TACATCTGCAAGCTGAATCAACAGCCCGAGCAACCAAGGTGGACAGAGAAAGTTGAGCCC 300  
DB 218 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
QY 301 AAATCTTGCAAACTCAACATGCGCCCGAGCAACCGTCCGAGCACTGAAGTCCGGGGCA 360  
DB 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAGCAACAGGACCCCTCATGATCTCCGGACCCCT 420  
DB 258 ProSerValPheLeuPheProLysProLysPheThrLeuMetIleSerArgThrPro 277  
QY 421 GAGTCAATGCGTGGTGGTGAAGTGAAGCAACCGTCCGAGTCAAGTTCAGTTCAGTGG 480  
DB 278 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
QY 481 TACGTGGAGCGGTGGAGGTGCTATGCGAGCAACAGGACCGCGGAGGAGCAGTACAAAC 540  
DB 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 317  
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
DB 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337  
QY 601 GAGTCAAGTCAAGTCTCCCAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 660  
DB 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrIleSer 357  
QY 661 AAAGCAAGGCGCGCCCGAGAGAACCAAGGTGACACCGTCCCGGATGAG 720  
DB 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377  
QY 721 CTGACCAAGTGGAGCAATGGGCGAGCGGAGCAACAACTACAGACCAACCGTCCCGGTG 840  
DB 398 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 417  
QY 841 CTGACTCCGAGCGGTCTCTTCTCTTCTACAGCAAGTCAAGTGGAGCAAGCGGTGG 900  
DB 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437  
QY 901 CAGCAGGGGAACGCTCTCTCATGCTCCGCTGATGATGAGGCTCTGCAACCAACCTACACG 960  
DB 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457  
QY 961 CAGAAGAGCCTCTCCCTCTCTCCGGGTAAA 990  
DB 458 GlnLysSerLeuSerLeuSerProGlyLys 467

## RESULT 6

US-11-158-505-23  
; Sequence 23, Application US/11158505  
; Publication No. US2006002921A1  
; GENERAL INFORMATION:  
; APPLICANT: WINSOR-HINES, DAWN  
; APPLICANT: RAO, PATRICIA  
; APPLICANT: RINGLER, DOUGLAS J  
; APPLICANT: FOMATH, PAUL  
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE  
; TITLE OF INVENTION: INDUCTION IN PRIMATES  
; FILE REFERENCE: TLN-031  
; CURRENT APPLICATION NUMBER: US/11/158,505  
; CURRENT FILING DATE: 2005-06-21  
; PRIOR APPLICATION NUMBER: 60/582,181  
; PRIOR FILING DATE: 2004-06-22  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 23  
; LENGTH: 467

! TYPE: PRT  
! ORGANISM: Artificial Sequence  
! FEATURE:  
! OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1  
! OTHER INFORMATION: heavy chain construct  
US-11-158-505-23

## Alignment Scores:

Pred. No.: 3,29e-115 Length: 467  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 7 Gaps: 0  
US-10-733-563-111 (1-990) x US-11-158-505-23 (1-467)

QY 1 GCCTCCACCAAGGCGCCCATCGGTCTTCCCTCGGCACCTCTCTCCAAAGAGCACTCTGGG 60  
DB 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157  
QY 61 GGCACAGCGCGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120  
DB 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177  
QY 121 TGGAACTCAGCGCGCTGACCAAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180  
DB 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240  
DB 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217  
QY 241 TACATCTGCAAGCTGAATCAACAGCCCGAGCAACCAAGGTGGACAGAGAAAGTTGAGCCC 300  
DB 218 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
QY 301 AAATCTTGCAAACTCAACATGCGCCCGAGCAACCGTCCCGGATGAG 360  
DB 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAGCAACAGGACCCCTCATGATCTCCGGACCCCT 420  
DB 258 ProSerValPheLeuPheProLysProLysPheThrLeuMetIleSerArgThrPro 277  
QY 421 GAGTCAATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
DB 278 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
QY 481 TACGTGGAGCGGTGGAGGTGCTATGCGAGCAACAGGACCGCGGAGGAGCAGTACAAAC 540  
DB 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 317  
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
DB 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337  
QY 601 GAGTCAAGTCAAGTCTCCCAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 660  
DB 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrIleSer 357  
QY 661 AAAGCAAGGCGCGCCCGAGAGAACCAAGGTGACACCGTCCCGGATGAG 720  
DB 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377  
QY 721 CTGACCAAGTGGAGCAATGGGCGAGCGGAGCAACAACTACAGACCAACCGTCCCGGTG 780  
DB 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397  
QY 781 GCCGTGGAGTGGAGCAATGGGCGAGCGGAGCAACAACTACAGACCAACCGTCCCGGTG 840  
DB 398 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 417

Qy	841	CTGGACTCCGAGCGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG	900
Db	418	LeuAepSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp	437
Qy	901	CAGCAGGGGAGCGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG	960
Db	438	GlnGlnGlyAenValPheSerCysSerValMetHisGluAlaLeuHisAenHisTyrThr	457
Qy	961	CAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA	990
Db	458	GlnLysSerLeuSerLeuSerProGlyLys	467
RESULT 7			
US-11-024-251-35			
; Sequence 35, Application US/11024251			
; Publication No. US20050266425A1			
; GENERAL INFORMATION:			
; APPLICANT: Zauderer, Maurice			
; APPLICANT: Paris, Mark			
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Ant			
; FILE REFERENCE: 1843.0230001			
; CURRENT APPLICATION NUMBER: US/11/024,251			
; CURRENT FILING DATE: 2004-12-29			
; PRIOR APPLICATION NUMBER: 60/533,241			
; PRIOR FILING DATE: 2003-12-31			
; NUMBER OF SEQ ID NOS: 129			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 35			
; LENGTH: 335			
; TYPE: PRT			
; ORGANISM: Artificial			
; FEATURE:			
; OTHER INFORMATION: IGG Secreted Constant Domain			
US-11-024-251-35			

QY	421	GAGGTCAATCGTGGTGCTGAGCGTGAACGACGAGACCCTGAGGTCAAGTTCAACTGG	480
Db	146	GluValThrCysValValIaspValSerHisGluAapProGluValLlyePheAenTrp	165
QY	481	TACGTGACGCCGTGGAGGTGCATAATCCAAAGACAAGAAGCCGCGGAGAGAGCAGGTACAAAC	540
Db	166	TyrValAapGlyValGluValHisAenAlalyThrLysProArgGluGluInTrpAen	185
QY	541	AGCACGTACCGTGGTTCAGCGTCTCATCCGCTCTGCACACGAGGACTGCTGAATCGCAAG	600
Db	186	SerThrTyArgValValSerValLeuThrValLeuHisGlnAepTrpPueuAenGlyLys	205
QY	601	GAGTACAGTGCAGAGTCTCCAACAAGCCCTCCAGAGCCCCCATCGAGAAAACCATCTCCC	660
Db	206	GluTyrlLysCysLyavalSerAsnLysalaLeuProAlaProileGluLysThriLeser	225
QY	661	AAAGCCAAAGGCGACGCCGAGAACCAACAGGTGTACACCTTCGCCCCCATTCCTCGGATGAG	720
Db	226	LysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSerArgAaspGlu	245
QY	721	CTGACCAAGAACACAGGTACAGCTGCACCTGCCTCGTGTCAAAGGCTTCTATCCAGCGCACATC	780
Db	246	LeuthrLysAenGlnValSerLeuThrCysLeuVallysGlyPheTyProSerAaspIle	265
QY	781	GCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAGAACAACTACAAGACCAACGCTCCCCGTG	840
Db	266	AlaValGluTrpGluSerAenGlyGlnProGluAenAenTyLysThrThrProProVal	285
QY	841	CTGAGATCCGACGGGTCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG	900
Db	286	LeuAepSerAaspGlySerPhePheLeuTyrsLysLeuThrValAaspLysSerArgTrp	305
QY	901	CAGCAGGGGACGCTTCTCTCATGCTCCGTGTGATGCATGAGGCTCTGCACAAACCACTACACG	960
Db	306	GlnGlnGlyAenValPheSerCysSerValMethHisGluAlaLeuHisAenHisTyThr	325
QY	961	CAGAAGAGCCCTCTCCCTGTCTCCCGGTAAA	990
Db	326	GlnLysSerLeuSerLeuSerProGlyLys	335
<b>RESULT 8</b>			
US-11-172-320-6			
; Sequence 6, Application US/11172320			
; Publication No. US2005024413A1			
GENERAL INFORMATION:			
; APPLICANT: Adolf, Guenther			
; APPLICANT: Baum, Anke			
; APPLICANT: Heider, Karl-Heinz			
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using			
Antibody			
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and			
Chemotherapeutic Agents			
; FILE REFERENCE: 1/1383			
; CURRENT APPLICATION NUMBER: US/11/172,320			
; CURRENT FILING DATE: 2005-06-30			
; PRIOR APPLICATION NUMBER: US/10/645,215			
; PRIOR FILING DATE: 2003-08-21			
; PRIOR APPLICATION NUMBER: EP 02 018 686.2			
; PRIOR FILING DATE: August 21, 2002			
; PRIOR APPLICATION NUMBER: US 60/405,956			
; PRIOR FILING DATE: August 26, 2002			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 6			
; LENGTH: 444			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain			
US-11-172-320-6			
Alignment Scores:			
Pred. No.: 1.38e-114 Length: 444			
Score: 1756.00 Matches: 328			

Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-172-320-6 (1-444)

QY 1 GCCTCCACAGGGCCCATCGGTCTTCCCTCGGACCCCTCTCCAGAGCACCTCTGGG 60  
DB 115 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 134  
QY 61 GGCACAGCGCCCTGGCTGCTCAAGGACTACTTCCCGAACCGGTGACGTGTCG 120  
DB 135 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 154  
QY 121 TGGAACTCAGGCGCCTGACACAGCGCGTGCACACCTTCCCGGTCTCTCAGTCTCA 180  
DB 155 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 174  
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGGTCCCTCCAGCAGCTTGGGCACCCAGACC 240  
DB 175 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 194  
QY 241 TACATCTGCAGCTGAATCAACAGCCCGACCAACCAAGGTGGACAAAGATTGAGCCC 300  
DB 195 TyrIleCysAsnValAsnHisLysProSerAenThrLysValAspLysValGluPro 214  
QY 301 AAATCTGTGACAAACTCACACATGCCCGTCCAGCAGCCTGAACTCGCGGGGCA 360  
DB 215 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuGlyGly 234  
QY 361 CGCTCAGCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCT 420  
DB 235 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 254  
QY 421 GAGTCAATGCTGCTGAGTGTGACCGGTCCAGCAAGACCTGAGGTCAAGTTCAGTGG 480  
DB 255 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 274  
QY 481 TACGTGGAGCGCGTGGAGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540  
DB 275 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 294  
QY 541 AGCAGTACCGTGTGCTCAGCGTCTCCCGTCTGACAGGAGTGGCTGATGAGTCAAG 600  
DB 295 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 314  
QY 601 GAGTACAGTGCAGGTCTCCAAAGCCCTCCAGCGCCCGCATCGAGAAACCAATCTCC 660  
DB 315 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 334  
QY 661 AAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCGCCCATCCCGGATGAG 720  
DB 335 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 354  
QY 721 CTGACCAAGAACCGGTGAGTCAAGTCTCCCTGGTCAAGAGTCTTATCCCGACGACATC 780  
DB 355 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 374  
QY 781 GCCGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACCACTACAGACCAACGCTCCCGT 840  
DB 375 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 394  
QY 841 CTGGACTCCGCGGTCTCTTCTCTCTACAGAGCTCACCGTGACAGGAGGAGTGG 900  
DB 395 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 414  
QY 901 CAGCAGGGGAAAGCTTCTTCTATGCTCCGTGTGATGAGGTCTGCACAAACCACTACACG 960  
DB 415 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 434  
QY 961 CAGAAAGCCCTCTCCCTGTCTCCCGGGTAAA 990

DB 435 GlnLysSerLeuSerLeuSerProGlyLys 444

RESULT 9  
US-11-173-969-6  
; Sequence 6, Application US/11173969  
; Publication No. US20050271672A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolif, G. et al.  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates  
; FILE REFERENCE: 1/1211  
; CURRENT APPLICATION NUMBER: US/11/173,969  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US/10/150,475  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: US 60/307,451  
; PRIOR FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanised  
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6  
US-11-173-969-6

Alignment Scores:  
Pred. No.: 1,38e-114 Length: 444  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-173-969-6 (1-444)

QY 1 GCCTCCACAGGGCCCATCGGTCTTCCCTCGGACCCCTCTCCAGAGCACCTCTGGG 60  
DB 115 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 134  
QY 61 GGCACAGCGCCCTGGCTGCTCAAGGACTACTTCCCGAACCGGTGACGTGTCG 120  
DB 135 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 154  
QY 121 TGGAACTCAGGCGCCTGACACAGCGCGTGCACACCTTCCCGGTCTCTCAGTCTCA 180  
DB 155 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 174  
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGGTCCCTCCAGCAGCTTGGGCACCCAGACC 240  
DB 175 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 194  
QY 241 TACATCTGCAACCGTGAATCAACAGCCCGACCAACCAAGGTGGACAAAGATTGAGCCC 300  
DB 195 TyrIleCysAsnValAsnHisLysProSerAenThrLysValAspLysValGluPro 214  
QY 301 AAATCTGTGACAAACTCACACATGCCCGTCCAGCAGCCTGAACTCGCGGGGCA 360  
DB 215 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuGlyGly 234  
QY 361 CGCTCAGCTTCTCTTCCCGCCCAAAACCAAGGAGACCCCTCATGATCTCCCGGACCCCT 420  
DB 235 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 254  
QY 421 GAGTCAATGCTGCTGAGTGTGACCGGTCCAGCAAGACCTGAGGTCAAGTTCAGTGG 480  
DB 255 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 274  
QY 481 TACGTGGAGCGCGTGGAGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540  
DB 275 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 294

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QY 541 AGCAGTACCGTGTGGTTCAGCGTCTCCACGCTGCTGACACGAGGACTGGCTGAATGGCAAG 600
Db |||||
QY 295 SerThrTyArgValValSerValLeuThrValLeuHisGlnAsePTrpLeuAsnGlyLys 314
Db |||||
QY 601 GAGTACAGTCAAGGCTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAAAACCATCTCC 660
Db |||||
QY 315 GlnTyLysCysLeuValSerAenLysAlaLeuProAlaProlleGluLysThrIleSer 334
Db |||||
QY 661 AAAGCCAAAGGGAGCCCGGAGAACCAAGGTGTACACCTGCGCCCGCCATCCCGGGATGAG 720
Db |||||
QY 335 LysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSerArgAsePglu 354
Db |||||
QY 721 CTGACCAAGAACCGAGTCCAGCTGACCTGCTCCCTGGTCAAGGCTTCTATCCAGCGACATC 780
Db |||||
QY 355 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAsePle 374
Db |||||
QY 781 GCCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAACCAACTCAAGACCAACCCCTCCCGTG 840
Db |||||
QY 375 AlaValGluTrpGluSerAenGlyGlnProGluAenAenTyLysThrProProVal 394
Db |||||
QY 841 CTGACCTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db |||||
QY 395 LeuAsePseAsePglySerPhePheLeuTySerLysLeuThrValAsePseAsePseArgTrp 414
Db |||||
QY 901 CAGCAGGGGAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db |||||
QY 415 GlnGlnGlyAenValPheSerCysValMetHisGlnAlaLeuHisAenHisTyThr 434
Db |||||
QY 961 CAGAAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db |||||
QY 435 GlnLysSerLeuSerLeuSerProGlyLys 444
Db |||||
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## RESULT 10

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US-11-158-505-33
; Sequence 33, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 33
; LENGTH: 451
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized CD8
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-33
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## Alignment Scores:

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Pred. No.: 1,38e-114 Length: 451
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 7 Gaps: 0
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US-10-733-563-111 (1-990) x US-11-158-505-33 (1-451)

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QY 1 GCCTCCACCAAGGCCCATCGGTCTTCCCTCGGACCCCTCTCCAGAGACCACTCTGGG 60
Db |||||
QY 122 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 141
Db |||||
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QY 61 GGCACAGGGCCCTGGGCTGCTGCTCAAGACTACTTCCCGACCGGTGACGGTGTGCG 120
Db |||||
QY 142 GlyThrAlaAlaLeuGlyCysLeuValLysAsePTrpPheProGluProValThrValSer 161
Db |||||
QY 121 TGGAACTCAGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTCTACAGTCTCTCA 180
Db |||||
QY 162 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 181
Db |||||
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGAC 240
Db |||||
QY 182 GlyLeuTySerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 201
Db |||||
QY 241 TACATCTGCAACGTGAATCAACAGCCCGCAGCAACACCAAGTGGGACAGAAAGTTGAGCCC 300
Db |||||
QY 202 TyrIleCysAenValAenHisLysProSerAenThrLysValAsePTrpLysValGluPro 221
Db |||||
QY 301 AAATCTTGTGACAAACTCAGCATGCCCCAGCGTCCAGCAGCTGAACCTCGCGGGSCA 360
Db |||||
QY 222 LysSerCysAsePTrpHisThrCysProProCysProAlaProGluLeuLeuGlyGly 241
Db |||||
QY 361 CCGTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db |||||
QY 242 ProSerValPheLeuPheProProLysProLysAsePTrpLeuMetIleSerArgThrPro 261
Db |||||
QY 421 GAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db |||||
QY 262 GluValThrCysValValValAsePTrpValSerHisGlnAsePTrpGluValLysPheAsePTrp 281
Db |||||
QY 481 TACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCGCGGAGGAGCAGTACAAAC 540
Db |||||
QY 282 TyrValAsePTrpValGluValHisAenAlaLysThrLysProArgGluGlnTyAsePTrp 301
Db |||||
QY 541 AGCAGTACCGTGTGGTTCAGCGTCTCTCCAGTCTCTGACAGGACTGGCTGAATGGCAAG 600
Db |||||
QY 302 SerThrTyArgValValSerValLeuThrValLeuHisGlnAsePTrpLeuAsnGlyLys 321
Db |||||
QY 601 GAGTACAGTGGCAGGTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAAAACCATCTCC 660
Db |||||
QY 322 GluTyLysCysLysValSerAenLysAlaLeuProAlaProlleGluLysThrIleSer 341
Db |||||
QY 661 AAAGCCAAAGGGAGCCCGGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGGATGAG 720
Db |||||
QY 342 LysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSerArgAsePglu 361
Db |||||
QY 721 CTGACCAAGAACCGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db |||||
QY 362 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAsePle 381
Db |||||
QY 781 GCCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAACCAACTCAAGACCAACCCCTCCCGTG 840
Db |||||
QY 382 AlaValGluTrpGluSerAenGlyGlnProGluAenAenTyLysThrProProVal 401
Db |||||
QY 841 CTGACTCTCCAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db |||||
QY 402 LeuAsePseAsePglySerPhePheLeuTySerLysLeuThrValAsePTrpLysSerArgTrp 421
Db |||||
QY 901 CAGCAGGGGAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db |||||
QY 422 GlnGlnGlyAenValPheSerCysSerValMetHisGlnAlaLeuHisAenHisTyThr 441
Db |||||
QY 961 CAGAAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db |||||
QY 442 GlnLysSerLeuSerLeuSerProGlyLys 451
Db |||||
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## RESULT 11

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US-11-022-289-7
; Sequence 7, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
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; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-7

Alignment Scores:
Pred. No.: 1,37e-114 Length: 551
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-022-289-7 (1-551)
QY 1 GCCTCCACAGGGCCCATCGTCTTCCCTGGCACCCCTCTCCACAGGACACCTCTGGG 60
DB 1 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSergly 20
QY 61 GGCACAGCGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGCAACCGGTGACGGTGGC 120
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspLysPheProGluProValThrValSer 40
QY 121 TGGAACTCAGCGGCCCTGACAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCA 180
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 181 GGACTCTACTCCCTCAGCAGGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240
DB 61 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 241 TACATCTGCAACGTGAATCAACAGCCCAAGGTTGGACAAGGTTGGACAAGGTTGGAC 300
DB 81 TyrIleCysAsnValAsnHisGlyProSerAsnThrLysValAspLysValGluPro 100
QY 301 AAATCTTGTGACAAACTCACACATGCCCGTCCAGCAGCCTGAACTCGCGGGGCA 360
DB 101 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 120
QY 361 CCGTCAGTCTTCTTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
DB 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATCGTGGTGGAGTGCAGTGCAGCAGCAGCAGCAGTCAAGTCAAGTCAACTGG 480
DB 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGACAGTACAAAC 540
DB 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 180
QY 541 AGCAGTACCGTGGTGGAGTGCCTTCACTGCTGACAGGACTGGCTGAATGGCAAG 600
DB 181 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 601 GAGTACAGTGCAGGTCCTCAACAAAGCCCTCCCGCCCGCCCATCGAGAAACCATCTCC 660
DB 201 GluTyLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220
QY 661 AAAGCAAAAGGCGCCCGGAGAACCAACAGGTGTACACCTGCGCCCGCCCGGATGAG 720
DB 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
QY 721 CTGACCAAGAACCAAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 CTGACCAAGAACCAAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
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QY 361 CCGTCAGTCTTCTCTCCCTCCCAAAACCCAGGACACCCCTCATGATCTCCGGACCCCT 420
Db 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATCGGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCACATGG 480
Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TACGTGACGCGGTGGAGGTGCATATGCCAAGACAAAGCCGCGGAGGACGAGTACAAAC 540
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180
QY 541 AGCAGTACCGGTGGTGGAGGTCTCTACCGCTCTGTCACACGAGGAGTGGCTGAATGGCAG 600
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 601 GAGTACAGTCAAGGTCTCCAAACAAAGCCCTCCAGGCCCCCATCGAGAAAACCATCTCC 660
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 220
QY 661 AAAGCCAAAGGCGACCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAG 720
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
QY 721 CTGACCAAGACCGGTGAGTGGGAGCAATGGGAGGAGAACAACTACAAAGACCCAGCCCTCC 780
Db 241 LeuThrLysAsnGlnValSerLysThrCysLeuValLysGlyPheTyrProSerAspIle 260
QY 781 GCCGTGAGTGGGAGGAGCAATGGGAGGAGAACAACTACAAAGACCCAGCCCTCCCGTG 840
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnIleTyrThrProProVal 280
QY 841 CTGCACTCCGACGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 900
Db 281 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
QY 901 CAGCAGGGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320
QY 961 CAGAAGAGCCCTCTCCCTGCTCCCGGTAAA 990
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330
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## RESULT 13

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US-11-022-289-4
; Sequence 4, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-4

Alignment Scores:
Pred. No.: 1.37e-114 Length: 557
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
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DB: 7 Gaps: 0
US-10-733-563-111 (1-990) x US-11-022-289-4 (1-557)
QY 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCGCACCCCTCTCCAAAGAGCACCTCTGGG 60
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20
QY 61 GGCAACAGCGCCCTGGGCTGCTGGTCAAGGACTTACTTCCCGCAACCGGTGACGGTGTG 120
Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGCGCGCTTACGAGCGGCGTGCACACCTTCCCGGTGCTCTACAGTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGACCGTGCCTTCCAGCAGCTTGGGCGCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 241 TACATCTGCAACGTGAATCAAGCCCGAGCAACCAAGGTGGACAAGAAAGTTGAGCCC 300
Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
QY 301 AAATCTTGTGACAAAACCTCACATGCCACCGTCCCGACGACCTGAACTCGCGGGGCA 360
Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 120
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCCCTCATGATCTCCCGACCCCT 420
Db 121 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATCGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 480
Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TAGCTGACGCGCTGGAGTGCATATGCCAAGACAAAGCGCGGAGGAGGAGTACAAAC 540
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180
QY 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 601 GAGTCAAGTGGCAAGGTCTCCAAAGCCCTCCAGGCCCCCATCGAGAAAACCATCTCC 660
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 220
QY 661 AAAGCCAAAGGCGACCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAG 720
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
QY 721 CTGACCAAGACCGGTGAGTGGGAGCAATGGGAGGAGAACAACTACAAAGACCCAGCCCTCC 780
Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260
QY 781 GCCGTGAGTGGGAGGAGCAATGGGAGGAGAACAACTACAAAGACCCAGCCCTCCCGTG 840
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnIleTyrThrProProVal 280
QY 841 CTGGACTCCCGACGGCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 281 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
QY 901 CAGCAGGGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320
QY 961 CAGAAGAGCCCTCTCCCTGCTCCCGGTAAA 990
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330
RESULT 14
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US-11-022-289-5
; Sequence 5, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-5

Alignment Scores:
Pred. No.: 1,37e-114 Length: 557
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 7 Gaps: 0

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QY 1 GCCTCCCAAGGGCCCATCGGTCTTCCCTGGCACCTCTCTCCAGAGCACCTCTCTGGG 60
DB 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20
QY 61 GGCACAGGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGCAACCGGTGACGTGTGG 120
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGGCGCCTGCACAGCGCGTGCACACCTTCCCGGTGTCTACAGTCTCA 180
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240
DB 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 241 TACATCTGCAAGCTGAATCACAAGCCCAAGCCCAACCAAGGTGGACAAGAAAGTTGAGCCC 300
DB 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
QY 301 AAATCTGTGACAAACTCACACATGCCCGTCCCGCCAGCACCTGAACTCGCGGGGCA 360
DB 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 120
QY 361 CGGTCAAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATATCTCCCGGACCCCT 420
DB 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATGCGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 480
DB 141 GluValThrCysValValAlaAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TACGTGGACGGGTGGAGGTGCATATCCCAAGACAAAGCCCGGAGAGGACGTACAAAC 540
DB 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180
QY 541 AGCAGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
DB 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 601 GAGTCAAGTGAAGGTCTCCAAAGCCCTTCCAGGCCCTCCAGGCCCTCCAGAAACCAATCTCC 660
DB 601 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
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DB 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220
QY 661 AAAGCCAAAGGCGCCCGGAGAACACACAGGTGTACACCTGCGCCCATCCCGGATGAG 720
DB 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
QY 721 CTGACCAAGAACACAGGTGACCTGACCTGCGTGGTCAAGGGCTTCTATCCACGACATC 780
DB 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260
QY 781 GCCGTGGAGTGGAGAGCAATGGCGAGCGCGGAGAGAACAACTACAGACACACGCTCCG 840
DB 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProVal 280
QY 841 CTGGAATCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGCACAAGAGCAGGTGG 900
DB 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
QY 901 CAGCAGGGGAACGTCTTCTCATGTCTTCTGATGATGATGATGATGATGATGATGATGAT 960
DB 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320
QY 961 CAGAAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
DB 321 GlnLysSerLeuSerLeuSerProGlyLys 330
RESULT 15
US-11-022-289-6
; Sequence 6, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-6

Alignment Scores:
Pred. No.: 1,37e-114 Length: 557
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 7 Gaps: 0

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DB 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20
QY 61 GGCACAGGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGCAACCGGTGACGTGTGG 120
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGGCGCCTGCACAGCGCGTGCACACCTTCCCGGTGTCTACAGTCTCA 180
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACC 240
DB 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 241 TACATCTGCAAGCTGAATCACAAGCCCAAGCCCAACCAAGGTGGACAAGAAAGTTGAGCCC 300
DB 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
QY 301 AAATCTGTGACAAACTCACACATGCCCGTCCCGCCAGCACCTGAACTCGCGGGGCA 360
DB 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 120
QY 361 CGGTCAAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATATCTCCCGGACCCCT 420
DB 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATGCGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 480
DB 141 GluValThrCysValValAlaAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TACGTGGACGGGTGGAGGTGCATATCCCAAGACAAAGCCCGGAGAGGACGTACAAAC 540
DB 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180
QY 541 AGCAGTACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
DB 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 601 GAGTCAAGTGAAGGTCTCCAAAGCCCTTCCAGGCCCTCCAGGCCCTCCAGAAACCAATCTCC 660
DB 601 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
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QY 241 TACATCTGCAAGTGAATCACAAGCCCGACCAAGGTGGACAGAAAGTTGAGCCC 300
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QY 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
Db |||||||
QY 301 AAATCTTTGTGACAAACATCACACATGCCCGCCCGCCAGCACCTGAACTCGCGGGGCA 360
Db |||||||
QY 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 120
Db |||||||
QY 361 CCGTCAGTCTTCTCTCCCGCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db |||||||
QY 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
Db |||||||
QY 421 GAGGTCACTGCGGTGGTGGAGTGCACGAGACCCCTGAGTCAAGTTCAACTGG 480
Db |||||||
QY 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
Db |||||||
QY 481 TACGTGACGGCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAC 540
Db |||||||
QY 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 180
Db |||||||
QY 541 AGCAGGTACCGTGTGGTGGTCTCACCGTCTCTGCACCAAGGACTGGCTCAATGGCAAG 600
Db |||||||
QY 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
Db |||||||
QY 601 GAGTACAAGTCCAAGTCTCCAAACAAGCCCTCCCGAGCCCGCCATCGAGAAACCATCTCC 660
Db |||||||
QY 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220
Db |||||||
QY 661 AAAGCCAAAGCGGAGCCCGGAGAACACACAGGTGTACACCCCTGCCCGCCATCCCGGATGAG 720
Db |||||||
QY 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
Db |||||||
QY 721 CTGACCAAGAACCAAGGTGAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCGCACATC 780
Db |||||||
QY 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260
Db |||||||
QY 781 GCCGTGGAGTGGGAGAGCAATGGCGCGGAGAACAACTACAAGACCCAGCCCTCCCGTG 840
Db |||||||
QY 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 280
Db |||||||
QY 841 CTGACTCCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 900
Db |||||||
QY 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
Db |||||||
QY 901 CAGCAGGGGAAACGTCTTCTCATGTCTCGTGATGATGAGGCTCTGCACAACCACTACACG 960
Db |||||||
QY 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320
Db |||||||
QY 961 CAGAAGAGCCCTCTCCCTGTCTCCGGTAAA 990
Db |||||||
QY 321 GlnLysSerLeuSerLeuSerProGlyLys 330
Db |||||||
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Search completed: January 28, 2006, 09:32:24  
Job time : 22.6351 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 56.0706 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-112

Perfect score: 553

Sequence: 1 RTVAAPSVFIPFPDSQLK.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	2	AAW40578 Human Kap
2	553	100.0	107	2	AAV50152 Human Kap
3	553	100.0	107	2	AAW92425 Human Kap
4	553	100.0	107	2	AAW08745 Human Kap
5	553	100.0	107	3	AAW27000 Human Kap
6	553	100.0	107	5	ABG31883 Human Kap
7	553	100.0	107	6	ABB98755 Human Kap
8	553	100.0	107	6	ABR42732 Anti-tiss
9	553	100.0	107	6	ABR42734 Anti-tiss
10	553	100.0	107	6	ABR55835 Anti-Ang
11	553	100.0	107	7	ADJ94622 Human Kap
12	553	100.0	107	8	ADJ77161 Anti-VAP-
13	553	100.0	107	8	ADL35096 Human IgG
14	553	100.0	107	8	ADL35094 Human IgG
15	553	100.0	107	8	ADM41539 Anti-inte
16	553	100.0	107	8	ADM18336 Amino aci
17	553	100.0	107	8	ADN97487 Human Kap
18	553	100.0	107	8	ADQ89334 Artificial
19	553	100.0	107	8	ADQ89334 Human Imm
20	553	100.0	107	8	ADS87911 Anti-IFN-
21	553	100.0	107	8	ADS94908 Anti-IFN-
22	553	100.0	107	8	ADT88871 Human IgG
23	553	100.0	107	8	ADT51583 Light cha
24	553	100.0	107	9	ADW08870 IGF-IR an

ALIGNMENTS

RESULT 1

AAW40578					
ID	AAW40578	standard; protein; 107 AA.			
XX	AAW40578;				
AC					
DT	21-JUL-1998	(first entry)			
XX					
DE	Human kappa CL domain protein fragment.				
XX					
KW	Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;				
KW	disorder; salvage receptor binding epitope; cell adherence interaction;				
KW	lymphocyte; T cell inflammatory response.				
XX					
OS	Homo sapiens.				
XX					
PN	US5739277-A.				
XX					
PD	14-APR-1998.				
XX					
PF	14-APR-1995;	95US-00422101.			
XX					
PR	14-APR-1995;	95US-00422101.			
XX					
PA	(GETH ) GENENTECH INC.				
PI	Snedecor BR, Presta LG;				
XX					
DR	WPI; 1998-250490/22.				
XX					
PT	Polypeptide(s) that are not Fc fragments and have an increased half-life				
PT	- are useful for the treatment of LFA-1 mediated disorders.				
XX					
PS	Disclosure; Fig 2; 38pp; English.				
XX					
CC	This protein fragment is derived from a human immunoglobulin kappa CL				
CC	domain and is used to describe a novel method to produce polypeptides				
CC	which contain an epitope from the Fc region of an Igg molecule and a				
CC	mutated salvage receptor binding epitope. They are useful for the				
CC	treatment of LFA-1 mediated disorders. These are conditions caused by				
CC	e.g. T cell inflammatory responses involving the LFA-1 receptor on lymphocytes,				
CC	in the polypeptides means that they have increased in vivo circulatory				
CC	half-lives when compared to normal Fc regions of Igg molecules				
XX					
SQ	Sequence 107 AA;				

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2  
AA50152  
ID AA50152 standard; protein; 107 AA.  
AC AA50152;  
XX  
DT 31-JAN-2000 (first entry)  
XX Human kappa light chain constant region.  
DE  
XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
KW humanisation; complementarity determining region; CDR; CDR grafting;  
KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;  
KW immune response; framework sequence; constant region; variable region;  
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;  
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;  
KW skin inflammation; tumour; immunogenicity; light chain.  
XX  
OS Homo sapiens.  
XX  
XX EP953639-A1.  
XX  
XX 03-NOV-1999.  
XX  
XX 30-APR-1998; 98EP-00107925.  
XX  
XX 30-APR-1998; 98EP-00107925.  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX  
XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;  
XX Rettig WJ;  
XX  
XX WPI; 1999-621833/54.  
XX  
XX N-PSDB; AAZ32777.  
XX  
XX New antibody protein, useful for treating cancer and for imaging presence  
XX of activated stromal fibroblasts in healing wound or inflamed skin.  
XX  
XX Disclosure; Fig 20; 143pp; English.

This sequence represents a human kappa light chain, the cDNA of which was used in the construction of a nucleotide encoding the light chain of a human reshaped monoclonal antibody F19. F19 (ATCC Accession number HB 8269) is a murine monoclonal antibody against fibroblast activation protein alpha (FAP). FAP is a cell surface molecule of reactive stromal fibroblasts, and its induction is a highly consistent molecular trait of the reactive stroma of many types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of the antibody in patients and impairs continued administration. The novel human reshaped F19 was humanised by grafting the murine complementarity determining regions (CDRs) of F19 onto human variable region framework sequences, and then joining these "reshaped human" variable regions to human constant regions. These modifications also result in the improved producibility in eukaryotic cell culture systems as compared to a chimeric antibody having the entire variable regions of F19 joined to a human constant regions. The human reshaped F19 antibody has low immunogenicity for humans and is useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, breast

CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder  
CC cancers, pancreatic cancers and metastatic cancers. It is also useful for  
CC the detection of activated stromal fibroblasts in a healing wound,  
CC inflamed skin or a tumour in a human patient  
XX  
SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3  
AAW92425  
ID AAW92425 standard; peptide; 107 AA.  
AC AAW92425;  
XX  
DT 23-APR-1999 (first entry)  
XX Human Kappa protein CL domain.  
DE  
XX Antibody; salvage receptor binding epitope; Fab; F(ab')<sub>2</sub>; immunoglobulin;  
KW CH region; CL region; kidney; FC region; CH1 domain; CH2 domain; IgG;  
KW kappa protein; renal clearance rate; circulatory half-life.  
XX  
OS Homo sapiens.  
XX  
XX US5869046-A.  
XX  
XX 09-FEB-1999.  
XX  
XX 14-APR-1995; 95US-00422092.  
XX  
XX 14-APR-1995; 95US-00422092.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Presta LG, Snedecor BR;  
XX  
XX WPI; 1999-152694/13.  
XX  
XX Production of antibody fragments with reduced renal clearance - by  
XX introducing salvage receptor binding epitope into CH1 or CL region.  
XX  
XX Disclosure; Col 55-58; 38pp; English.

This invention describes a method for preparing a variant Fab or F(ab')<sub>2</sub> polypeptide having increased half-life in vivo, where the polypeptide contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is cleared from the kidneys and does not contain an IGG FC region. The method involves altering the polypeptide within the CH1 or CL region to incorporate a salvage receptor binding epitope taken from two loops of a CH2 domain of an IGG FC region. The polypeptides have a reduced renal clearance rate and an increased circulatory half-life. This sequence represents a human kappa protein CL domain used in the method of the invention

SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNKGEC 107  
Db 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNKGEC 107

RESULT 4  
AA08745  
ID AAY08745 standard; protein; 107 AA.  
AC AAY08745;  
XX 10-AUG-1999 (first entry)  
XX Human Kappa-CL domain.  
XX IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
XX IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;  
XX cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
XX CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;  
XX antibody.  
XX Homo sapiens.  
XX US5914112-A.  
XX 22-JUN-1999.  
XX 22-JAN-1997; 97US-00788800.  
XX 23-JAN-1996; 96US-0093038P.  
XX (GETH ) GENENTECH INC.  
XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
XX Thomas GR, Bednar MM, Gross CE;  
XX WPI; 1999-370483/31.  
XX Anti-CD18 antibodies in stroke.  
XX Disclosure; Fig 4A-B; 25pp; English.

This invention describes a method for improving the clinical outcome in focal ischaemic stroke by administering novel anti-CD18 antibody which has cerebroprotective properties. The invention particularly describes a method of treating focal ischaemic stroke caused by the obstruction of a main cerebral artery which comprises administering an anti-CD18 antibody to increase the blood flow or reduce the infarct size, where: (1) the antibody binds to an extracellular domain of CD18 and inhibits or reduces the ability of the cell expressing CD18 to bind to endothelium, (2) the antibody binds CD18 with an affinity of less than 4 nm, or (3) the antibody dissociates CD11b/CD18 complex. This sequence represents the human Kappa-CL domain which is used to illustrate the method of the invention

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNKGEC 107  
Db 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNKGEC 107

RESULT 5  
AAB27000  
ID AAB27000 standard; protein; 107 AA.  
XX AAB27000;  
XX 25-JAN-2001 (first entry)  
XX Human kappa CL domain.  
XX Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;  
XX mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;  
XX psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;  
XX inflammation; vaccine.  
XX Homo sapiens.  
XX US6121022-A.  
XX 19-SEP-2000.  
XX 14-APR-1995; 95US-00422112.  
XX 14-APR-1995; 95US-00422112.  
XX (GETH ) GENENTECH INC.  
XX Preeta LG, Snedecor BR;  
XX WPI; 2000-610925/58.  
XX New nucleic acid encoding new modified polypeptides with increased  
XX circulatory half-life useful for preventing/treating LFA-1-mediated  
XX disorders, e.g. reducing inflammatory responses or inducing tolerance to  
XX immunostimulants.  
XX Disclosure; Fig 2; 38pp; English.

The present sequence was used in a method for improving the in vivo half-life of polypeptides. The polypeptides comprise an Ig constant domain or an Ig-like constant domain, and a salvage receptor binding epitope within the Ig or Ig-like domain. The salvage receptor epitope is taken from two loops of the CH2 domain of an FC region of an Ig molecule. The modified polypeptides are useful for preventing or treating LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated diseases, B-cell lymphomas. They are also useful for wound repair, reducing inflammatory responses and inducing tolerance to immunostimulants. They may also be used in diagnostic assays. The nucleic acids and modified polypeptides are useful for the passive immunisation of patients, as well as for affinity purification of an antigen from recombinant cell culture or natural sources

Query Match 100.0%; Score 553; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNKGEC 107  
Db 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNKGEC 107

RESULT 6  
ABG31883  
ID ABG31883 standard; protein; 107 AA.  
XX AC ABG31883;

XX DT 05-NOV-2002 (first entry)  
 XX DE Human kappa CL domain.  
 XX KW Human; kappa CL domain; cerebral blood flow; infarct size;  
 KW focal ischaemic stroke; main cerebral artery;  
 KW tissue plasminogen activator; anti-CD18 antibody; stroke;  
 KW acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.  
 XX OS Homo sapiens.  
 XX OS US2002081294-A1.  
 XX PN 27-JUN-2002.  
 XX PD 20-DEC-2000; 2000US-00811384.  
 XX PF 23-JAN-1996; 96US-0093038P.  
 XX PR 22-JAN-1997; 97US-00788800.  
 XX PR 17-FEB-1999; 99US-00251652.  
 XX XX (GETH ) GENENTECH INC.  
 XX PA Bednar MM, Gross CE, Thomas GR, Gross LJ;  
 XX PI WPI; 2002-626528/67.  
 XX DR Increasing cerebral blood flow and/or reducing infarct size in focal  
 XX PT ischemic stroke using anti-CD18 antibody and tissue plasminogen activator  
 XX PT is useful to improve clinical outcome in acute ischemic stroke.  
 XX PS Disclosure; Fig 4; 27pp; English.  
 XX CC The invention relates to a method of increasing cerebral blood flow and/  
 CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
 CC of a main cerebral artery in a human, comprising co-administering tissue  
 CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
 CC stroke. The method is used to improve the clinical outcome in acute  
 CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
 CC for treating thromboembolic stroke, particularly where thrombolytic  
 CC therapy has been unsuccessful or is contra-indicated. The present  
 CC sequence represents the human kappa CL domain used in the method of the  
 CC invention

XX SQ Sequence 107 AA;  
 Query Match 100.0%; Score 553; DB 5; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7  
 ABB98755  
 ID ABB98755 standard; protein; 107 AA.  
 XX AC ABB98755;  
 XX XX 23-JAN-2003 (first entry)  
 XX DE Human kappa light constant chain.  
 XX KW Human; cytostatic; antitumour; immunosuppressive; antiallergic;  
 KW humanised; antibody; fibroblast activation protein alpha; FAPalpha;  
 KW cancer; monoclonal antibody F19; colorectal cancer;

KW non-small cell lung carcinoma; breast cancer; pancreatic cancer; tumour;  
 KW systemic autoimmune disease; allergy; light chain; constant region.  
 XX OS Homo sapiens.  
 XX PN WO200283171-A2.  
 XX PD 24-OCT-2002.  
 XX PF 11-APR-2002; 2002WO-EP004041.  
 XX PR 12-APR-2001; 2001US-0283868P.  
 XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 XX PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
 XX PI Amelsberg A, Scott A, Tanswell P;  
 XX XX WPI; 2003-058609/05.  
 XX DR N-PSDB; ABV74601.  
 XX PT Use of a humanized antibody which specifically binds to fibroblast  
 XX PT activation protein alpha for manufacturing a medicament for treating  
 XX PT cancer.  
 XX PS Claim 7; Page 55; 57pp; English.  
 XX CC The present invention relates to the use of a humanised antibody (I),  
 CC which specifically binds to fibroblast activation protein alpha  
 CC (FAPalpha), for manufacturing a medicament for treating cancer. (I) has  
 CC the complementary determining region (CDR) of the monoclonal antibody  
 CC F19, but has framework modifications resulting in improved producibility  
 CC in host cells as compared to a chimeric antibody having the variable  
 CC regions of F19 and foreign constant regions. To generate (I), a chimeric  
 CC antibody was constructed having variable regions of the light and heavy  
 CC chains of F19 and human light and heavy constant regions. (I) is useful  
 CC for treating a patient suffering from a pathological condition  
 CC characterised by expression of FAPalpha, such as colorectal cancer, non-  
 CC small cell lung carcinoma, breast cancer, pancreatic cancer, tumours,  
 CC systemic autoimmune diseases and allergies. The present sequence is human  
 CC kappa light constant chain which was used to produce (I)

XX SQ Sequence 107 AA;  
 Query Match 100.0%; Score 553; DB 6; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8  
 ABR42732  
 ID ABR42732 standard; protein; 107 AA.  
 XX AC ABR42732;  
 XX XX 26-AUG-2003 (first entry)  
 XX DE Anti-tissue factor humanized antibody light chain constant region.  
 XX KW Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antiinflammatory; mouse; human; hOAT.  
 XX OS Mus sp.  
 XX OS Homo sapiens.  
 XX OS Chimeric.

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XX PN WO2003037911-A2.
XX PD
XX PP 08-MAY-2003.
XX PR 29-OCT-2002; 2002WO-US034727.
XX PR 29-OCT-2001; 2001US-0343306P.
XX PR 21-NOV-2001; 2001US-00990586.
XX PA (SUNO-) SUNOL MOLECULAR CORP.
XX PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX DR WPI; 2003-468399/44.
XX PT New humanized antibody that binds specifically to human tissue factor,
XX PT useful for in vivo diagnostic methods, or for inhibiting blood
XX PT coagulation or blood clot formation, angiogenesis, tumor metastases or
XX PT inflammation in a mammal.
XX PS Example 10; Fig 14A; 110pp; English.
XX CC The present sequence is the protein sequence of the light chain constant
XX CC region of anti-human tissue factor (TF) humanized antibody hOAT
XX CC (humanised CH36-IgG1). Humanized antibodies of the invention provide
XX CC superior anticoagulant activity by binding native human TF with high
XX CC affinity and specificity. The antibodies bind human TF, either alone or
XX CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
XX CC Factor IX) binding to TF or the complex, and thereby reducing blood
XX CC coagulation. The humanized antibodies are useful for inhibiting blood
XX CC coagulation or blood clot formation, angiogenesis, tumor metastases or
XX CC inflammation in a mammal. They are also useful as drug carriers, as
XX CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
XX CC diagnosis
XX SQ Sequence 107 AA;
    Query Match 100.0%; Score 553; DB 6; Length 107;
    Best Local Similarity 100.0%; Pred. No. 4.1e-48;
    Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||
QY 61 SKDSTYSLSSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db |||||
QY 61 SKDSTYSLSSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db |||||
RESULT 9
ABR42734
ID ABR42734 standard; protein; 107 AA.
AC ABR42734;
XX 26-AUG-2003 (first entry)
XX DE Anti-tissue factor humanized antibody light chain constant region.
XX KW Tissue factor; humanization; antibody; anticoagulant; cytostatic;
XX KW antiinflammatory; mouse; human; hOAT.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX PN WO2003037911-A2.
XX PD 08-MAY-2003.
XX PR 29-OCT-2002; 2002WO-US034727.

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XX PR 29-OCT-2001; 2001US-0343306P.
XX PR 21-NOV-2001; 2001US-00990586.
XX PA (SUNO-) SUNOL MOLECULAR CORP.
XX PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX DR WPI; 2003-468399/44.
XX PT New humanized antibody that binds specifically to human tissue factor,
XX PT useful for in vivo diagnostic methods, or for inhibiting blood
XX PT coagulation or blood clot formation, angiogenesis, tumor metastases or
XX PT inflammation in a mammal.
XX PS Example 10; Fig 15A; 110pp; English.
XX CC The present sequence is the protein sequence of the light chain constant
XX CC region of anti-human tissue factor (TF) humanized antibody hPAT
XX CC (humanised CH36-IgG4). Humanized antibodies of the invention provide
XX CC superior anticoagulant activity by binding native human TF with high
XX CC affinity and specificity. The antibodies bind human TF, either alone or
XX CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
XX CC Factor IX) binding to TF or the complex, and thereby reducing blood
XX CC coagulation. The humanized antibodies are useful for inhibiting blood
XX CC coagulation or blood clot formation, angiogenesis, tumor metastases or
XX CC inflammation in a mammal. They are also useful as drug carriers, as
XX CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
XX CC diagnosis
XX SQ Sequence 107 AA;
    Query Match 100.0%; Score 553; DB 6; Length 107;
    Best Local Similarity 100.0%; Pred. No. 4.1e-48;
    Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||
QY 61 SKDSTYSLSSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db |||||
QY 61 SKDSTYSLSSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db |||||
RESULT 10
ABR55835
ID ABR55835 standard; protein; 107 AA.
XX ABR55835;
XX 02-SEP-2003 (first entry)
XX DE Anti-Ang-2 antibody kappa constant region.
XX KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
XX KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
XX KW angiogenesis; antibody.
XX OS Homo sapiens.
XX PN WO2003030833-A2.
XX PD 17-APR-2003.
XX PF 11-OCT-2002; 2002WO-US032613.
XX PR 11-OCT-2001; 2001US-0328604P.
XX PR 10-OCT-2002; 2002US-00269805.
XX PA (AMGE-) AMGEN INC.
XX PI Oliner JD;

```

XX WPI; 2003-504963/47.

XX New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful

PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,

PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

XX

XX Example 4; Page 96; 161pp; English.

XX

CC The invention relates to a specific binding agent, which comprises at

CC least one peptide selected from any of 62 peptides (ABR55769-830) or its

CC fragment. The binding agents are antibodies that recognize and bind to

CC angiopoietin-2 (Ang-2). The specific binding agent, particularly the

CC antibody, is useful for inhibiting undesired angiogenesis, treating

CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-

CC 2 activity, modulating vascular permeability or plasma leakage, or

CC treating a disease (e.g. ocular neovascular disease, obesity,

CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,

CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic

CC disease, bone-related disease, or psoriasis) in a mammal. The present

CC sequence represents a human kappa constant region of an anti-Ang-2

CC antibody

XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 6; Length 107;

Best Local Similarity 100.0%; Pred. No. 4.1e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 11

ADJ94622

ID ADJ94622 standard; protein; 107 AA.

XX

AC ADJ94622;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human kappa chain (CK) constant region.

XX

KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;

KW IVIAB variable region; B-cell lymphoma; leukaemia; autoimmune disease;

KW thrombocytopenia; lupus; rheumatoid arthritis; kappa chain; human; CK;

XX

OS Homo sapiens.

XX

PN WO2003068821-A2.

XX

PD 21-AUG-2003.

XX

PF 14-FEB-2003; 2003WO-GB000665.

XX

PR 14-FEB-2002; 2002US-0356132P.

PR 07-OCT-2002; 2002US-0416232P.

XX

PA (IMMU-) IMMUNOMEDICS INC.

PA (MCCA/) MCCA J. D.

XX

PI Hansen H, Qu Z, Goldenberg DM;

XX

DR WPI; 2003-697522/66.

DR N-PSDB; ADJ94621.

XX

PT New humanized anti-CD20 monoclonal antibody (Mab) that retains

PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting

PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,

XX leukemia or an autoimmune disease.

XX Example 1; Fig 7B; 106pp; English.

XX

CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody

CC (Mab) or its antigen-binding fragment containing the complementarity

CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable

CC region and the framework regions (FRs) of at least one human IVIAB

CC variable region. The antibodies of the invention are useful for

CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune

CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The

CC present amino acid sequence represents a human kappa chain (CK) constant

CC region.

XX

SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 4.1e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 12

ADF77161

ID ADF77161 standard; protein; 107 AA.

XX

AC ADF77161;

XX

DT 26-FEB-2004 (first entry)

XX

DE Anti-VAP-1 monoclonal antibody L chain constant region.

XX

KW complementarity determining region; CDR; mouse;

KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;

KW chimeric; inflammatory disorder; rheumatoid arthritis;

KW inflammatory bowel disease; autoimmune disease; psoriasis;

XX immunoscintigraphic imaging.

XX

OS Homo sapiens.

XX

PN WO2003093319-A1.

XX

PD 13-NOV-2003.

XX

PF 28-APR-2003; 2003WO-FI000330.

XX

PR 29-APR-2002; 2002FI-00000807.

XX

PA (BIOT-) BIOTIE THERAPIES CORP.

XX

PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;

XX

DR WPI; 2004-022642/02.

XX

PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and

PT encoding nucleic acid molecules, useful for diagnosing and treating

PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.

XX

PS Claim 18; SEQ ID NO 22; 56pp; English.

XX

CC This sequence represents the constant region of a human anti-Vascular

CC Adhesion Protein-1 (VAP-1) antibody light chain. This sequence may be

CC used in the production of a chimeric mouse-human anti-VAP-1 antibody. The

CC nucleic acid molecules, polypeptides or antibodies are useful in treating

CC VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis,  
 CC inflammatory bowel disease, autoimmune diseases or psoriasis. The  
 CC chimeric VAP-1 antibody is further used for in vitro and in vivo  
 CC diagnostic applications, including in vivo immunoscintigraphic imaging of  
 CC inflammation sites. The chimeric MAB's of the invention have improved  
 CC kinetic properties compared to the corresponding murine antibodies.

XX Sequence 107 AA;  
 SQ Query Match 100.0%; Score 553; DB 8; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

## RESULT 13

ADL35096  
 ID ADL35096 standard; protein; 107 AA.

AC ADL35096;

DT 03-JUN-2004 (first entry)

XX Human IgG4 (hPAT) kappa light chain constant domain protein SeqID 99.

DE antibody; variable domain; framework region; FR; huFR;  
 KW immune system molecule; kappa; anti-tissue factor; hPAT; human.

XX Homo sapiens.

XX WO2004020579-A2.

XX 11-MAR-2004.

XX 06-AUG-2003; 2003WO-US024637.

XX 29-AUG-2002; 2002US-00230880.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Wong HC, Stinson JR, Mosquera LA;

XX WPI; 2004-239169/22.

XX Producing humanized antibodies for diagnostic and therapeutic purposes  
 PT comprises optimizing similarity between individual antibody framework  
 PT regions to help identify human framework regions suitable for making the  
 PT antibodies.

XX Disclosure; SEQ ID NO 99; 137pp; English.

XX This invention relates to a novel method for producing a humanised  
 CC antibody variable (V) domain or its fragment by optimising sequence  
 CC similarity between individual antibody framework regions (FRs) in order  
 CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
 CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
 CC suitable binding affinity with reduced immunogenicity in humans. The  
 CC present invention describes a method of mutagenising DNA of non-human FRs  
 CC to encode humanised FRs having an amino acid sequence that is  
 CC substantially identical to the selected human FR previously identified  
 CC through sequence similarity searching. As such, this method provides  
 CC humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2  
 CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
 CC products to treat and/or diagnose diseases in humans and animals.  
 CC Furthermore, the method expands the number of best fit possibilities that  
 CC can be generated and provides a rational basis for assembling nearly all

CC humanised immune system molecules of interest. This polypeptide sequence  
 CC is the human IgG4 kappa light chain constant domain protein of the  
 CC invention.

XX Sequence 107 AA;

XX Query Match 100.0%; Score 553; DB 8; Length 107;  
 XX Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

## RESULT 14

ADL35094  
 ID ADL35094 standard; protein; 107 AA.

XX ADL35094;

XX 03-JUN-2004 (first entry)

XX Human IgG1 (hOAT) kappa light chain constant domain protein SeqID 97.

DE antibody; variable domain; framework region; FR; huFR;  
 KW immune system molecule; kappa; anti-tissue factor; hOAT; human.

XX Homo sapiens.

XX WO2004020579-A2.

XX 11-MAR-2004.

XX 06-AUG-2003; 2003WO-US024637.

XX 29-AUG-2002; 2002US-00230880.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Wong HC, Stinson JR, Mosquera LA;

XX WPI; 2004-239169/22.

XX Producing humanized antibodies for diagnostic and therapeutic purposes  
 PT comprises optimizing similarity between individual antibody framework  
 PT regions to help identify human framework regions suitable for making the  
 PT antibodies.

XX Disclosure; SEQ ID NO 97; 137pp; English.

XX This invention relates to a novel method for producing a humanised  
 CC antibody variable (V) domain or its fragment by optimising sequence  
 CC similarity between individual antibody framework regions (FRs) in order  
 CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
 CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
 CC suitable binding affinity with reduced immunogenicity in humans. The  
 CC present invention describes a method of mutagenising DNA of non-human FRs  
 CC to encode humanised FRs having an amino acid sequence that is  
 CC substantially identical to the selected human FR previously identified  
 CC through sequence similarity searching. As such, this method provides  
 CC humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2  
 CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
 CC products to treat and/or diagnose diseases in humans and animals.  
 CC Furthermore, the method expands the number of best fit possibilities that  
 CC can be generated and provides a rational basis for assembling nearly all  
 CC humanised immune system molecules of interest. This polypeptide sequence  
 CC is the human IgG1 kappa light chain constant domain protein of the  
 CC invention.

```

XX SQ      Sequence 107 AA;
Query Match      100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Db      1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60

QY      61 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 15
ADM41539
ID ADM41539 standard; protein; 107 AA.
XX
AC ADM41539;
XX
DT 03-JUN-2004 (first entry)
XX
DE Anti-interleukin-1 receptor type 1 antibody kappa chain constant region.
XX
KW Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW prozoocaine; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW anticonvulsant; dermatological; antigen; antiparkinsonian; antidiabetic;
KW cyostatic.
XX
OS Homo sapiens.
XX
FN WO2004022718-A2.
XX
PD 18-MAR-2004.
XX
PF 05-SEP-2003; 2003WO-US027978.
XX
PR 06-SEP-2002; 2002US-0408719P.
XX
PA (ANGE-) AMGEN INC.
XX
PI Varnum B, Vezina C, Witte A, Qian X, Martin P, Huang H;
PI Elliott G;
XX
DR WPI; 2004-248462/23.
DR N-PSDB; ADM41538.
XX
PT Isolated human antibody that specifically binds interleukin-1 receptor
PT type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
PS Disclosure; SEQ ID NO 4; 179pp; English.
XX
CC The present sequence is that of a human anti-interleukin-1 receptor type
CC 1 (IL-1R1) monoclonal antibody (Mab) kappa chain constant region. Human
CC Mabs to IL-1R1 were prepared using the HCo7 strain of transgenic mice,
CC which expresses human antibody genes. These mice were immunised with
CC purified recombinant IL-1R1, and splenocytes from immunised mice were
CC fused to a mouse myeloma cell line to generate hybridomas. Hybridomas
CC which secreted a MAb that bound with high avidity to IL-1R1 were
CC selected. The Mabs inhibit IL-1 signalling by competing with IL-1beta and
CC IL-1alpha binding to IL-1R. These Mabs, as well as single chain
CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies
CC and (Fab')2 antibodies derived from them, are used in methods of treating
CC IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.
CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral
CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,
CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
CC Clostridium associated illnesses, coronary conditions, cancer including

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CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,
CC fibromyalgia, glomerulonephritis, graft versus host disease,
CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,
CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,
CC septic shock, side effects of radiation therapy, temporal mandibular
CC joint disease, sleep disturbance, uveitis, or an inflammatory condition
CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic
XX surgery, infection or other disease processes.
XX
SQ      Sequence 107 AA;
Query Match      100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
Db      1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60

QY      61 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

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Search completed: January 28, 2006, 09:38:16  
Job time : 57.0706 secs



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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:23:14 ; Search time 10.9249 Seconds  
(without alignments)  
942.358 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPPDEQLKS.....EVTHQGLSPVTKSFNRGEC 107  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 80: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	215	2 JE0243	Ig kappa chain NIG
2	553	100.0	215	2 JE0244	Ig kappa chain NIG
3	553	100.0	215	2 JE0242	Ig kappa chain NIG
4	550	99.5	135	2 S52059	JC-kappa protein -
5	548	99.1	106	1 K3HU	Ig kappa chain C r
6	537	97.1	216	2 JE0241	Ig kappa chain Am3
7	520	94.0	215	2 A23746	Ig kappa chain V-1
8	513	92.8	99	2 A37927	Ig kappa chain C r
9	507	91.7	99	2 S26653	Ig kappa chain C r
10	372	67.3	240	2 S06084	Ig kappa chain pre
11	367	66.4	106	1 K1RTB	Ig kappa chain C r
12	366	66.2	178	2 PT0219	Ig kappa chain V-C
13	359	64.9	106	1 K1RTA	Ig kappa chain C r
14	358	64.7	217	2 S42772	Ig kappa chain - m
15	358	64.7	218	2 S68241	Ig kappa chain V r
16	358	64.7	219	2 S38865	Ig kappa chain C r
17	352	63.7	218	2 JC5810	monoclonal antibod
18	352	63.7	219	2 S52028	Ig kappa chain - m
19	352	63.7	219	2 PC4203	Ig kappa chain - m
20	352	63.7	219	2 S16112	Ig kappa chain V r
21	352	63.7	220	2 A31790	Ig kappa chain V r
22	352	63.7	225	2 S37484	Ig kappa chain - m
23	352	63.7	234	2 S14237	Ig kappa chain pre
24	352	63.7	234	2 S01320	Ig kappa chain pre
25	352	63.7	235	2 S25058	Ig kappa chain - m
26	350	63.3	106	1 K1MS	Ig kappa chain C r
27	350	63.3	126	2 K1M5	gene Pvt-1a/Ig-Ck
28	348	62.9	225	2 JL0029	Ig kappa chain pre
29	345	62.4	230	2 S33161	Ig kappa chain - s

30	321	58.0	214	2 S68212	Ig kappa chain (Ma
31	312	56.4	210	2 A56169	Ig kappa chain V r
32	308.5	55.8	106	2 G20907	Ig kappa-B4 chain
33	306.5	55.4	106	1 K4RBS	Ig kappa-2 chain C
34	277.5	50.2	229	2 A20969	Ig kappa chain pre
35	257.5	46.6	103	1 K4RB	Ig kappa-B4 chain
36	256	46.3	104	2 F53275	Ig kappa-1 chain C
37	246.5	44.6	104	1 K9RB	Ig kappa-B9 chain
38	245	44.3	238	2 A49633	Ig lambda-like cha
39	241	43.6	104	1 K5RBV	Ig kappa chain C r
40	237	42.9	118	2 A46518	Ig Li chain J-C re
41	231	41.8	103	2 B26167	Ig lambda chain C
42	231	41.8	213	2 A21177	Ig light chain pre
43	225	40.7	108	1 K3FG	Ig light chain C r
44	223.5	40.4	103	1 K5RB	Ig kappa-B5 chain
45	222	40.1	197	2 S29593	Ig kappa chain (WM

ALIGNMENTS

RESULT 1

JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243  
R:Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, P.; Yamaki, H.; T  
Submitted to JFID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>

A:Cross-references: UNIPARC:UPI0000176984

C:Superfamily: immunoglobulin V region; immunoglobulin homology

P:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.6e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQD 60
DB	109	RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQD 168
QY	61	SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
DB	169	SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, P.; Yamaki, H.; T

Submitted to JFID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

A:Cross-references: UNIPARC:UPI0000176982

C:Superfamily: immunoglobulin V region; immunoglobulin homology

P:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.6e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQD 60
----	---	--

Db 109 RTVA<sup>PSVF</sup>IP<sup>PSDE</sup>QL<sup>SGTAS</sup>VV<sup>CLLNN</sup>FYP<sup>REAKVQ</sup>KY<sup>VDNAL</sup>OS<sup>GN</sup>QS<sup>SVTEQD</sup> 168

<b>Qy</b>	61 SKDSTYSLSSTLTLSKADYEKHKYVACEVTHQGSSPVTKSFNRGEC 107 
<b>D<sub>b</sub></b>	169 SKDSTYSLSSTLTLSKADYEKHKYVACEVTHQGSSPVTKSFNRGEC 215 

RESULT 3  
JE0242  
IG kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JPTD, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
A:Cross-references: UNIPARC:UPI0000176983  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domains: immunoglobulin homology <IMV>

Query Match	100.08;	Score	553;	DB	2;	Length	215;
Best Local Similarity	100.00;	Pred. No.	1.6e-46;				
Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0						
Qy	1	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALGSGNSQESVTE	60				
Db	109	RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALGSGNSQESVTE	168				

Qy 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 169 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4  
S52059 JC-kappa protein - human  
C/Species: Homo sapiens (man)  
C/Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 08-Sep-2000  
C/Accession: S52059  
R/Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.; EMBO J. 13, 5937-5943, 1994  
A/Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy chain  
A/Reference number: S52059; MUID:55112804; PMID:7813432  
A/Accession: S52059  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-135 <FRA>  
A/Cross-references: UNIPARC:UPI00001184D0  
C/Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 99.5%; Score 550; DB 2; Length 135;  
Best Local Similarity 99.1%; Pred. No. 1.8e-46;  
Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLINNFYFPKVKVQWVKDNALSGNSQESVTEQ 60  
DB 29 RTVAAPSVFIFPPSDEQLKSGTASVCLINNFYFPKVKVQWVKDNALSGNSQESVTEQ 88

	61	SKDSTYSLSSTLTLSKADYEKHVYACEVTHQGLSSPVTKSFNRGEC	107
Qy		: :	
	89	SKDSTYSLSSTLTLSKADYEKHLYACEVTHQGLSSPVTKSFNRGEC	135
Dd			

RESULT 5  
K3HU  
Ig kappa chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1980 #sequence revision 02-Jul-1998 #text change 09-Jul-2004

C;Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02116  
R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.  
Biochemistry 9, 3155-3161, 1970  
A>Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequence  
A:Reference number: A90562; MUID:71064023; PMID:5489770  
A:Contents: myeloma protein Eu  
A:Accession: B90562  
A:Molecule type: protein  
A:Residues: 1-106 <GOT>  
A:Cross-references: UNIPROT:P01834; UNIPARC:UIP000002F106  
A>Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation: Eu, disulfide bonds  
R;Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
A>Title: Die Primerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Subg  
A:Reference number: A91651; MUID:72188439; PMID:5027703  
A:Contents: Bence Jones protein Ti  
A:Accession: A91651  
A:Molecule type: protein  
A:Residues: 1-106 <SUT>  
A:Cross-references: UNIPARC:UIP000002F106  
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.  
Cell 22, 197-207, 1980  
A>Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserve  
A:Reference number: A90806; MUID:81042304; PMID:6775818  
A:Accession: A90806  
A:Molecule type: DNA  
A:Residues: 1-106 <HIE>  
A:Cross-references: UNIPARC:UIP000002F106; GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g3  
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, F.  
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, I  
A:Reference number: A94417  
A:Contents: Bence Jones protein Roy  
A:Accession: A94417  
A:Molecule type: protein  
A:Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>  
A:Cross-references: UNIPARC:UIP000017376D  
A>Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu  
R;Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
A>Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).  
A:Reference number: A91639; MUID:68242259; PMID:5586923  
A:Contents: Bence Jones protein Cum  
A:Accession: A91639  
A:Molecule type: protein  
A:Residues: 1-56, 'Q', 58-106 <HI2>  
A:Cross-references: UNIPARC:UIP000017376E  
R;Titani, K.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A>Title: The amino acid sequief of a kappa type Bence-Jones protein. III. The complete  
A:Reference number: A92047; MUID:69234734; PMID:4893682  
A:Contents: Bence Jones protein Ag  
A:Accession: A92047  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <TIT>  
A:Cross-references: UNIPARC:UIP000017376F  
R;Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 56-59, 1970  
A>Title: Macroglobulin structures: variable sequence of light and heavy chains.  
A:Reference number: A94242; MUID:70201507; PMID:5447531  
A:Contents: Waldenström's macroglobulin Ou  
A:Accession: A94242  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <KOH>  
A:Cross-references: UNIPARC:UIP000017376F  
R;Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A>Title: Km typing with PCR: application to population screening.

A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A:Cross-references: UNIPARC:UPI0000173770  
A>Note: allotype inv(3)  
R:Steiner, V.; Chang, J.Y.  
PDBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
A:Contents: annotation  
C:Genetics:

A:Gene: GDB:IGKC  
A:Cross-references: GDB:120088; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 99.1%; Score 548; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.1e-46;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61

Db 1 TVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 61 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

#### RESULT 6

Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
A:Accession: J80241  
R:Alim, M.A.; Yamaki, S.; Hoessain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
A:Reference number: J80241  
A:Accession: J80241  
A:Molecule type: protein  
A:Residues: 1-216 <ALI>  
A:Cross-references: UNIPARC:UPI0000176981  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 537; DB 2; Length 216;  
Best Local Similarity 97.2%; Pred. No. 5.7e-45;  
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 110 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169

QY 61 SKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 170 SKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

#### RESULT 7

Ig kappa chain V-III (KAU cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
A:Accession: A23746

R:Leoni, J.; Ghiso, J.; Goni, P.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin  
A:Reference number: A23746; MUID:91131575; PMID:1993660

A:Accession: A23746  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
A:Cross-references: UNIPARC:UPI0000176985  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 520; DB 2; Length 215;  
Best Local Similarity 98.1%; Pred. No. 2.6e-43;  
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 109 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

Db 169 SKDSYSLSTLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGEC 214

#### RESULT 8

A37927  
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
A:Accession: A37927  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: A37927  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
A:Cross-references: UNIPARC:UPI0000176ED6  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 513; DB 2; Length 99;  
Best Local Similarity 99.0%; Pred. No. 5e-43;  
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 FIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 68

Db 1 FIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 60

QY 69 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 61 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 99

#### RESULT 9

S26653  
Ig kappa chain C region - chimpanzee (fragment)  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
A:Accession: S26653  
R:Erlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybrids 1, 23-26, 1990  
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies: r  
A:Reference number: S26652; MUID:91355693; PMID:2129418  
A:Accession: S26653  
A:Status: translation not shown

A:Molecule type: mRNA  
A:Residues: 1-99 <EHR>  
A:Cross-references: UNIPARC:UPI0000176ED5; EMBL:X65287

C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;19-88/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 507; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.9e-42;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 TVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDS 61  
Db 1 TVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDS 60  
  
Qy 62 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTK 100  
Db 61 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTK 99

RESULT 10  
S06084  
Ig kappa chain precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C;Accession: S06084  
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA  
A;Reference number: S06084; MUID:90016888; PMID:2508067  
A;Accession: S06084  
A;Molecule type: mRNA  
A;Residues: 1-240 <CRO>  
C;Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-240/Product: Ig kappa chain #status predicted <MAT>  
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 372; DB 2; Length 240;  
Best Local Similarity 65.4%; Pred. No. 7.4e-29;  
Matches 70; Conservative 13; Mismatches 24; Indels 0; Gaps 0;  
  
Qy 1 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60  
Db 134 RADAAPTVISFPPSTEQLATGASVVCCLMNNFYPRDISVKWKIDGTERDGVLDSDVDQD 193  
  
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 194 SKDSTYMSSTLSLKADYKSHNLYTCVVHKTSSSPVVKSFNRNEC 240

RESULT 11  
KIRTB  
Ig kappa chain C region (allele b) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
C;Accession: A93901; A92807; A02117  
R;Sheppard, H.W.; Gutman, G.A.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981  
A;Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le  
A;Reference number: A93901; MUID:82082587; PMID:6273908  
A;Accession: A93901  
A;Molecule type: DNA  
A;Residues: 1-106 <SHE>  
C;Cross-references: UNIPROT:P01835; UNIPARC:UPI000012DB83; GB:V01241; GB:J00745; GB:J025  
A;Experimental source: strain LOU  
R;Starace, V.; Querinjean, P.  
J. Immunol. 115, 59-62, 1975  
A;Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation  
A;Reference number: A92807; MUID:75212238; PMID:807630  
A;Contents: Bence Jones protein S211  
A;Accession: A92807  
A;Molecule type: protein  
A;Residues: 1,'N',3-29,'K',31-47,49-78,'Q',80-86,'Q',88-98,'W',99,'N',101-106 <STA>

A;Cross-references: UNIPARC:UPI0000173771  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;19-88/Domain: immunoglobulin homology <IMM>  
F;26-86/Disulfide bonds: #status predicted  
F;106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 66.4%; Score 367; DB 1; Length 106;  
Best Local Similarity 65.4%; Pred. No. 8.7e-29;  
Matches 68; Conservative 14; Mismatches 22; Indels 0; Gaps 0;  
  
Qy 4 AAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 63  
Db 3 AAPTVISFPPSTEQLATGASVVCCLMNNFYPRDISVKWKIDGTERDGVLDSDVDQDSKD 62

Qy 64 STYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 63 STYMSSTLTLSKADYKSHNLYTCVVHKTSSSPVVKSFNRNEC 106

RESULT 12  
PT0219  
Ig kappa chain V-C region (PLC18) - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 11-Jan-2000  
C;Accession: PT0219  
R;Lammers, B.M.; Beaman, K.D.; Kim, Y.B.  
Mol. Immunol. 28, 877-880, 1991  
A;Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.  
A;Reference number: PT0219; MUID:91342694; PMID:1715030  
A;Accession: PT0219  
A;Molecule type: mRNA  
A;Residues: 1-178 <LAM>  
A;Cross-references: UNIPARC:UPI0001151A1; GB:M59321; NID:G164508; PIDN:AAA03520.1; PID:9

A;Experimental source: spleen, strain Minnesota Miniature  
A;Note: the authors translated the codon CTC for residue 141 as Ser  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-70/Domain: V region (fragment) <VRG>  
F;12-18/Region: complementarity-determining 1  
F;19-51/Region: framework 1  
F;52-60/Region: complementarity-determining 2  
F;61-70/Region: framework 2  
F;71-178/Domain: C region <CRG>  
F;96-156/Disulfide bonds: #status predicted  
F;176/Disulfide bonds: interchain #status predicted

Query Match 66.2%; Score 366; DB 2; Length 178;  
Best Local Similarity 64.5%; Pred. No. 2e-28;  
Matches 69; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60  
Db 70 RADAKPSVFIPPSDEQLATPTVSVCCLNNFYPRDISVKWKIDGTERDGVLDSDVDQD 129  
  
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 130 SKDSTYSLSTLSPTSQYLSHNLYSCVTHKTLASPLVTSFNRNEC 176

RESULT 13  
KIRTA  
Ig kappa chain C region (allele a) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 18-Aug-1982 #sequence\_revision 10-Sep-1982 #text\_change 09-Jul-2004  
C;Accession: A02118  
R;Sheppard, H.W.; Gutman, G.A.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981  
A;Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le  
A;Reference number: A93901; MUID:82082587; PMID:6273908  
A;Accession: A02118

A:Molecule type: DNA  
A:Residues: 1-106 <SHE>  
A:Cross-references: UNIPROT:P01836; UNIPARC:UIP00001148A8; GB:J02574; GB:J00745; NID:g20  
A:Experimental source: strain DA  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into large superfamily: immunoglobulin C region; immunoglobulin homology  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status predicted  
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 64.9%; Score 359; DB 1; Length 106;  
Best Local Similarity 63.5%; Pred. No. 5.2e-28;  
Matches 66; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 4 AAPSVPFPSPDEQLKSGTASVVCLNNFPREAKVQWKVDNALQSGNSQSSTVEQDSKD 63  
| | | | | | | | | | | | | | | | | | | | | | : | | | |  
Db 3 AAPTVSIFFPSNEQLTSGATVVCVFNFPRIISIVKWKIDGSEQRDGLVLSVTDDQSD 62  
| | | | | | | | | | | | | | | | | | | | | | : | | | |  
QY 64 STYSLSSTLTLSKADYEKHVKYACVETHOGLSSPVTKSFNRGEC 107  
| | | | | | | | | | | | | | | | | | | | | | : | | | |  
Db 63 STYSMSSTLTLTKVEYERHNLTCVHVHTKTSPPVVKSPFRNEC 106  
| | | | | | | | | | | | | | | | | | | | | | : | | | |

RESULT 14  
S42772  
Ig kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42772  
R:Schellekens, G.A.  
submitted to the EMBL Data Library, November 1993  
A:Reference number: S42771  
A:Accession: S42772  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-217 <SCH>  
A:Cross-references: UNIPARC:UIP00001161CD; EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 64.7%; Score 358; DB 2; Length 217;  
Best Local Similarity 61.7%; Pred. No. 1.5e-27;  
Matches 66; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPIPPSPDEQLKSGTASVVCLNNFPREAKVQWKVDNALQSGNSQSSTVEQD 60  
| | | | | | | | | | | | | | | | | | | | | | : | | | |  
Db 111 RADAAPTYSIPIPPSPSQELTSGGASVVCFLNFYPKDINVKWKIDGSRQNGVLNSWTDQD 170  
| | | | | | | | | | | | | | | | | | | | | | : | | | |  
QY 61 SKDSTYSLSSTLTLSKADYEKHVKYACEVTHOGLSSPVTKSFNRGEC 107  
| | | | | | | | | | | | | | | | | | | | | | : | | | |  
Db 171 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTGPVKSPFRNEC 217  
| | | | | | | | | | | | | | | | | | | | | | : | | | |

RESULT 15  
S68241  
Ig kappa chain V region (Mab13-1) - mouse (fragment)  
N:Alternate names: immunoglobulin light chain  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S68241; S68214  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
submitted to the EMBL Data Library, March 1994  
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin  
A:Reference number: S68241  
A:Accession: S68241  
A:Molecule type: mRNA  
A:Residues: 1-218 <TAK>  
A:Cross-references: UNIPARC:UIP000011B263; EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PI  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995

A>Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin I  
A:Reference number: S68211; MUID:96085223; PMID:7498516  
A:Accession: S68214  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 'NI', 3-212 <TAM>  
A:Cross-references: UNIPARC:UPT0000176980; EMBL:D296570  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin

Query Match 64.7%; Score 358; DB 2; Length 218;  
Best Local Similarity 61.7%; Pred. No. 1.5e-27;  
Matches 66; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPDEQLKSTASVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 112 RADAAPTVSIAPPSSSEQLTSGCAGVCFVFNPFYFDINVRWKIDGSEKQNGVLNSWTDQD 171

Qy 61 SKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 172 SKOSTYSGMSSTLTUKDEYRHNSTCEATHKSTSPVTKSFNRGEC 218

Search completed: January 28, 2006, 09:45:39  
Job time : 10.9249 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:21:24 ; Search time 56.7132 Seconds  
(without alignments)  
1331.110 Million cell updates/sec

Title: US-10-733-563-112

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPPSDEQLKS.....EVTHQGLSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	553	100.0	120	2	Q6P5R5 HUMAN	Q6P5R5 homo sapien
2	553	100.0	234	2	Q5E9E6 HUMAN	Q5E9E6 homo sapien
3	553	100.0	234	2	Q72473 HUMAN	Q72473 homo sapien
4	553	100.0	235	2	Q6GMV9 HUMAN	Q6GMV9 homo sapien
5	553	100.0	235	2	Q6GMW0 HUMAN	Q6GMW0 homo sapien
6	553	100.0	235	2	Q6PUF2 HUMAN	Q6PUF2 homo sapien
7	553	100.0	236	2	Q6GMX0 HUMAN	Q6GMX0 homo sapien
8	553	100.0	236	2	Q6P5S8 HUMAN	Q6P5S8 homo sapien
9	553	100.0	236	2	Q6PIH4 HUMAN	Q6PIH4 homo sapien
10	553	100.0	236	2	Q6PIL8 HUMAN	Q6PIL8 homo sapien
11	553	100.0	236	2	Q6PIT5 HUMAN	Q6PIT5 homo sapien
12	553	100.0	236	2	Q723Y4 HUMAN	Q723Y4 homo sapien
13	553	100.0	236	2	Q6PIH7 HUMAN	Q6PIH7 homo sapien
14	553	100.0	236	2	Q6GMX9 HUMAN	Q6GMX9 homo sapien
15	553	100.0	236	2	Q6GMX8 HUMAN	Q6GMX8 homo sapien
16	553	100.0	236	2	Q6GMW1 HUMAN	Q6GMW1 homo sapien
17	553	100.0	236	2	Q502W4 HUMAN	Q502W4 homo sapien
18	553	100.0	239	2	Q6P491 HUMAN	Q6P491 homo sapien
19	553	100.0	239	2	Q8TCD0 HUMAN	Q8TCD0 homo sapien
20	553	100.0	240	2	Q6PIH6 HUMAN	Q6PIH6 homo sapien
21	549	99.3	239	2	Q8NEK0 HUMAN	Q8NEK0 homo sapien
22	548	99.1	106	1	KAC_HUMAN	P01834 homo sapien
23	548	99.1	234	2	Q5G9I9 HUMAN	Q5G9I9 homo sapien
24	369	66.7	234	2	Q4KM66 RAT	Q4KM66 rattus norv
25	369	66.7	234	2	Q8M838 RAT	Q8M838 rattus norv
26	367	66.4	106	1	KACB_RAT	P01835 rattus norv
27	359	64.9	106	1	KACA_RAT	P01836 rattus norv
28	358	64.7	219	2	Q55ZC0 MOUSE	Q55ZC0 mus musculus
29	352	63.7	234	2	Q5XK94 MOUSE	Q5XK94 mus musculus
30	352	63.7	235	2	Q5XFY8 MOUSE	Q5XFY8 mus musculus
31	352	63.7	235	2	Q58EV6 MOUSE	Q58EV6 mus musculus

32	352	63.7	236	2	Q7TS98 MOUSE	Q7TS98 mus musculus
33	352	63.7	236	2	Q52L95 MOUSE	Q52L95 mus musculus
34	352	63.7	237	2	Q569Y8 MOUSE	Q569Y8 mus musculus
35	352	63.7	238	2	Q6J5J7 MOUSE	Q6J5J7 mus musculus
36	352	63.7	238	2	Q58EU4 MOUSE	Q58EU4 mus musculus
37	352	63.7	239	2	Q58EU8 MOUSE	Q58EU8 mus musculus
38	352	63.7	240	2	Q52L64 MOUSE	Q52L64 mus musculus
39	352	63.7	241	2	Q63ZX4 MOUSE	Q63ZX4 mus musculus
40	350	63.3	106	1	KAC_MOUSE	P01837 mus musculus
41	306.5	55.4	106	1	KACB_RABBIT	P01839 oryctolagus
42	292	52.8	189	2	Q569I7_HUMAN	Q569I7 homo sapien
43	259.5	46.9	116	2	Q6LEJ1_RABBIT	Q6LEJ1 oryctolagus
44	259.5	46.9	116	2	Q6LEJ2_RABBIT	Q6LEJ2 oryctolagus
45	257.5	46.6	103	1	KAC4_RABBIT	P01840 oryctolagus

## ALIGNMENTS

RESULT 1  
Q6P5R5 HUMAN PRELIMINARY; PRT; 120 AA.  
AC Q6P5R5  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Glandular pool- thyroid;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Strausberg R.L., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Glandular pool- thyroid;  
RG NIH MGC Project;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
histocompatibility complex class I molecules (by similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted (by similarity).  
DR EMBL; BC062732; AAHG2732.1; -; mRNA.  
DR HSSP; P01837; 1KCU.  
DR SMR; Q6P5R5; 3-120.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; C1-set; 1.

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DR SMART: SM00407: IGc1: 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immune response; Immunoglobulin domain; MHC I.
SQ SEQUENCE 120 AA; 13153 MW; B42FA2928C5C8F1F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.4e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 14 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 73

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 74 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 120

RESULT 2
QSEF66 HUMAN
ID Q5BFE6 HUMAN PRELIMINARY; PRT; 234 AA.
AC Q5BFE6
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Anti-Rhd monoclonal T125 kappa light chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894991; AAW82027.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light
FT CHAIN chain.
SQ SEQUENCE 234 AA; 25698 MW; 866DDC01E4FDD7D5EA CRC64;

Query Match 100.0%; Score 553; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 3
Q72473 HUMAN
ID Q72473_HUMAN PRELIMINARY; PRT; 234 AA.

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AC Q72473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krawinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAHS6256.1; -; mRNA.
DR HSSP; P01834; 1HEX.
DR SMR; Q72473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 4
Q6GMV9 HUMAN
ID Q6GMV9 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073793; AAH73793.1; -; mRNA.  
DR SMR; Q6GMV9; 21-235.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; CI-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;  
  
Query Match 100.0%; Score 553; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 129 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 188  
  
QY 61 SKDSTYLSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 189 SKDSTYLSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 235  
  
RESULT 5  
ID Q6GMW0 HUMAN PRELIMINARY; PRT; 235 AA.  
AC Q6GMW0;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE IGKV1-5 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Director MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073792; AAH73792.1; -; mRNA.  
DR SMR; Q6GMW0; 21-233.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; CI-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;  
  
Query Match 100.0%; Score 553; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 129 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 188  
  
QY 61 SKDSTYLSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 189 SKDSTYLSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 235  
  
RESULT 6  
ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.  
AC Q6PJF2;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)

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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -; mRNA.
DR HSSP; P01837; 1KCU.
DR SMR; O6PJ2; 21-235.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 129 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 188

Qy 61 SKDSTYLSSTLTLSKADYKHKYKVCETHQGLSSPVTKSFNRGEC 107
Db 189 SKDSTYLSSTLTLSKADYKHKYKVCETHQGLSSPVTKSFNRGEC 235

RESULT 7
ID Q6GNX0_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GNX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -; mRNA.
DR SMR; O6GMX0; 23-236.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

Qy 61 SKDSTYLSSTLTLSKADYKHKYKVCETHQGLSSPVTKSFNRGEC 107
Db 190 SKDSTYLSSTLTLSKADYKHKYKVCETHQGLSSPVTKSFNRGEC 236

RESULT 8
ID Q6PS58_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PS58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RA Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC062704; AAH62704.1; -; mRNA.  
 DR HSSP; P01837; 1KCJ.  
 DR SMR; Q6P588; 21-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig c1.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;  
 Query Match 100.0%; Score 553; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189  
 QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 190 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236  
 RESULT 9  
 ID Q6PIH4\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIH4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034146; AAH34146.1; -; mRNA.  
 DR HSSP; P01607; 1AE2.  
 DR SMR; Q6PIH4; 23-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig c1.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06BEE26 CRC64;  
 Query Match 100.0%; Score 553; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189  
 QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 190 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236  
 RESULT 10  
 ID Q6PIL8\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIL8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;



RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Skeletal Muscle;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Casavant T.L., Scheetz T.E.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN (2)  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal Muscle;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005332; AAH05332.1; -; mRNA.  
 DR HSP; P01834; 1HEZ.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein; Immunoglobulin domain.  
 SQ SEQUENCE 236 AA; 25702 MW; 7B8FE4ED23084BC6 CRC64;  
  
 Query Match 100.0%; Score 553; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYREAKVQWKVDNALQSGNSQESVTEQD 189  
  
 QY 61 SKDSTYSLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSPNRGEC 107  
 DB 190 SKDSTYSLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSPNRGEC 236  
  
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 ID Q6PIH7\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIH7;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Casavant T.L., Scheetz T.E.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN (2)  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RG NIH MGC Project;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034141; AAH34141.1; -; mRNA.  
 DR HSP; P01607; 1AR2.  
 DR SMR; Q6PIH7; 23-236.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 DR SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;  
  
 Query Match 100.0%; Score 553; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFPYREAKVQWKVDNALQSGNSQESVTEQD 189  
  
 QY 61 SKDSTYSLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSPNRGEC 107  
 DB 190 SKDSTYSLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSPNRGEC 236  
  
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 ID Q6QMX9\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6QMX9;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -; mRNA.
DR SMR; Q6GMX9; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 2.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 189

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNREGC 107
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RESULT 15
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AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -; mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 2.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 189

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNREGC 107
Db 190 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNREGC 236

Search completed: January 28, 2006, 09:44:19
Job time : 56.7132 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 15.7447 Seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPPDEQLKS.....EVTHQGLSSPVTKSFRNGEC 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	1	US-08-422-101-8
2	553	100.0	107	1	US-08-422-091-8
3	553	100.0	107	1	US-08-422-092-8
4	553	100.0	107	1	US-08-788-800-5
5	553	100.0	107	2	US-08-422-093-8
6	553	100.0	107	2	US-08-422-113-8
7	553	100.0	107	2	US-09-301-593-20
8	553	100.0	212	2	US-10-011-125A-5
9	553	100.0	213	2	US-08-630-820-6
10	553	100.0	213	2	US-08-397-411-12
11	553	100.0	213	2	US-09-273-453-6
12	553	100.0	213	2	US-09-996-288-209
13	553	100.0	213	2	US-09-996-288-211
14	553	100.0	213	2	US-09-996-288-213
15	553	100.0	213	2	US-09-996-288-215
16	553	100.0	213	2	US-09-996-288-217
17	553	100.0	213	2	US-09-996-288-219
18	553	100.0	213	2	US-09-996-288-221
19	553	100.0	213	2	US-09-996-288-223
20	553	100.0	213	2	US-09-996-288-225
21	553	100.0	213	2	US-09-996-288-227
22	553	100.0	213	2	US-09-996-288-229
23	553	100.0	213	2	US-09-996-288-231
24	553	100.0	213	2	US-09-996-288-233
25	553	100.0	213	2	US-09-996-288-235
26	553	100.0	213	2	US-09-996-288-237
27	553	100.0	213	2	US-09-996-288-239

28	553	100.0	213	2	US-09-996-288-241	Sequence 241, App
29	553	100.0	213	2	US-09-996-288-243	Sequence 243, App
30	553	100.0	213	2	US-09-996-288-245	Sequence 245, App
31	553	100.0	213	2	US-09-996-288-247	Sequence 247, App
32	553	100.0	213	2	US-09-996-288-251	Sequence 251, App
33	553	100.0	213	2	US-09-996-288-253	Sequence 253, App
34	553	100.0	213	2	US-09-996-288-255	Sequence 255, App
35	553	100.0	213	2	US-09-996-288-257	Sequence 257, App
36	553	100.0	213	2	US-09-996-265-209	Sequence 209, App
37	553	100.0	213	2	US-09-996-265-211	Sequence 211, App
38	553	100.0	213	2	US-09-996-265-213	Sequence 213, App
39	553	100.0	213	2	US-09-996-265-215	Sequence 215, App
40	553	100.0	213	2	US-09-996-265-217	Sequence 217, App
41	553	100.0	213	2	US-09-996-265-219	Sequence 219, App
42	553	100.0	213	2	US-09-996-265-221	Sequence 221, App
43	553	100.0	213	2	US-09-996-265-223	Sequence 223, App
44	553	100.0	213	2	US-09-996-265-225	Sequence 225, App
45	553	100.0	213	2	US-09-996-265-227	Sequence 227, App

ALIGNMENTS

RESULT 1  
US-08-422-101-8  
; Sequence 8, Application US/08422101  
; Patent No. 5739277  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,101  
; FILING DATE: 14-Apr-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-422-101-8

Query Match 100.0%; Score 553; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.7e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPDEQLKSCTASVVLNNFYPREAKVQMKVONALQSGNSQSVTQD 60  
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Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQD 60
QY      61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2
US-08-422-091-8
; Sequence 8, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
; APPLICANT: Leonard Preetia
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,091
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-091-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQD 60
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQD 60
QY      61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-08-422-092-8
; Sequence 8, Application US/08422092
; Patent No. 5869046
; GENERAL INFORMATION:
; APPLICANT: Leonard Preetia
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997

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; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,092
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-092-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQD 60
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQD 60
QY      61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-08-788-800-5
; Sequence 5, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997

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; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-788-800-5

Query Match      100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-08-422-093-8
; Sequence 8, Application US/08422093
; Patent No. 6096871
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-422-093-8

Query Match      100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
; Sequence 8, Application US/08422112
; Patent No. 6121022
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-422-112-8

Query Match      100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
; Sequence 20, Application US/09301593A
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; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Productivity
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-20

Query Match      100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-10-011-125A-5
; Sequence 5, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: PI604R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-5

Query Match      100.0%; Score 553; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 9
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US-08-630-820-6
; Sequence 6, Application US/08630820
; Patent No. 6008023
; GENERAL INFORMATION:
; APPLICANT: Oppler, Martin
; APPLICANT: BOSSLET, Klaus
; APPLICANT: CZECH, Joerg
; TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
; TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
; NUMBER OF SEQUENCES: 7
; TITLE OF INVENTION: IN E. COLI
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,820
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19513676.4
; FILING DATE: 11-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/306
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-820-6

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 10
US-08-397-411-12
; Sequence 12, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
```

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/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/397,411
/ FILING DATE: 01-MAR-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/859,583
/ FILING DATE: 27-MAR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 011823-004901
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 213 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-397-411-12

Query Match 100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 11
US-09-273-453-6
; Sequence 6, Application US/09273453
; Patent No. 6602688
; GENERAL INFORMATION:
; APPLICANT: OPPER, Martin
; BOSSLER, Klaus
; CZECH, Joerg
; TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
; ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
; IN E. COLI
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/273,453
; FILING DATE: 22-Mar-1999
; PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: 08/630,820
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 18748/306
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 213 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
/ US-09-273-453-6

Query Match 100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 12
US-09-996-288-209
; Sequence 209, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Lealie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 209
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-996-288-209

Query Match 100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 13
US-09-996-288-211
; Sequence 211, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
```

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; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-211

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
US-09-996-288-213
; Sequence 213, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-213

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15
US-09-996-288-215
; Sequence 215, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
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; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-215
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Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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Search completed: January 28, 2006, 09:47:29  
Job time : 15.7447 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 45.6276 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPSDEQLKS.....EVTHQGLSPVTKSFNRGEC 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	3	US-09-301-593-20
2	553	100.0	107	3	US-09-811-384-5
3	553	100.0	107	3	US-09-990-586-97
4	553	100.0	107	3	US-09-990-586-99
5	553	100.0	107	4	US-10-121-464-18
6	553	100.0	107	4	US-10-269-805-67
7	553	100.0	107	4	US-10-153-006-20
8	553	100.0	107	4	US-10-310-113-166
9	553	100.0	107	4	US-10-310-113-168
10	553	100.0	107	4	US-10-230-880-97
11	553	100.0	107	4	US-10-230-880-99
12	553	100.0	107	4	US-10-366-709-54
13	553	100.0	107	4	US-10-404-286-5
14	553	100.0	107	4	US-10-656-769-4
15	553	100.0	107	4	US-10-679-620-60
16	553	100.0	107	4	US-10-733-563-112
17	553	100.0	107	5	US-10-815-449-10
18	553	100.0	107	5	US-10-684-957-4
19	553	100.0	107	5	US-10-886-838-8
20	553	100.0	107	5	US-10-822-300-9
21	553	100.0	107	5	US-10-687-118-9
22	553	100.0	107	5	US-10-873-932A-41
23	553	100.0	107	5	US-10-891-658-8
24	553	100.0	107	5	US-10-937-596-29
25	553	100.0	107	5	US-10-893-576-44
26	553	100.0	107	5	US-10-810-881A-40
27	553	100.0	107	5	US-10-981-936-40

28	553	100.0	107	6	US-11-001-980-4	Sequence 4, Appli
29	553	100.0	107	6	US-11-001-980-8	Sequence 8, Appli
30	553	100.0	107	6	US-11-132-143-60	Sequence 60, Appl
31	553	100.0	107	6	US-11-102-403-23	Sequence 23, Appl
32	553	100.0	109	4	US-10-272-899A-12	Sequence 12, Appl
33	553	100.0	109	4	US-10-733-563-116	Sequence 116, App
34	553	100.0	134	4	US-10-272-899A-66	Sequence 66, Appl
35	553	100.0	212	4	US-10-011-125-5	Sequence 5, Appli
36	553	100.0	212	4	US-10-320-231A-77	Sequence 77, Appl
37	553	100.0	212	5	US-10-867-506-77	Sequence 77, Appl
38	553	100.0	213	3	US-09-796-848A-38	Sequence 38, Appl
39	553	100.0	213	3	US-09-796-848A-40	Sequence 40, Appl
40	553	100.0	213	3	US-09-796-848A-42	Sequence 42, Appl
41	553	100.0	213	3	US-09-796-848A-44	Sequence 44, Appl
42	553	100.0	213	3	US-09-796-848A-46	Sequence 46, Appl
43	553	100.0	213	3	US-09-796-848A-48	Sequence 48, Appl
44	553	100.0	213	3	US-09-796-848A-50	Sequence 50, Appl
45	553	100.0	213	3	US-09-796-848A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1  
US-09-301-593-20  
; Sequence 20, Application US/09301593A  
; Publication No. US20020052480A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: PAD-Specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301.593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086.049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-20

Query Match	100.0%	Score 553;	DB 3;	Length 107;
Best Local Similarity	100.0%	Pred. No. 1.7e-51;		
Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	RTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD	60	
Db	1	RTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD	60	
QY	61	SKDSTYLSSTLTLSKADYEHKHYKHYACVTHQGLSSPVTKSFNRGEC	107	
Db	61	SKDSTYLSSTLTLSKADYEHKHYKHYACVTHQGLSSPVTKSFNRGEC	107	

RESULT 2  
US-09-811-384-5  
; Sequence 5, Application US/09811384  
; Patent No. US20020081294A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15



Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
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DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
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QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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## RESULT 6

US-10-269-805-67

; Sequence 67, Application US/10269805

; Publication No. US20030124129A1

; GENERAL INFORMATION:

; APPLICANT: OLINER, JONATHAN D.

; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

; FILE REFERENCE: A-722

; CURRENT APPLICATION NUMBER: US/10/269,805

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: US 60/328,604

; PRIOR FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 67

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-269-805-67

Query Match 100.0%; Score 553; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-51;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
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DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
|||||

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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## RESULT 7

US-10-159-006-20

; Sequence 20, Application US/10159006

; Publication No. US20030143229A1

; GENERAL INFORMATION:

; APPLICANT: Park, John B.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890002

; CURRENT APPLICATION NUMBER: US/10/159,006

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 09/301,593

; PRIOR FILING DATE: 1999-04-29

; PRIOR APPLICATION NUMBER: EP 98107925.4

; PRIOR FILING DATE: 1998-04-30

; PRIOR APPLICATION NUMBER: US 60/086,049

; PRIOR FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-159-006-20

Query Match 100.0%; Score 553; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-51;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
|||||

DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
|||||

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

## RESULT 8

US-10-310-113-166

; Sequence 166, Application US/10310113

; Publication No. US20030176664A1

; GENERAL INFORMATION:

; APPLICANT: JIAO, JIN-AN

; APPLICANT: WONG, HING C.

; APPLICANT: NIEVES, ESPERANZA LILIANA

; APPLICANT: MOSQUERA, LUIS A.

; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

; FILE REFERENCE: 58122(71758)

; CURRENT APPLICATION NUMBER: US/10/310,113

; CURRENT FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 09/990,586

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/343,306

; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 09/293,854

; PRIOR FILING DATE: 1999-04-16

; PRIOR APPLICATION NUMBER: 08/814,806

; PRIOR FILING DATE: 1997-03-10

; NUMBER OF SEQ ID NOS: 169

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 166

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-310-113-166

Query Match 100.0%; Score 553; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-51;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
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DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
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QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

## RESULT 9

US-10-310-113-168

; Sequence 168, Application US/10310113

; Publication No. US20030176664A1

; GENERAL INFORMATION:

; APPLICANT: JIAO, JIN-AN

; APPLICANT: WONG, HING C.

; APPLICANT: NIEVES, ESPERANZA LILIANA

; APPLICANT: MOSQUERA, LUIS A.

; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

; FILE REFERENCE: 58122(71758)

; CURRENT APPLICATION NUMBER: US/10/310,113

; CURRENT FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 09/990,586

; PRIOR FILING DATE: 2001-11-21

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; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 10
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 11
US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
```

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; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 12
US-10-366-709-54
; Sequence 54, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-709-54

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 13
US-10-404-286-5
; Sequence 5, Application US/10404286
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Publication No. US20040057951A1  
GENERAL INFORMATION:  
APPLICANT: Bednar, Martin M.  
Thomas, G. Roger  
Gross, Cordell B.  
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/404,286  
FILING DATE: 31-Mar-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/811384  
FILING DATE: 20-DEC-2000  
APPLICATION NUMBER: 09/251652  
FILING DATE: 17-FEB-2000  
APPLICATION NUMBER: 08/788800  
FILING DATE: 22-JAN-1997  
APPLICATION NUMBER: 60/093038  
FILING DATE: 23-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, David W.  
REGISTRATION NUMBER: NONE  
REFERENCE/DOCKET NUMBER: P1729C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1739  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-404-286-5

Query Match 100.0%; Score 553; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 14  
US-10-656-769-4  
Sequence 4, Application US/10656769  
Publication No. US2004009712A1  
GENERAL INFORMATION:  
APPLICANT: Varnum, Brian  
APPLICANT: Witte, Allison  
APPLICANT: Vezina, Chris  
APPLICANT: Wong, Lu Min  
APPLICANT: Qian, Xueming  
TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody  
FILE REFERENCE: 01,1554  
CURRENT APPLICATION NUMBER: US/10/656,769

CURRENT FILING DATE: 2003-09-05  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-656-769-4

Query Match 100.0%; Score 553; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 15  
US-10-679-620-60  
Sequence 60, Application US/10679620  
Publication No. US20040110930A1  
GENERAL INFORMATION:  
APPLICANT: Large Scale Biology  
APPLICANT: Reiml, Stephen J.  
APPLICANT: Edwards, Patricia C.  
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING  
FILE REFERENCE: 34150-004A  
CURRENT APPLICATION NUMBER: US/10/679,620  
CURRENT FILING DATE: 2003-10-03  
PRIOR APPLICATION NUMBER: 60/415,940  
PRIOR FILING DATE: 2002-10-03  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 60  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: huscFabmlA6, see Example 15  
US-10-679-620-60

Query Match 100.0%; Score 553; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

Search completed: January 28, 2006, 10:11:23  
Job time : 45.6276 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 6.42643 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPSPDEQLKS.....EVTHQGLSSPVTKSPNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US03\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	6	US-10-999-866-40
2	553	100.0	107	6	US-10-886-383-8
3	553	100.0	107	6	US-10-988-207-21
4	553	100.0	107	7	US-11-025-713-5
5	553	100.0	107	7	US-11-075-351-61
6	553	100.0	107	7	US-11-061-821-40
7	553	100.0	107	7	US-11-102-621-9
8	553	100.0	110	7	US-11-024-251-27
9	553	100.0	213	7	US-11-172-320-4
10	553	100.0	213	7	US-11-172-320-8
11	553	100.0	213	7	US-11-174-186-42
12	553	100.0	213	7	US-11-120-338-13
13	553	100.0	213	7	US-11-120-338-16
14	553	100.0	213	7	US-11-173-969-4
15	553	100.0	213	7	US-11-173-969-8
16	553	100.0	213	7	US-11-102-621-118
17	553	100.0	213	7	US-11-102-621-135
18	553	100.0	213	7	US-11-107-028-31
19	553	100.0	213	7	US-11-107-028-44
20	553	100.0	213	7	US-11-106-820-24
21	553	100.0	213	7	US-11-106-820-29
22	553	100.0	213	7	US-11-106-820-44
23	553	100.0	213	7	US-11-158-505-34
24	553	100.0	214	7	US-11-025-712-11
25	553	100.0	214	7	US-11-094-625-9

26	553	100.0	214	7	US-11-102-621-129	Sequence 129, App
27	553	100.0	214	7	US-11-128-900-71	Sequence 71, Appl
28	553	100.0	214	7	US-11-154-337-14	Sequence 14, Appl
29	553	100.0	214	7	US-11-154-337-16	Sequence 16, Appl
30	553	100.0	215	7	US-11-102-621-141	Sequence 141, App
31	553	100.0	215	7	US-11-166-906-2	Sequence 2, Appl
32	553	100.0	218	6	US-10-923-327-6	Sequence 6, Appl
33	553	100.0	218	6	US-10-923-327-8	Sequence 8, Appl
34	553	100.0	218	6	US-10-923-327-10	Sequence 10, Appl
35	553	100.0	218	6	US-10-923-327-12	Sequence 12, Appl
36	553	100.0	218	6	US-10-923-327-17	Sequence 17, Appl
37	553	100.0	218	7	US-11-084-554-11	Sequence 11, Appl
38	553	100.0	218	7	US-11-158-505-4	Sequence 4, Appl
39	553	100.0	218	7	US-11-158-505-28	Sequence 28, Appl
40	553	100.0	218	7	US-11-004-590-229	Sequence 229, App
41	553	100.0	219	7	US-11-080-587-8	Sequence 8, Appl
42	553	100.0	232	7	US-11-106-820-23	Sequence 23, Appl
43	553	100.0	233	7	US-11-128-900-15	Sequence 15, Appl
44	553	100.0	233	7	US-11-128-900-67	Sequence 67, Appl
45	553	100.0	234	7	US-11-128-900-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-10-999-866-40  
; Sequence 40, Application US/10999866  
; GENERAL INFORMATION:  
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND  
; FILE REFERENCE: CEN5042NP  
; CURRENT APPLICATION NUMBER: US/10/999,866  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: 60/527,794  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 40  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(107)  
; OTHER INFORMATION: Light chain kappa constant region (IgKc)  
US-10-999-866-40

Query Match	100.0%	Score 553;	DB 6;	Length 107;
Best Local Similarity	100.0%	Pred. No. 1.3e-51;		
Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	RTVAAPSVFIPPSPDEQLKSGTASVVC	LNFPY	PREAKVQMKVDNALSGNSQESVTEQD 60
DB	1	RTVAAPSVFIPPSPDEQLKSGTASVVC	LNFPY	PREAKVQMKVDNALSGNSQESVTEQD 60
QY	61	SKDSTYSLSSTLTLSKADYERKHVYACV	THQGLSS	PTVKSPNRGEC 107
DB	61	SKDSTYSLSSTLTLSKADYERKHVYACV	THQGLSS	PTVKSPNRGEC 107

RESULT 2  
US-10-886-383-8  
; Sequence 8, Application US/10886383  
; Publication No. US20060005571A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann-La Roche Inc.  
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses  
; FILE REFERENCE: 21695  
; CURRENT APPLICATION NUMBER: US/10/886,383  
; CURRENT FILING DATE: 2004-07-08

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; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-383-8

Query Match      100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-10-988-207-21
; Sequence 21, Application US/10988207
; Publication No. US20060008457A1
; GENERAL INFORMATION:
; APPLICANT: TeGenero AG
; APPLICANT: Hanke, Thomas
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A
; FILE REFERENCE: TEG/US/0409
; CURRENT APPLICATION NUMBER: US/10/988.207
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: DE 103 52 900.4
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 21
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mab TGN1412 constant region light chain
US-10-988-207-21

Query Match      100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-11-025-712-5
; Sequence 5, Application US/11025712
; Publication No. US2005025108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

```
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/025,712
; FILING DATE: 28-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2003
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-DEC-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-025-712-5

Query Match      100.0%; Score 553; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-11-075-351-61
; Sequence 61, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-61

Query Match      100.0%; Score 553; DB 7; Length 107;
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-11-172-320-4

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 10
US-11-172-320-8
; Sequence 8, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-11-172-320-8

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 11
US-11-174-186-42
; Sequence 42, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
```

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; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: light chain
US-11-174-186-42

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 12
US-11-120-338-13
; Sequence 13, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-13

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 13
US-11-120-338-16
; Sequence 16, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
```

```
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 16
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-16

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
US-11-173-969-4
; Sequence 4, Application US/11/173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: 4
US-11-173-969-4

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15
US-11-173-969-8
; Sequence 8, Application US/11/173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
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; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 8 Light Chain SEQ ID NO: 8
US-11-173-969-8

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: January 28, 2006, 10:12:15
Job time : 6.42643 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p\_model

Run on: January 28, 2006, 08:12:21 ; Search time 50.1261 Seconds  
(without alignments)  
5627.428 Million cell updates/sec

Title: US-10-733-563-113

Perfect score: 564

Sequence: 1 cgtacggtggtgcaccatc.....gcttcaacagggagagtgt 321

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CGN 1.1.624 @runat\_27012006.180005.4773 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq 21.1\*

1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	98.0	107	2 AAW40578	Human kap
2	553	98.0	107	2 AAY50152	Human kap
3	553	98.0	107	2 AAW92425	Human kap
4	553	98.0	107	2 AAY08745	Human kap
5	553	98.0	107	3 AAB27000	Human kap
6	553	98.0	107	5 ABG31883	Human kap
7	553	98.0	107	6 ABB98755	Human kap
8	553	98.0	107	6 ABR42732	Anti-tiss
9	553	98.0	107	6 ABR42734	Anti-tiss

10	553	98.0	107	6 ABR55835	Anti-Ang-
11	553	98.0	107	7 ADJ94622	Human kap
12	553	98.0	107	8 ADJ77161	Anti-VAP-
13	553	98.0	107	8 ADL35096	Human IGG
14	553	98.0	107	8 ADL35094	Human IGG
15	553	98.0	107	8 ADM41539	Anti-inte
16	553	98.0	107	8 ADK18336	Amino aci
17	553	98.0	107	8 ADN97487	Artificia
18	553	98.0	107	8 ADQ89334	Human inm
19	553	98.0	107	8 ADS87911	Anti-IFN-
20	553	98.0	107	8 ADS94908	Anti-IFN-
21	553	98.0	107	8 ADT88871	Human IGG
22	553	98.0	107	8 ADT51583	Light cha
23	553	98.0	107	8 ADU68013	Mouse ant
24	553	98.0	107	9 ADW08870	IGF-IR an
25	553	98.0	107	9 ADW07454	Human kap
26	553	98.0	107	9 ADW24748	Variable
27	553	98.0	107	9 ADW24790	Variable
28	553	98.0	107	9 ADX98272	Human ant
29	553	98.0	107	9 ADY26693	Human ant
30	553	98.0	107	9 ADY74804	Human lig
31	553	98.0	107	9 ADZ08815	Mammalian
32	553	98.0	107	9 ADZ08946	Amyloid a
33	553	98.0	107	9 ADZ44472	Human inm
34	553	98.0	107	9 AEA25951	Human inm
35	553	98.0	107	9 AEA16547	Human MCP
36	553	98.0	107	9 AEA45321	Apolipop
37	553	98.0	107	9 AEA45323	Apolipop
38	553	98.0	107	9 AEA37411	Anti-huma
39	553	98.0	107	9 AEA37415	Anti-huma
40	553	98.0	107	9 AEB09607	Human C k
41	553	98.0	107	9 AEB72782	Anti-Ltal
42	553	98.0	108	8 ADL22765	Human ant
43	553	98.0	108	8 ADW15047	Human Fab
44	553	98.0	108	9 AEA52525	Human ant
45	553	98.0	109	8 ADJ95916	Human kap

ALIGNMENTS

RESULT 1

AAW40578

ID AAW40578 standard; protein; 107 AA.

XX AAW40578;

XX 21-JUL-1998 (first entry)

XX Human kappa CL domain protein fragment.

XX Immunoglobulin G; Igg molecule; human; Fc region; LFA-1 receptor;  
XX disorder; salvage receptor binding epitope; cell adherence interaction;  
XX lymphocyte; T cell inflammatory response.

XX Homo sapiens.

XX US5739277-A.

XX 14-APR-1998.

XX 14-APR-1995; 95US-00422101.

XX 14-APR-1995; 95US-00422101.

XX (GETH ) GENENTECH INC.

XX Snedecor BR, Presta LG;

XX WPI; 1998-250490/22.

XX Polypeptide(s) that are not Fc fragments and have an increased half-life  
XX - are useful for the treatment of LFA-1 mediated disorders.

PS Disclosure; Fig 2; 38pp; English.

XX This protein fragment is derived from a human immunoglobulin kappa CL  
CC domain and is used to describe a novel method to produce polypeptides  
CC which contain an epitope from the FC region of an IgG molecule and a  
CC mutated salvage receptor binding epitope. They are useful for the  
CC treatment of LFA-1 mediated disorders. These are conditions caused by  
CC cell adherence interactions involving the LFA-1 receptor on lymphocytes,  
CC e.g. T cell inflammatory responses. The mutated salvage receptor sequence  
CC in the polypeptides means that they have increased in vivo circulatory  
CC half-lives when compared to normal FC regions of IgG molecules  
XX  
SQ Sequence 107 AA;

Alignment Scores:  
Pred. No.: 4.93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x AAW40578 (1-107)

Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGACGAGTTGAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAACCTGCCTCTGTGTGCTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40  
Qy 121 TGGAGGTGGATACCGCTCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGACCTACAGCTCAGCAGCACCCCTGAGCAGCAAGAGCAGCTACAG 240  
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80  
Qy 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 2

AA50152  
ID AAY50152 standard; protein; 107 AA.

XX  
AC AAY50152;  
XX  
DT 31-JAN-2000 (first entry)

XX Human kappa light chain constant region.

XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
KW humanisation; complementarity determining region; CDR; CDR grafting;  
KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;  
KW immune response; framework sequence; constant region; variable region;  
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;  
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;  
KW skin inflammation; tumour; immunogenicity; light chain.

OS Homo sapiens.

XX EP953639-A1.

XX 03-NOV-1999.

XX 30-APR-1998; 98EP-00107925.

XX 30-APR-1998; 98EP-00107925.  
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
PA Park JB, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;  
PI Rettig WJ;  
XX WPI; 1999-621833/54.  
DR N-PSDB; AAZ32777.

XX New antibody protein, useful for treating cancer and for imaging presence  
PT of activated stromal fibroblasts in healing wound or inflamed skin.

XX Disclosure; Fig 20; 143pp; English.

XX This sequence represents a human kappa light chain, the cDNA of which was  
CC used in the construction of a nucleotide encoding the light chain of a  
CC human reshaped monoclonal antibody F19. F19 (ATCC Accession number HB  
CC 8259) is a murine monoclonal antibody against fibroblast activation  
CC protein alpha (FAP). FAP is a cell surface molecule of reactive stromal  
CC fibroblasts, and its induction is a highly consistent molecular trait of  
CC the reactive stroma of many types of epithelial cancer. Although F19 may  
CC be useful in vitro, e.g., for diagnosis, its applications for in vivo use  
CC in humans are problematic as it elicits a human anti-mouse response which  
CC reduces the efficacy of the antibody in patients and impairs continued  
CC administration. The novel human reshaped F19 was humanised by grafting  
CC the murine complementarity determining regions (CDRs) of F19 onto human  
CC variable region framework sequences, and then joining these "reshaped  
CC human" variable regions to human constant regions. These modifications  
CC also result in the improved producibility in eukaryotic cell culture  
CC systems as compared to a chimeric antibody having the entire variable  
CC regions of F19 joined to a human constant regions. The human reshaped F19  
CC antibody has low immunogenicity for humans and is useful for treating  
CC cancers e.g., colorectal cancers, non-small cell lung cancers, breast  
CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder  
CC cancers, pancreatic cancers and metastatic cancers. It is also useful for  
CC the detection of activated stromal fibroblasts in a healing wound,  
CC inflamed skin or a tumour in a human patient

XX Sequence 107 AA;

Alignment Scores:  
Pred. No.: 4.93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x AAY50152 (1-107)

Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGACGAGTTGAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAACCTGCCTCTGTGTGCTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40  
Qy 121 TGGAGGTGGATACCGCTCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGACCTACAGCTCAGCAGCACCCCTGAGCAGCAAGAGCAGCTACAG 240  
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80  
Qy 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGAGAGTGT 321

```
Db      101 SerPheAsnArgGlyGluCys 107
|||||
RESULT 3
AAW92425
ID      AAW92425 standard; peptide; 107 AA.
XX
AC      AAW92425;
XX
DT      23-APR-1999 (first entry)
XX
DE      Human Kappa protein CL domain.
XX
KW      Antibody; salvage receptor binding epitope; Fab; F(ab')2; immunoglobulin;
KW      CH region; CL region; kidney; Fc region; CH1 domain; CH2 domain; IgG;
KW      kappa protein; renal clearance rate; circulatory half-life.
XX
OS      Homo sapiens.
XX
PN      US5869046-A.
XX
PD      09-FEB-1999.
XX
PF      14-APR-1995; 95US-00422092.
XX
PR      14-APR-1995; 95US-00422092.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Presta LG, Snedecor BR;
XX
DR      WPI; 1999-152694/13.
XX
PT      Production of antibody fragments with reduced renal clearance - by
PT      introducing salvage receptor binding epitope into CH1 or CL region.
XX
PS      Disclosure; Col 55-58; 38pp; English.
XX
CC      This invention describes a method for preparing a variant Fab or F(ab')2
CC      polypeptide having increased half-life in vivo, where the polypeptide
CC      contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is
CC      cleared from the kidneys and does not contain an IgG Fc region. The
CC      method involves altering the polypeptide within the CH1 or CL region to
CC      incorporate a salvage receptor binding epitope taken from two loops of a
CC      CH2 domain of an IgG Fc region. The polypeptides have a reduced renal
CC      clearance rate and an increased circulatory half-life. This sequence
CC      represents a human kappa protein CL domain used in the method of the
CC      invention
XX
SQ      Sequence 107 AA;

Alignment Scores:
Pred. No.:      4,93e-55      Length:      107
Score:          553.00      Matches:      107
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    98.05%      Indels:      0
DB:             2      Gaps:      0

US-10-733-563-113 (1-321) x AAW92425 (1-107)

Qy      1 CGTAGCGTGCTGCACCATCTGTCTTCCATCTTCCGCCATCTGATGAGCGTTGAAATCT 60
|||||
Db      1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluLeuLysSer 20

Qy      61 GGAAGTGGCTGTGTGTGCTGTGTAATACATTCTATCCAGAGAGGCCAAAGTACAG 120
|||||
Db      21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40

Qy      121 TGGAGGTGGATACGCCCTCCATCGGTAACTCCAGGAGAGTGTCACAGAGCAGAC 180
|||||
Db      41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
```

```
Qy      181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACCTGAGCAAGAGCAGCTACGAG 240
|||||
Db      61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80

Qy      241 AAACACAAAGTCTACGCTTGGAGAGTCACCCATCAGGGCGCTGAGCTCGCCCCCTCAAAAG 300
|||||
Db      81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100

Qy      301 AGCTTCAACAGGGGAGAGTGT 321
|||||
Db      101 SerPheAsnArgGlyGluCys 107

RESULT 4
AAW08745
ID      AAW08745 standard; protein; 107 AA.
XX
AC      AAW08745;
XX
DT      10-AUG-1999 (first entry)
XX
DE      Human Kappa-CL domain.
XX
KW      IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
KW      IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
KW      cerebroprotective; cerebral artery obstruction; blood flow; infarct;
KW      CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
KW      antibody.
XX
OS      Homo sapiens.
XX
PN      US5914112-A.
XX
PD      22-JUN-1999.
XX
PF      22-JAN-1997; 97US-00788800.
XX
PR      23-JAN-1996; 96US-0093038P.
XX
PA      (GETH ) GENENTECH INC.
PA      (UYVB-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI      Thomas GR, Bednar MM, Gross CB;
XX
DR      WPI; 1999-370483/31.
XX
PT      Anti-CD18 antibodies in stroke.
XX
PS      Disclosure; Fig 4A-B; 25pp; English.
XX
CC      This invention describes a method for improving the clinical outcome in
CC      focal ischaemic stroke by administering novel anti-CD18 antibody which
CC      has cerebroprotective properties. The invention particularly describes a
CC      method of treating focal ischaemic stroke caused by the obstruction of a
CC      main cerebral artery which comprises administering an anti-CD18 antibody
CC      to increase the blood flow or reduce the infarct size, where: (1) the
CC      antibody binds to an extracellular domain of CD18 and inhibits or reduces
CC      the ability of the cell expressing CD18 to bind to endothelium (2) the
CC      antibody binds CD18 with an affinity of less than 4 nm, or (3) the
CC      antibody dissociates CD11b/CD18 complex. This sequence represents the
CC      human Kappa-CL domain which is used to illustrate the method of the
CC      invention
XX
SQ      Sequence 107 AA;

Alignment Scores:
Pred. No.:      4.93e-55      Length:      107
Score:          553.00      Matches:      107
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    98.05%      Indels:      0
DB:             2      Gaps:      0

US-10-733-563-113 (1-321) x AAW08745 (1-107)
```

QY 1 CGTACGGTGGCTGCACCATCTGTCTTTCATCTTCCGGCCATCTGATGACGAGTTCGAATCT 60  
 Db |||||||  
 QY 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20  
 Db |||||||  
 QY 61 GGAACCTGCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db |||||||  
 QY 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
 Db |||||||  
 QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGGTAACCTCCAGGAGAGTGTCCACAGAGCAGGAC 180  
 Db |||||||  
 QY 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
 Db |||||||  
 QY 181 AGCAAGGACAGCAGCTCAGCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
 Db |||||||  
 QY 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
 Db |||||||  
 QY 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCCACAAAG 300  
 Db |||||||  
 QY 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
 Db |||||||  
 QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db |||||||  
 QY 101 SerPheAsnArgGlyGluCys 107  
 Db |||||||

RESULT 5  
 AAB27000  
 ID AAB27000 standard; protein; 107 AA.  
 AC AAB27000;  
 XX  
 XX  
 DT 25-JAN-2001 (first entry)  
 XX  
 DE Human kappa CL domain.  
 XX  
 KW Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;  
 KW mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;  
 KW psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;  
 KW inflammation; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6121022-A.  
 XX  
 PD 19-SEP-2000.  
 XX  
 PF 14-APR-1995; 95US-00422112.  
 XX  
 PR 14-APR-1995; 95US-00422112.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Presta LG, Snedecor BR;  
 XX  
 XX WPI; 2000-610925/58.  
 DR  
 XX  
 PT New nucleic acid encoding new modified polypeptides with increased  
 PT circulatory half-life useful for preventing/treating LFA-1-mediated  
 PT disorders, e.g. reducing inflammatory responses or inducing tolerance to  
 PT immunostimulants.  
 XX  
 PS Disclosure; Fig 2; 38pp; English.  
 XX

The present sequence was used in a method for improving the in vivo half-life of polypeptides. The polypeptides comprise an Ig constant domain or an Ig-like constant domain, and a salvage receptor binding epitope within the Ig or Ig-like domain. The salvage receptor epitope is taken from two loops of the CH2 domain of an Fc region of an Ig molecule. The modified polypeptides are useful for preventing or treating LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated diseases, B-cell lymphomas. They are also useful for wound repair, reducing inflammatory responses and inducing tolerance to immunostimulants. They

CC may also be used in diagnostic assays. The nucleic acids and modified polypeptides are useful for the passive immunisation of patients, as well as for affinity purification of an antigen from recombinant cell culture or natural sources  
 XX  
 SQ Sequence 107 AA;  
 Alignment Scores:  
 Pred. NO.: 4.93e-55 Length: 107  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-733-563-113 (1-321) x AAB27000 (1-107)  
 QY 1 CGTACGGTGGCTGCACCATCTGTCTTTCATCTTCCGGCCATCTGATGACGAGTTCGAATCT 60  
 Db |||||||  
 QY 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20  
 Db |||||||  
 QY 61 GGAACCTGCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db |||||||  
 QY 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
 Db |||||||  
 QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGGTAACCTCCAGGAGAGTGTCCACAGAGCAGGAC 180  
 Db |||||||  
 QY 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
 Db |||||||  
 QY 181 AGCAAGGACAGCAGCTCAGCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
 Db |||||||  
 QY 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
 Db |||||||  
 QY 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCCACAAAG 300  
 Db |||||||  
 QY 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
 Db |||||||  
 QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db |||||||  
 QY 101 SerPheAsnArgGlyGluCys 107  
 Db |||||||

RESULT 6  
 ABG31883  
 ID ABG31883 standard; protein; 107 AA.  
 AC ABG31883;  
 XX  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human kappa CL domain.  
 XX  
 KW Human; kappa CL domain; cerebral blood flow; infarct size;  
 KW focal ischaemic stroke; main cerebral artery;  
 KW tissue plasminogen activator; anti-CD18 antibody; stroke;  
 KW acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002081294-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 20-DEC-2000; 2000US-00811384.  
 XX  
 PR 23-JAN-1996; 96US-0093038P.  
 PR 22-JAN-1997; 97US-00788800.  
 PR 17-FEB-1999; 99US-00251652.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Bednar MM, Gross CB, Thomas GR, Gross LJ;  
 XX WPI; 2002-626528/67.  
 DR

XX Increasing cerebral blood flow and/or reducing infarct size in focal  
PT ischemic stroke using anti-CD18 antibody and tissue plasminogen activator  
PT is useful to improve clinical outcome in acute ischemic stroke.  
XX  
XX  
PS Disclosure; Fig 4; 27pp; English.

XX The invention relates to a method of increasing cerebral blood flow and/  
CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
CC of a main cerebral artery in a human, comprising co-administering tissue  
CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
CC stroke. The method is used to improve the clinical outcome in acute  
CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
CC for treating thromboembolic stroke, particularly where thrombolytic  
CC therapy has been unsuccessful or is contra-indicated. The present  
CC sequence represents the human kappa CL domain used in the method of the  
XX invention

SQ Sequence 107 AA;

Alignment Scores:  
Pred. No.: 4,93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-113 (1-321) x ABG31883 (1-107)

QY 1 CGTAGCGGTGGTGCACCAATCTGCTTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20  
QY 61 GGAAGTGGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGCCAAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGTAAACGCCCTCCAAATCGGCTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGAGCAGTACGAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTAGCCTGCGAAGTCCCAATCGGCTAACTCCAGGAGAGTGTCCAGAGCAGGAC 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 7

ABB98755  
ID ABB98755 standard; protein; 107 AA.

AC ABB98755;

XX 23-JAN-2003 (first entry)

XX Human kappa light constant chain.

XX Human; cytostatic; antitumour; immunosuppressive; anti-allergic;  
KW humanised; antibody; fibroblast activation protein alpha; FAPalpa;  
KW cancer; monoclonal antibody F19; colorectal cancer;  
KW non-small cell lung carcinoma; breast cancer; pancreatic cancer; tumour;  
KW systemic autoimmune disease; allergy; light chain; constant region.

XX Homo sapiens.

XX WO200283171-A2.

RESULT 8

XX 24-OCT-2002.  
PD  
XX  
XX 11-APR-2002; 2002WO-EP004041.  
PP  
XX 12-APR-2001; 2001US-0283868P.  
PR  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
PA  
XX Amelsberg A, Scott A, Tanswell P;  
PI  
XX WPI; 2003-058609/05.  
DR  
XX N-PSDB; ABV74601.  
DR  
XX Use of a humanized antibody which specifically binds to fibroblast  
PT activation protein alpha for manufacturing a medicament for treating  
PT cancer.

XX Claim 7; Page 55; 57pp; English.

XX The present invention relates to the use of a humanised antibody (I),  
CC which specifically binds to fibroblast activation protein alpha (I),  
CC (FAPalpa), for manufacturing a medicament for treating cancer. (I) has  
CC the complementary determining region (CDR) of the monoclonal antibody  
CC F19, but has framework modifications resulting in improved producibility  
CC in host cells as compared to a chimeric antibody having the variable  
CC regions of F19 and foreign constant regions. To generate (I), a chimeric  
CC antibody was constructed having variable regions of the light and heavy  
CC chains of F19 and human light and heavy constant regions. (I) is useful  
CC for treating a patient suffering from a pathological condition  
CC characterised by expression of FAPalpa, such as colorectal cancer, non-  
CC small cell lung carcinoma, breast cancer, pancreatic cancer, tumour,  
CC systemic autoimmune diseases and allergies. The present sequence is human  
CC kappa light constant chain which was used to produce (I)

XX Sequence 107 AA;

Alignment Scores:  
Pred. No.: 4,93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 6 Gaps: 0

US-10-733-563-113 (1-321) x ABB98755 (1-107)

QY 1 CGTAGCGGTGGTGCACCAATCTGCTTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20  
QY 61 GGAAGTGGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCTCCAGAGCAGGAC 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGTAAACGCCCTCCAAATCGGCTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCCTACAGCCTCAGAGCAGCCCTGAGCCCTGAGCAAGAGCAGTACGAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTAGCCTGCGAAGTCCCAATCGGCTAACTCCAGGAGAGTGTCCAGAGCAGGAC 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

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ABR42732
ID ABR42732 standard; protein; 107 AA.
XX
AC ABR42732;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-tissue factor humanized antibody light chain constant region.
XX
KW Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW antiinflammatory; mouse; human; hOAT.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO2003037911-A2.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-US034727.
XX
PR 29-OCT-2001; 2001US-0343306P.
PR 21-NOV-2001; 2001US-00990586.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR WPI; 2003-468399/44.
XX
PT New humanized antibody that binds specifically to human tissue factor,
PT useful for in vivo diagnostic methods, or for inhibiting blood
PT coagulation or blood clot formation, angiogenesis, tumor metastases or
PT inflammation in a mammal.
XX
PS Example 10; Fig 14A; 110pp; English.
XX
CC The present sequence is the protein sequence of the light chain constant
CC region of anti-human tissue factor (TF) humanized antibody hOAT
CC (humanised ch36-IgG1). Humanized antibodies of the invention provide
CC superior anticoagulant activity by binding native human TF with high
CC affinity and specificity. The antibodies bind human TF, either alone or
CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
CC Factor IX) binding to TF or the complex, and thereby reducing blood
CC coagulation. The humanized antibodies are useful for inhibiting blood
CC coagulation or blood clot formation, angiogenesis, tumour metastases or
CC inflammation in a mammal. They are also useful as drug carriers, as
CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
CC diagnosis
XX
SQ Sequence 107 AA;

Alignment Scores:
Pred. No.: 4.93e-55 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 6 Gaps: 0

US-10-733-563-113 (1-321) x ABR42732 (1-107)

QY 1 CGTAGGGTGGACACATCTGTCTTCACTTCCGCCATCTGATGACAGTTGAATCT 60
Dd 1 ArgThrValAlaAlaProSerValPheIleProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATCGCTCTGTGTGCTGCTGAATCACTTCTATCCAGAGAGCCAAAGTACAG 120
Dd 21 GlyThrAlaSerValValCysLeuLeuAsnAnPheTyProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAACGCCCTCCAAATCGGGGTAACTCCAGGAGAGTGTCCACAGAGCAGGAC 180
Dd 121 TGGAGGTGGATAACGCCCTCCAAATCGGGGTAACTCCAGGAGAGTGTCCACAGAGCAGGAC 180

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Db 41 TrpLysValAspAsnAlaLeuGlnSerClyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGACCTACAGCCTCAGCAGACACCTGACCTTGAGCAAGACGACTTACCAG 240
Dd 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyArgLys 80
QY 241 AAACACAAAGTCTACGGCTGCGAAGTCACCCATCAGGGCCTGAGCTGCCCGTCCACAAG 300
Dd 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Dd 101 SerPheAsnArgGlyGluCys 107

RESULT 9
ABR42734
ID ABR42734 standard; protein; 107 AA.
XX
AC ABR42734;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-tissue factor humanized antibody light chain constant region.
XX
KW Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW antiinflammatory; mouse; human; hOAT.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO2003037911-A2.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-US034727.
XX
PR 29-OCT-2001; 2001US-0343306P.
PR 21-NOV-2001; 2001US-00990586.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR WPI; 2003-468399/44.
XX
PT New humanized antibody that binds specifically to human tissue factor,
PT useful for in vivo diagnostic methods, or for inhibiting blood
PT coagulation or blood clot formation, angiogenesis, tumor metastases or
PT inflammation in a mammal.
XX
PS Example 10; Fig 15A; 110pp; English.
XX
CC The present sequence is the protein sequence of the light chain constant
CC region of anti-human tissue factor (TF) humanized antibody hFAT
CC (humanised ch36-IgG4). Humanized antibodies of the invention provide
CC superior anticoagulant activity by binding native human TF with high
CC affinity and specificity. The antibodies bind human TF, either alone or
CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
CC Factor IX) binding to TF or the complex, and thereby reducing blood
CC coagulation. The humanized antibodies are useful for inhibiting blood
CC coagulation or blood clot formation, angiogenesis, tumour metastases or
CC inflammation in a mammal. They are also useful as drug carriers, as
CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
CC diagnosis
XX
SQ Sequence 107 AA;

Alignment Scores:
Pred. No.: 4.93e-55 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```

Query Match: 98.05% Indels: 0  
DB: 6 Gaps: 0  
US-10-733-563-113 (1-321) x ABR42734 (1-107)  
QY 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAGGAGCAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107  
RESULT 10  
ABR55835  
ID ABR55835 standard; protein; 107 AA.  
XX AC ABR55835;  
XX DT 02-SEP-2003 (first entry)  
XX DE Anti-Ang-2 antibody kappa constant region.  
XX KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
XX KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
XX KW angiogenesis; antibody.  
XX OS Homo sapiens.  
XX FN WO2003030833-A2.  
XX PD 17-APR-2003.  
XX PF 11-OCT-2002; 2002WO-US032613.  
XX PR 11-OCT-2001; 2001US-0328604P.  
XX PR 10-OCT-2002; 2002US-00269805.  
XX XX (AMGE-) AMGEN INC.  
XX PA Oliner JD;  
XX PI WPI; 2003-504963/47.  
XX DR New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful  
XX PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
XX PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX XX Example 4; Page 96; 161pp; English.  
XX PS The invention relates to a specific binding agent, which comprises at  
XX CC least one peptide selected from any of 62 peptides (ABR55769-830) or its  
XX CC fragment. The binding agents are antibodies that recognize and bind to  
XX CC angiotensin-2 (Ang-2). The specific binding agent, particularly the  
XX CC antibody, is useful for inhibiting undesired angiogenesis, treating  
XX CC cancer, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
XX CC 2 activity, modulating vascular permeability or plasma leakage, or

CC treating a disease (e.g. ocular neovascular disease, obesity,  
CC haemangioma, haemangioma, arteriosclerosis, inflammatory disease,  
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
CC disease, bone-related disease, or psoriasis) in a mammal. The present  
CC sequence represents a human kappa constant region of an anti-Ang-2  
CC antibody  
XX SQ Sequence 107 AA;  
Alignment Scores: 4.93e-55 Length: 107  
Pred. No.: 553.00 Matches: 107  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 98.05% Gaps: 0  
DB: 6  
US-10-733-563-113 (1-321) x ABR55835 (1-107)  
QY 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAGGAGCAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAAAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107  
RESULT 11  
ADJ94622  
ID ADJ94622 standard; protein; 107 AA.  
XX AC ADJ94622;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human kappa chain (CK) constant region.  
XX XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;  
XX KW IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;  
XX KW thrombocytopenia; lupus; rheumatoid arthritis; kappa chain; human; CK;  
XX KW constant region.  
XX OS Homo sapiens.  
XX FN WO2003068821-A2.  
XX PD 21-AUG-2003.  
XX XX 14-FEB-2003; 2003WO-GB000665.  
XX PR 14-FEB-2002; 2002US-0356132P.  
XX PR 07-OCT-2002; 2002US-0416232P.  
XX XX (IMMU-) IMMUNOMEDICS INC.  
XX PA (MCCA/) MCCA J D.  
XX XX Hansen H, Qu Z, Goldenberg DM;

```

XX DR WPI; 2003-697522/66.
XX DR N-FSDB; ADJ94621.
XX
PT PT New humanized anti-CD20 monoclonal antibody (Mab) that retains
PT PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,
PT PT leukemia or an autoimmune diseases.
XX PS
XX PS Example 1; Fig 7B; 106pp; English.
XX
CC CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
CC CC (Mab) or its antigen-binding fragment containing the complementarity
CC CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
CC CC region and the framework regions (FRs) of at least one human IV1AB
CC CC variable region. The antibodies of the invention are useful for
CC CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
CC CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
CC CC present amino acid sequence represents a human kappa chain (CK) constant
CC CC region.
XX
SQ Sequence 107 AA;
Alignment Scores:
Pred. No.: 4.93e-55 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-113 (1-321) x ADJ94622 (1-107)
Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGACAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAGTGGTGTGTGTGCTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGGTGGATTAACGCCCTCCAACTCGGTAACTCCAGGAGAGTGTCCACAGAGCAGAC 180
Db 41 TrpLysValAlaAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGACCTACAGCCTCAGCAGCACCCCTGACCCCTGAGCAAGACGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107
RESULT 12
ADP77161
ID ADP77161 standard; protein; 107 AA.
XX
AC ADP77161;
XX
DT 26-FEB-2004 (first entry)
XX
DE Anti-VAP-1 monoclonal antibody L chain constant region.
XX
KW complementarity determining region; CDR; mouse;
KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
KW chimeric; inflammatory disorder; rheumatoid arthritis;
KW inflammatory bowel disease; autoimmune disease; psoriasis;
KW immunoscintigraphic imaging.
XX

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OS Homo sapiens.
XX
FN WO2003093319-A1.
XX
PD 13-NOV-2003.
XX
PF 28-APR-2003; 2003WO-FI000330.
XX
PR 29-APR-2002; 2002FI-00000807.
XX
PA (BIOT-) BIOTIE THERAPIES CORP.
XX
PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;
XX
WIPI; 2004-022642/02.
XX
New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
PT encoding nucleic acid molecules, useful for diagnosing and treating
PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
XX
Claim 18; SEQ ID NO 22; 56pp; English.
XX
This sequence represents the constant region of a human anti-Vascular
CC Adhesion Protein-1 (VAP-1) antibody light chain. This sequence may be
CC used in the production of a chimeric mouse-human anti-VAP-1 antibody. The
CC nucleic acid molecules, polypeptides or antibodies are useful in treating
CC VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis,
CC inflammatory bowel disease, autoimmune diseases or psoriasis. The
CC chimeric VAP-1 antibody is further used for in vitro and in vivo
CC diagnostic applications, including in vivo immunoscintigraphic imaging of
CC inflammation sites. The chimeric MAb's of the invention have improved
CC kinetic properties compared to the corresponding murine antibodies.
XX
SQ Sequence 107 AA;
Alignment Scores:
Pred. No.: 4.93e-55 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 8 Gaps: 0
US-10-733-563-113 (1-321) x ADP77161 (1-107)
Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGACAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAGTGGTGTGTGTGCTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGGTGGATTAACGCCCTCCAACTCGGTAACTCCAGGAGAGTGTCCACAGAGCAGAC 180
Db 41 TrpLysValAlaAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGACCTACAGCCTCAGCAGCACCCCTGACCCCTGAGCAAGACGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107
RESULT 13
ADL35096
ID ADL35096 standard; protein; 107 AA.
XX

```



AC ADL35096;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human IgG4 (hFAT) kappa light chain constant domain protein SeqID 99.  
XX  
KW antibody; variable domain; framework region; FR; huFR;  
XX immune system molecule; kappa; anti-tissue factor; hFAT; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004020579-A2.  
XX  
PD 11-MAR-2004.  
XX  
PF 06-AUG-2003; 2003WO-US024637.  
XX  
PR 29-AUG-2002; 2002US-00230880.  
XX  
PA (SUNO-) SUNOL MOLECULAR CORP.  
XX  
PI Wong HC, Stinson JR, Mosquera LA;  
XX WPI; 2004-239169/22.  
XX  
DR  
XX  
XX Producing humanized antibodies for diagnostic and therapeutic purposes  
PT comprises optimizing similarity between individual antibody framework  
PT regions to help identify human framework regions suitable for making the  
PT antibodies.  
XX  
PS Disclosure; SEQ ID NO 99; 137pp; English.  
XX  
XX This invention relates to a novel method for producing a humanised  
CC antibody variable (V) domain or its fragment by optimising sequence  
CC similarity between individual antibody framework regions (FRs) in order  
CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
CC suitable binding affinity with reduced immunogenicity in humans. The  
CC present invention describes a method of mutagenising DNA of non-human FRs  
CC to encode humanised FRs having an amino acid sequence that is  
CC substantially identical to the selected human FR previously identified  
CC through sequence similarity searching. As such, this method provides  
CC humanised light or heavy chain V domains of the sequence huFR1-huFR2  
CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
CC products to treat and/or diagnose diseases in humans and animals.  
CC Furthermore, the method expands the number of best fit possibilities that  
CC can be generated and provides a rational basis for assembling nearly all  
CC humanised immune system molecules of interest. This polypeptide sequence  
CC is the human IgG4 kappa light chain constant domain protein of the  
CC invention.  
XX  
SQ Sequence 107 AA;  
  
Alignment Scores:  
Pred. No.: 4.93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-733-563-113 (1-321) x ADL35096 (1-107)  
  
QY 1 CQTACGGTGGCTGCACCATCTCTCTTCATCTCCGCCATCTGAGCAGTTGAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20  
  
QY 61 GGAAGTGGCTCTGTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40  
  
QY 121 TGGAAAGTGGATAACGCCCTCCAAATCGGGTAACTCCCAAGGAGAGTGTCCAGAGCAGAC 180  
DB 121 TGGAAAGTGGATAACGCCCTCCAAATCGGGTAACTCCCAAGGAGAGTGTCCAGAGCAGAC 180

DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCAGCACCTGACCCCTGAGCAAGCAGACTACGAG 240  
DB 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80  
QY 241 AAACCAAAAGTCTACGCTTCCGGAAGTCAACCCATCAGGCGCTGAGCTCGCCCTCACAAG 300  
DB 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGCGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107  
  
RESULT 14  
ADL35094  
ID ADL35094 standard; protein; 107 AA.  
XX  
AC ADL35094;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human IgG1 (hOAT) kappa light chain constant domain protein SeqID 97.  
XX  
KW antibody; variable domain; framework region; FR; huFR;  
XX immune system molecule; kappa; anti-tissue factor; hOAT; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004020579-A2.  
XX  
PD 11-MAR-2004.  
XX  
PF 06-AUG-2003; 2003WO-US024637.  
XX  
PR 29-AUG-2002; 2002US-00230880.  
XX  
PA (SUNO-) SUNOL MOLECULAR CORP.  
XX  
PI Wong HC, Stinson JR, Mosquera LA;  
XX WPI; 2004-239169/22.  
XX  
DR  
XX  
XX Producing humanized antibodies for diagnostic and therapeutic purposes  
PT comprises optimizing similarity between individual antibody framework  
PT regions to help identify human framework regions suitable for making the  
PT antibodies.  
XX  
PS Disclosure; SEQ ID NO 97; 137pp; English.  
XX  
XX This invention relates to a novel method for producing a humanised  
CC antibody variable (V) domain or its fragment by optimising sequence  
CC similarity between individual antibody framework regions (FRs) in order  
CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
CC suitable binding affinity with reduced immunogenicity in humans. The  
CC present invention describes a method of mutagenising DNA of non-human FRs  
CC to encode humanised FRs having an amino acid sequence that is  
CC substantially identical to the selected human FR previously identified  
CC through sequence similarity searching. As such, this method provides  
CC humanised light or heavy chain V domains of the sequence huFR1-huFR2  
CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
CC products to treat and/or diagnose diseases in humans and animals.  
CC Furthermore, the method expands the number of best fit possibilities that  
CC can be generated and provides a rational basis for assembling nearly all  
CC humanised immune system molecules of interest. This polypeptide sequence  
CC is the human IgG1 kappa light chain constant domain protein of the  
CC invention.  
XX  
SQ Sequence 107 AA;  
  
Alignment Scores:  
Pred. No.: 4.93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 8 Gaps: 0

Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-113 (1-321) x ADL35094 (1-107)

Qy 1 CGTACGGTGGCTGCACCATCTGCTTCTTCATCTCCGCCCATCTGATGACGAGTTCGAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAAGTGCCTGTGTGTGCTGCTGTAATCTTATCCAGAGAGGCGCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
Qy 121 TGGAAAGTGGATAACGCCCTCCAAATCGGGTAACTCCAGAGAGAGTGTCCACAGAGCAGGAC 180  
Db 41 TrpLysValAlaAspAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGAGACACCTACAGCCTCAGCAGCAGCCCTGACCCCTGAGCAAGAGAGTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
Qy 241 AAACACAAAGTCTAGCGCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCCGTCACAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 15  
ID ADM41539  
AC ADM41539;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Anti-interleukin-1 receptor type 1 antibody kappa chain constant region.  
XX  
KW Human; monoclonal antibody; antibody; interleukin-1; receptor;  
KW antiasthmatic; antiinflammatory; dermatological; antiallergic;  
KW protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;  
KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;  
KW anticonvulsant; dermatological; antigen; antiparkinsonian; antidiabetic;  
KW cytostatic.  
XX  
OS Homo sapiens.  
XX  
FN WO2004022718-A2.  
XX  
PD 18-MAR-2004.  
XX  
PF 05-SEP-2003; 2003WO-US027978.  
XX  
PR 06-SEP-2002; 2002US-0408719P.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;  
PI Elliott G;  
XX  
DR WPI; 2004-248462/23.  
XX  
DR N-PSDB; ADM41538.  
XX  
PT Isolated human antibody that specifically binds interleukin-1 receptor  
PT type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as  
PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.  
XX  
PS Disclosure; SEQ ID NO 4; 179pp; English.  
XX

CC The present sequence is that of a human anti-interleukin-1 receptor type  
CC 1 (IL-1R1) monoclonal antibody (MAB) kappa chain constant region. Human  
CC MABs to IL-1R1 were prepared using the HCo7 strain of transgenic mice,  
CC which expresses human antibody genes. These mice were immunised with  
CC purified recombinant IL-1R1, and splenocytes from immunised mice were  
CC fused to a mouse myeloma cell line to generate hybridomas. Hybridomas  
CC which secreted a MAb that bound with high avidity to IL-1R1 were  
CC selected. The MABs inhibit IL-1 signalling by competing with IL-1beta and  
CC IL-1alpha binding to IL-1R. These MABs, as well as single chain  
CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies  
CC and (Fab')2 antibodies derived from them, are used in methods of treating  
CC IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.  
CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral  
CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,  
CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,  
CC Clostridium associated illnesses, coronary conditions, cancer including  
CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,  
CC fibromyalgia, glomerulonephritis, graft versus host disease,  
CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,  
CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,  
CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,  
CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,  
CC septic shock, side effects of radiation therapy, temporal mandibular  
CC joint disease, sleep disturbance, uveitis, or an inflammatory condition  
CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic  
CC surgery, infection or other disease processes.  
CC  
CC SQ Sequence 107 AA;

Alignment Scores:

Pred. No.: 4,93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-113 (1-321) x ADM41539 (1-107)

Qy 1 CGTACGGTGGCTGCACCATCTGCTTCTTCATCTCCGCCCATCTGATGACGAGTTCGAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAAGTGCCTGTGTGTGCTGCTGTAATCTTATCCAGAGAGGCGCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
Qy 121 TGGAAAGTGGATAACGCCCTCCAAATCGGGTAACTCCAGAGAGAGTGTCCACAGAGCAGGAC 180  
Db 41 TrpLysValAlaAspAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGAGACACCTACAGCCTCAGCAGCAGCCCTGACCCCTGAGCAAGAGAGTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
Qy 241 AAACACAAAGTCTAGCGCTGCGAAGTCAACCCATCAGGGCCTGAGCTCGCCGTCACAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107

Search completed: January 28, 2006, 08:33:47  
Job time : 53.1261 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:20:11 ; Search time 8.75601 Seconds  
(without alignments)  
7054.719 Million cell updates/sec

Title: US-10-733-563-113  
Perfect score: 564  
Sequence: 1 cgtacggtggtgcaccatc.....gcttcaacagggagagtgt 321

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgm2\_1/USPFO\_spool\_p/US10733563/runat\_27012006\_180006\_4797/app\_query.fasta\_1.2716  
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1 83 @runat\_27012006\_180006\_4797 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=1120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	98.0	215	2 JEO243	Ig kappa chain NIG
2	553	98.0	215	2 JEO244	Ig kappa chain NIG
3	553	98.0	215	2 JEO242	Ig kappa chain NIG
4	550	97.5	135	2 S52059	JC-kappa protein -
5	548	97.2	106	1 K3HU	Ig kappa chain C r
6	537	95.2	216	2 JEO241	Ig kappa chain Am3
7	520	92.2	215	2 A23746	Ig kappa chain V-1
8	513	91.0	99	2 A37927	Ig kappa chain C r
9	507	89.9	99	2 S26653	Ig kappa chain C r
10	372	66.0	240	2 S06084	Ig kappa chain pre
11	367	65.1	106	1 K1RTB	Ig kappa chain C r
12	366	64.9	178	2 PT0219	Ig kappa chain C r
13	359	63.7	106	1 K1RTA	Ig kappa chain C r
14	358	63.5	217	2 S42772	Ig kappa chain - m

15	358	63.5	218	2 S68241	Ig kappa chain V r
16	358	63.5	219	2 S38865	Ig kappa chain - m
17	352	62.4	218	2 JCS810	monoclonal antibod
18	352	62.4	219	2 S52028	Ig kappa chain - m
19	352	62.4	219	2 PC4203	Ig kappa chain (no
20	352	62.4	219	2 S16112	Ig kappa chain V r
21	352	62.4	220	2 A31790	Ig kappa chain - m
22	352	62.4	225	2 S37484	Ig kappa chain V r
23	352	62.4	234	2 S14237	Ig kappa chain - m
24	352	62.4	234	2 S01320	Ig kappa chain pre
25	352	62.4	235	2 S25058	Ig kappa chain pre
26	350	62.1	106	1 K1MS	Ig kappa chain - m
27	350	62.1	126	2 I54782	gene Pvt-1a/Ig-Ck
28	348	61.7	225	2 J10029	Ig kappa chain C r
29	345	61.2	230	2 S31611	Ig kappa chain pre
30	321	56.9	214	2 S68212	Ig kappa chain - a
31	312	55.3	210	2 A56169	Ig kappa chain (Ma
32	308.5	54.7	106	2 G20907	Ig kappa chain V r
33	306.5	54.3	106	1 K4RBBS	Ig kappa-B4 chain
34	277.5	49.2	229	2 A20969	Ig kappa-2 chain C
35	257.5	45.7	103	1 K4RB	Ig kappa chain pre
36	256	45.4	104	2 F53275	Ig kappa-B4 chain
37	246.5	43.7	104	1 K9RB	Ig kappa-1 chain C
38	245	43.4	238	2 A49633	Ig kappa-B9 chain
39	241	42.7	104	1 K9RBV	Ig lambda-like Cha
40	237	42.0	118	2 A46518	Ig kappa chain C r
41	231	41.0	103	2 B26167	Ig L1 chain J-C re
42	231	41.0	213	2 A21177	Ig lambda chain C
43	225	39.9	108	1 K3FG	Ig light chain pre
44	223.5	39.6	103	1 K9RB	Ig light chain C r
45	222	39.4	197	2 S29593	Ig kappa-B5 chain
					Ig kappa chain (WM

ALIGNMENTS

RESULT 1

JEO243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JEO243  
R:Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A:Reference number: JEO243  
A:Accession number: JEO243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
A:Cross-references: UNIPARC:UPI0000176984  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 3.34e-47 Length: 215  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x JEO243 (1-215)

QY	1	CGTACGGTGGCGTGCACCATCTCTTCATCTTCCGCCCATCTGATGACGAGTTGAATCT	60
DB	109	ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuIysSer	128
QY	61	GGAACCTGCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAG	120
DB	129	GlyThrAlaSerValValCysLeuLeuAsnAsnPhenPheProArgGluAlaIysValGln	148
QY	121	TGGAAGGTGGTAACGCCCTCAATCGGTTAACTCCAGGAGAGTGTCCAGAGCAGAC	180
DB	149	TrpIysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAap	168



QY 61 GGAACCTGCTCTGTGTGTGCTGCTGTAATACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db 49 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 68  
QY 121 TCGAAGGTGGATAACGCCCTCCAAATCGGTAACTCCAGAGAGTCTCACAGCAGGAC 180  
Db 69 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 88  
QY 181 AGCAAGGACAGCACCTTACAGCCTTCAGCAGCAGCCCTGACCCCTGAGCAAAAGCAGATACAG 240  
Db 89 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 108  
QY 241 AAACACAAAGTACGCTGCGAAGTACCCATCAGGCGCTGAGCTGCGCCCTCACAAAG 300  
Db 109 LysHisLysLeuTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 128  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 129 SerPheAsnArgGlyGluCys 135  
RESULT 5  
K3HU  
Ig kappa chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1980 #sequence\_revision 02-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02  
R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.  
Biochemistry 9, 3155-3161, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequence  
A:Reference number: A90562; MUID:71064023; PMID:5489770  
A:Contents: myeloma protein Eu  
A:Accession: B90562  
A:Molecule type: protein  
A:Residues: 1-106 <GOT>  
A:Cross-references: UNIPROT:P01834; UNIPARC:UPI000002F106  
A:Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation: Eu, disulfide bonds  
R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub  
A:Reference number: A91651; MUID:72188439; PMID:5027703  
A:Contents: Bence Jones protein Ti  
A:Accession: A91651  
A:Molecule type: protein  
A:Residues: 1-106 <SUT>  
A:Cross-references: UNIPARC:UPI000002F106  
R:Hietter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.  
Cell 22, 197-207, 1980  
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv  
A:Reference number: A90806; MUID:81042304; PMID:6775818  
A:Accession: A90806  
A:Molecule type: DNA  
A:Residues: 1-106 <HIE>  
A:Cross-references: UNIPARC:UPI000002F106; GB:J00241; NID:933140; PIDN:CAA23823.1; PID:9  
A:Note: the sequence was determined from the germline gene  
R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,  
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,  
A:Reference number: A94417  
A:Contents: Bence Jones protein Roy  
A:Accession: A94417  
A:Molecule type: protein  
A:Residues: 1-44, 'A', '46-56', 'Q', '58-82', 'L', '84-106 <HIL>  
A:Cross-references: UNIPARC:UPI000017376D  
A:Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu  
R:Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
A:Title: Die vollständige Aminosäuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).  
A:Reference number: A91639; MUID:68242259; PMID:5586923  
A:Contents: Bence Jones protein Cum

A:Accession: A91639  
A:Molecule type: protein  
A:Residues: 1-56, 'Q', '58-106 <H12>  
A:Cross-references: UNIPARC:UPI000017376E  
R:Tritani, K.; Shinoda, I.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete s  
A:Reference number: A92047; MUID:69234734; PMID:4893682  
A:Contents: Bence Jones protein Ag  
A:Accession: A92047  
A:Molecule type: protein  
A:Residues: 1-13, 'N', '15-106 <TIT>  
A:Cross-references: UNIPARC:UPI000017376F  
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 56-59, 1970  
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.  
A:Reference number: A94242; MUID:70201507; PMID:5447531  
A:Contents: Waldenstrom's macroglobulin Ou  
A:Accession: A94242  
A:Molecule type: protein  
A:Residues: 1-13, 'N', '15-106 <KOH>  
A:Cross-references: UNIPARC:UPI000017376F  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A:Cross-references: UNIPARC:UPI0000173770  
A:Note: allotype Inv(3)  
R:Steiner, V.; Chang, J.Y.  
PDBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
A:Contents: annotation  
C:Genetics:  
A:Gene: GDB:IGKC  
A:Cross-references: GDB:120088; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into la;  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental  
Alignment Scores:  
Pred. No.: 1,09e-46 Length: 106  
Score: 548.00 Matches: 106  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.16% Indels: 0  
DB: 1 Gaps: 0  
US-10-733-563-113 (1-321) x K3HU (1-106)  
QY 4 ACGGTGGCTGCACCATCTGTCTTCATCTCCGCCATCTGTATGACAGTGTGAATCTGGA 63  
Db 1 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSerGly 20  
QY 64 ACTGCTCTGTGTGTGCTGCTCTGAATACTTCTATCCAGAGAGCCAAAGTACAGTG 123  
Db 21 ThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGlnTrp 40  
QY 124 AAGTGGTAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTCCACAGAGCAGCAGC 183  
Db 41 LysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAspSer 60  
QY 184 AAGGACAGCACCTTACAGCCTCAGCAGCACCTTGACCCCTGAGCAAGACAGATACCAGAAA 243

Db 61 LysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLeuSerLysAlaAspTyrGluLys 80  
Qy 244 CACAAAGTCTAGGCTGGAAGTCAACCATCGGCGCTGAGCTCGCCGTCACAAAGAGC 303  
|||||  
Db 81 HisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer 100  
|||||  
Qy 304 TTCAACAGGGGAGAGTGT 321  
|||||  
Db 101 PheAsnArgGlyGluCys 106  
|||||  
RESULT 6  
Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: J050241  
F:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
A:Reference number: J050241  
A:Accession: J050241  
A:Molecule type: protein  
A:Residues: 1-216 <ALI>  
A:Cross-references: UNIPARC:UPI0000176981  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-92/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 1.33e-45 Length: 216  
Score: 537.00 Matches: 104  
Percent Similarity: 97.20% Conservative: 0  
Best Local Similarity: 97.20% Mismatches: 3  
Query Match: 95.21% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x J050241 (1-216)  
Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAATCT 60  
Db 110 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 129  
|||||  
Qy 61 GGAAGTGGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db 130 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 149  
|||||  
Qy 121 TGAAGGTGGATAACGCTCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 150 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 169  
|||||  
Qy 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGAGCAGGAGAGTGTCCAGAG 240  
Db 170 SerLysAspSerThrTyrSerLeuSerSerThrThrLeuThrSerLysAlaAspTyrGlu 189  
|||||  
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 190 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 209  
|||||  
Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 210 SerPheAsnArgGlyGluCys 216  
|||||  
RESULT 7  
Ig kappa chain V-III (KAU cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: A23746  
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl  
A:Reference number: A23746; MUID:91131575; PMID:1993660  
A:Accession: A23746  
A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
A:Cross-references: UNIPARC:UPI0000176985  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 6.64e-44 Length: 215  
Score: 520.00 Matches: 104  
Percent Similarity: 98.11% Conservative: 0  
Best Local Similarity: 98.11% Mismatches: 2  
Query Match: 92.20% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x A23746 (1-215)  
Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAATCT 60  
Db 109 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 128  
|||||  
Qy 61 GGAAGTGGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db 129 GlyThrAlaSerValValGlyLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 148  
|||||  
Qy 121 TGAAGGTGGATAACGCTCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 149 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 168  
|||||  
Qy 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGAGCAGGAGAGTGTCCAGAG 240  
Db 169 SerLysAspSerThrTyrSerLeuSerSerThrThrLeuThrSerLysAlaAspTyrGlu 188  
|||||  
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 189 LysHisLysValTyrAlaGlyGluValThrHisGlnGlyLeuSerSerProValThrLys 208  
|||||  
Qy 301 AGCTTCAACAGGGGAGAG 318  
Db 209 SerPheAsnArgGlyGlu 214  
|||||  
RESULT 8  
A37927  
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
C:Accession: A37927  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: A37927  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
A:Cross-references: UNIPARC:UPI0000176ED6  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:12-81/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 3.45e-43 Length: 99  
Score: 513.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 98.99% Mismatches: 0  
Query Match: 90.96% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x A37927 (1-99)  
Qy 25 TTCATCTTCCCGCCATCTGATGAGCAGTTGAATCTGGAATCGCTGTGTGTGCTG 84  
Db 1 PheIlePheProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeu 20  
|||||

QY 85 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAACGCCCTCCAA 144  
 Db 21 LeuAsnAsnPhetyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGln 40  
 QY 145 TCGGGTAACTCCAGAGAGAGTGTCCAGAGCAGGACAGCAAGCAGACCTACAGCTTC 204  
 Db 41 SerGlyAsnSerGlnGluSerValThrGluGlnAspSerLysAspSerThrTrpSerLeu 60  
 QY 205 AGCAGCACCTGACCTCGAGCAAGCAGACTACGAGAAACACAAAGTCTACCGCTGCCGAA 264  
 Db 61 SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysLeuTyrAlaCysGlu 80  
 QY 265 GTACCCATCAGGCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 321  
 Db 81 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGluCys 99

RESULT 9  
 S26653  
 Ig kappa chain C region - chimpanzee (fragment)  
 C:Species: Pan troglodytes (chimpanzee)  
 C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
 C:Accession: S26653  
 R: Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.B.; Isaacson, C.; Oestberg, L.  
 Hum. Antibodies Hybridomas 1, 23-26, 1990  
 A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
 A:Reference number: S26652; MUID:91355693; PMID:2129418  
 A:Accession: S26653  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <EHR>  
 A:Cross-references: UNIPARC:UPI0000176BD5; EMBL:X65287  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 P:19-88/Domain: immunoglobulin homology <IMW>

Alignment Scores:  
 Pred. No.: 1.37e-42 Length: 99  
 Score: 507.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 89.8% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x S26653 (1-99)

QY 4 ACGGTGGCTGCACCATCTGTCTTCATCTCCGCCCATCTGATGACAGTTGAAATCTGGA 63  
 Db 1 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSerGly 20  
 QY 64 ACTGCCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAGTGG 123  
 Db 21 ThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGlnTrp 40  
 QY 124 AAGTGTGAATAAGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTCAAGAGCAGCAGC 183  
 Db 41 LysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAspSer 60  
 QY 184 AAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGCAGACTACAGAAA 243  
 Db 61 LysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGluLys 80  
 QY 244 CACAAAGTCTAGCCTCGGAGAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
 Db 81 HisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 99

RESULT 10  
 S06084  
 Ig kappa chain precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
 C:Accession: S06084  
 R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989  
 A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.  
 A:Reference number: S06084; MUID:90016888; PMID:2508067  
 A:Accession: S06084  
 A:Molecule type: mRNA  
 A:Residues: 1-240 <CRO>  
 A:Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 P:1-20/Domain: signal sequence #status predicted <SIG>  
 P:21-240/Product: Ig kappa chain #status predicted <MAT>  
 P:153-222/Domain: immunoglobulin homology <IMW>

Alignment Scores:  
 Pred. No.: 4.12e-29 Length: 240  
 Score: 372.00 Matches: 70  
 Percent Similarity: 77.57% Conservative: 13  
 Best Local Similarity: 65.42% Mismatches: 24  
 Query Match: 65.96% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x S06084 (1-240)

QY 1 CQTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
 Db 134 ArgAlaAspAlaAlaProThrValSerIlePheProProSerThrGluGlnLeuAlaThr 153  
 QY 61 GGAACCTGCCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAG 120  
 Db 154 GlyGlyAlaSerValValCysLeuMetAsnAsnPheTyrProArgAspIleSerValLys 173  
 QY 121 TGGAAAGTGGATAACGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTCAAGAGCAGGAC 180  
 Db 174 TrpLysIleAspGlyThrGluArgArgAspGlyValLeuAspSerValThrAspGlnAsp 193  
 QY 181 AGCAAGGACAGCAGCCTCAGCAGCTCAGCAGCCCTGACCCCTGAGCAAGAGCAGCTACGAG 240  
 Db 194 SerLysAspSerThrTyrSerMetSerSerThrLeuSerLeuSerLysAlaAspTyrGlu 213  
 QY 241 AAACACAAAGTCAAGCCTCGCGAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
 Db 214 SerHisAsnLeuTyrThrCysGluValValHisLysThrSerSerSerProValLys 233  
 QY 301 AGCTTCAACAGGGGAGAGTGT 321  
 Db 234 SerPheAsnArgAsnGluCys 240

RESULT 11  
 KIRTB  
 Ig kappa chain C region (allele b) - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
 C:Accession: A93901; A92807; A02117  
 R:Sheppard, H.W.; Gutman, G.A.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981  
 A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the lev  
 A:Reference number: A93901; MUID:82082587; PMID:6273908  
 A:Accession: A93901  
 A:Molecule type: DNA  
 A:Residues: 1-106 <SHS>  
 A:Cross-references: UNIPROT:P01835; UNIPARC:UPI000012DB83; GB:V01241; GB:J00745; GB:J025:  
 A:Experimental source: strain LOU  
 R:Starace, V.; Querinjean, P.  
 J. Immunol. 115, 59-62, 1975  
 A:Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation  
 A:Reference number: A92807; MUID:75212238; PMID:807630  
 A:Contents: Bence Jones protein S211  
 A:Accession: A92807  
 A:Molecule type: protein  
 A:Residues: 1, 'N', 3-29, 'K', 31-47, 49-78, 'Q', 80-86, 'Q', 88-98, 'W', 99, 'N', 101-106 <STA>  
 A:Cross-references: UNIPARC:UPI0000173771  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la;

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer

F:19-88/Domain: immunoglobulin homology <IMM>

F:26-86/Disulfide bonds: #status predicted

F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Alignment Scores:

Pred. No.:	1.35e-28	Length:	106
Score:	367.00	Matches:	68
Percent Similarity:	78.85%	Conservative:	14
Best Local Similarity:	65.38%	Mismatches:	22
Query Match:	65.07%	Indels:	0
DB:	1	Gaps:	0

US-10-733-563-113 (1-321) x K1RTB (1-106)

Qy	10	GCTGCACCATCTGCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCC	69
Db	3	AlaAlaProThrValSerIlePheProProSerThrGluGlnLeuAlaThrGlyGlyAla	22
Qy	70	TCTGTGTGCTGCTGCTGAATACTTATCCAGAGGCCAAAGTACAGTGGAGGTG	129
Db	23	SerValValCysLeuMetAsnAsnPheTyrProArgAspIleSerValYstIrpIysile	42
Qy	130	GATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGACGACGACGAGGAC	189
Db	43	AspGlyThrGluArgArgAspGlyValLeuAspSerValThrAspGlnAspSerIysAsp	62
Qy	190	AGCACCTACAGCTCAGCAGACACCTGACCTCCAGCAAGCAGACTACGAGAAACACAAA	249
Db	63	SerThrTyrSerMetSerSerThrLeuSerLeuThrIysAlaAspTyrGluSerHisAsn	82
Qy	250	GTCTACGCTCGGAAGTCACCCATCAGGCGCTGAGCTCGCCGTCACAAAGAGCTTCAAC	309
Db	83	LeuTyrThrCysGluValValHisIysThrSerSerProValValIysSerPheAsn	102
Qy	310	AGGGGAGAGTCT 321	
Db	103	ArgAsnGluCys 106	

RESULT 12

PT0219

Ig kappa chain V-C region (PIC18) - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 11-Jan-2000

C:Accession: PT0219

R:Lammers, B.M.; Beaman, K.D.; Kim, Y.B.

Mol. Immunol. 28, 877-880, 1991

A:Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.

A:Reference number: PT0219; MUID:91342694; PMID:1715030

A:Accession: PT0219

A:Molecule type: mRNA

A:Residues: 1-178 <LAM>

A:Cross-references: UNIPARC:UPI00001151A1; GB:M59321; NID:g164508; PIDN:AAA03520.1; PID:

A:Experimental source: spleen, strain Minnesota Miniature

A:Note: the authors translated the codon CTC for residue 141 as Ser

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-70/Domain: V region (fragment) <VRG>

F:12-18/Region: complementarity-determining 1

F:52-60/Region: complementarity-determining 2

F:61-70/Region: framework 2

F:71-178/Domain: C region <CRG>

F:96-156/Disulfide bonds: #status predicted

F:176/Disulfide bonds: interchain #status predicted

Alignment Scores:

Pred. No.:	1.66e-28	Length:	178
Score:	366.00	Matches:	69
Percent Similarity:	76.64%	Conservative:	13
Best Local Similarity:	64.49%	Mismatches:	25
Query Match:	64.89%	Indels:	0

DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x PT0219 (1-178)

Qy	1	CGTACGGTGGTGACACCATCTGCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCT	60
Db	70	ArgAlaAspAlaIysProSerValPheIlePheProProSerIysGluGlnLeuAlaThr	89
Qy	61	GGAACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAG	120
Db	90	ProThrValSerValCysLeuIleAsnAsnPhePheProArgGluIleSerValIys	109
Qy	121	TGGAAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGACGAGGAC	180
Db	110	TrpIysValAspGlyValValGlnSerSerGlyHisProAspSerValThrGluGlnAsp	129
Qy	181	AGCAAGGACACACCTCAGCAGCTCAGCAGACCCCTGACCCCTGAGCAAAAGCAGACTACGAG	240
Db	130	SerIysAspSerThrTyrSerLeuSerSerThrLeuSerLeuProThrSerGlnTyrLeu	149
Qy	241	AAACACAAAGTCTACGCTCGGAAGTCACCCATCAGGCGCTGAGCTCGCCGTCACAAAG	300
Db	150	SerHisAsnLeuTyrSerCysGluValThrHisIysThrIysThrLeuAlaSerProLeuValThr	169
Qy	301	AGCTTCAACAGGGGAGAGTGT 321	
Db	170	SerPheAsnArgAsnGluCys 176	

RESULT 13

K1RTA

Ig kappa chain C region (allele a) - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Aug-1982 #sequence\_revision 10-Sep-1982 #text\_change 09-Jul-2004

C:Accession: A02118

R:Sheppard, H.W.; Gutman, G.A.

Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981

A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the lev

A:Reference number: A93901; MUID:82082587; PMID:6273908

A:Accession: A02118

A:Molecule type: DNA

A:Residues: 1-106 <SHE>

A:Cross-references: UNIPROT:P01836; UNIPARC:UPI00001148A8; GB:J00745; NID:g204

A:Experimental source: strain DA

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lai

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer

F:19-88/Domain: immunoglobulin homology <IMM>

F:26-86/Disulfide bonds: #status predicted

F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Alignment Scores:

Pred. No.:	8.54e-28	Length:	106
Score:	359.00	Matches:	66
Percent Similarity:	78.85%	Conservative:	16
Best Local Similarity:	63.46%	Mismatches:	22
Query Match:	63.65%	Indels:	0
DB:	1	Gaps:	0

US-10-733-563-113 (1-321) x K1RTA (1-106)

Qy	10	GCTGCACCATCTGCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCC	69
Db	3	AlaAlaProThrValSerIlePheProProSerMetGluGlnLeuThrSerGlyGlyAla	22
Qy	70	TCTGTGTGCTGCTGCTGAATACTTATCCAGAGGCCAAAGTACAGTGGAGGTG	129
Db	23	ThrValValCysPheValAsnAsnPheTyrProArgAspIleSerValYstIrpIysile	42
Qy	130	GATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGACGAGGACGACGAGGAC	189
Db	43	AspGlySerGluGlnArgAspGlyValLeuAspSerValThrAspGlnAspSerIysAsp	62





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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 ; Search time 49.2425 Seconds  
(without alignments)  
9198.340 Million cell updates/sec

Title: US-10-733-563-113  
Perfect score: 564  
Sequence: 1 cgtacggtggtgcaccatc.....gcttcaacagggagagtgt 321

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgm2\_1/USPTO\_spool\_p/US10733563/runat\_27012006.180005.4782/app\_query.fasta\_1.2716  
-DB=UniProt -QFWT=fascan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptp -NORM=ext -HRAPISE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CGN 1.1.632 @runat\_27012006.180005.4782 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=1120 -WARN\_TIMEOUT=30 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	98.0	120	Q6P5R5 HUMAN	Q6P5R5 homo sapien
2	553	98.0	234	Q6P5R5 HUMAN	Q6P5R5 homo sapien
3	553	98.0	234	Q6P5R5 HUMAN	Q6P5R5 homo sapien
4	553	98.0	235	Q6GMV9 HUMAN	Q6GMV9 homo sapien
5	553	98.0	235	Q6GMW0 HUMAN	Q6GMW0 homo sapien
6	553	98.0	235	Q6P5R5 HUMAN	Q6P5R5 homo sapien
7	553	98.0	236	Q6GMX0 HUMAN	Q6GMX0 homo sapien
8	553	98.0	236	Q6P5R5 HUMAN	Q6P5R5 homo sapien
9	553	98.0	236	Q6P5R5 HUMAN	Q6P5R5 homo sapien
10	553	98.0	236	Q6P5R5 HUMAN	Q6P5R5 homo sapien
11	553	98.0	236	Q6P5R5 HUMAN	Q6P5R5 homo sapien
12	553	98.0	236	Q6P5R5 HUMAN	Q6P5R5 homo sapien
13	553	98.0	236	Q6P5R5 HUMAN	Q6P5R5 homo sapien
14	553	98.0	236	Q6GMX9 HUMAN	Q6GMX9 homo sapien
15	553	98.0	236	Q6GMX8 HUMAN	Q6GMX8 homo sapien
16	553	98.0	236	Q6GMW1 HUMAN	Q6GMW1 homo sapien

17	553	98.0	236	2	Q502W4 HUMAN	Q502W4 homo sapien
18	553	98.0	239	2	Q6P491 HUMAN	Q6P491 homo sapien
19	553	98.0	239	2	Q8TCD0 HUMAN	Q8TCD0 homo sapien
20	553	98.0	240	2	Q6PIH6 HUMAN	Q6PIH6 homo sapien
21	549	97.3	239	2	Q8NEK0 HUMAN	Q8NEK0 homo sapien
22	548	97.2	106	1	KAC_HUMAN	P01834 homo sapien
23	548	97.2	234	2	Q569I9 HUMAN	Q569I9 homo sapien
24	369	65.4	234	2	Q4KM66 RAT	Q4KM66 rattus norv
25	369	65.4	234	2	Q5M838 RAT	Q5M838 rattus norv
26	367	65.1	106	1	KACB_RAT	P01835 rattus norv
27	359	63.7	106	1	KACA_RAT	P01836 rattus norv
28	358	63.5	219	2	Q5ZC0 MOUSE	Q5ZC0 mus musculus
29	352	62.4	234	2	Q5XKG4 MOUSE	Q5XKG4 mus musculus
30	352	62.4	235	2	Q5XFY8 MOUSE	Q5XFY8 mus musculus
31	352	62.4	235	2	Q58EV6 MOUSE	Q58EV6 mus musculus
32	352	62.4	236	2	Q7TS98 MOUSE	Q7TS98 mus musculus
33	352	62.4	236	2	Q52L95 MOUSE	Q52L95 mus musculus
34	352	62.4	237	2	Q569Y8 MOUSE	Q569Y8 mus musculus
35	352	62.4	238	2	Q66J87 MOUSE	Q66J87 mus musculus
36	352	62.4	238	2	Q58EU4 MOUSE	Q58EU4 mus musculus
37	352	62.4	239	2	Q58EU8 MOUSE	Q58EU8 mus musculus
38	352	62.4	240	2	Q52L64 MOUSE	Q52L64 mus musculus
39	352	62.4	241	2	Q63ZX4 MOUSE	Q63ZX4 mus musculus
40	350	62.1	106	1	KAC_MOUSE	P01837 mus musculus
41	306.5	54.3	106	1	KACB_RABIT	P01839 oryctolagus
42	292	51.8	189	2	Q569I7 HUMAN	Q569I7 homo sapien
43	259.5	46.0	116	2	Q6LEJ1_RABIT	Q6LEJ1 oryctolagus
44	259.5	46.0	116	2	Q6LEJ2_RABIT	Q6LEJ2 oryctolagus
45	257.5	45.7	103	1	KAC4_RABIT	P01840 oryctolagus

ALIGNMENTS

RESULT 1  
Q6P5R5 HUMAN  
ID Q6P5R5 HUMAN PRELIMINARY; PRT; 120 AA.  
AC Q6P5R5;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Glandular pool- thyroid;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;  
 RG NIH MGC Project;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 DR EMBL; BC062732; AAC62732.1; -, mRNA.  
 DR HSSP; P01837; 1KCQ.  
 DR SMR; Q6PSR5; 3-120.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF07654; CI-set; 1.  
 DR SMART; SM00407; IGcl; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Immune response; Immunoglobulin domain; MHC I.  
 SQ SEQUENCE 120 AA; 13153 MW; B42FA2928C5CF1F CRC64;

Alignment Scores:  
 Pred. No.: 1.24e-48 Length: 120  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PSR5\_HUMAN (1-120)

QY 1 CGTAGGGTGGTGGACCATCTGCTTCATCTCCCGCATCTGATGACAGTTGAAATCT 60  
 Db 14 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 33  
 QY 61 GGAATCGCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db 34 GlyThrAlaSerValValCysLeuLeuAenAnPheTyrProArgGluAlaLysValGln 53  
 QY 121 TGGAGGTGGATAACGCCCTCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGAC 180  
 Db 54 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 73  
 QY 181 AGCAGGACACACCTACAGCTCAGCAGCCCTGACCCCTGACGACAGCAGCTACAGAG 240  
 Db 74 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 93  
 QY 241 AAACACAAAGTCTACGCTCGGAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
 Db 94 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 113  
 QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 114 SerPheAsnArgGlyGluCys 120

# RESULT 2

QSEPF6\_HUMAN  
 ID QSEPF6\_HUMAN PRELIMINARY; PRT; 234 AA.  
 AC QSEPF6;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Anti-Rhd monoclonal T125 kappa light chain precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Gaucher C., Klein P., Boliard R.;  
 RT "Sequence determination of the recombinant human anti-Rhd monoclonal  
 antibody T125.";  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY894991; AA882027.1; -, mRNA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; CI-set; 1.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Signal.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light  
 SQ SEQUENCE 234 AA; 25698 MW; 866DCD1B4FD7D5EA CRC64;

## Alignment Scores:

Pred. No.: 1.35e-48 Length: 234  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x QSEPF6\_HUMAN (1-234)

QY 1 CGTAGGGTGGTGGACCATCTGCTTCATCTCCCGCATCTGATGACAGTTGAAATCT 60  
 Db 128 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 147  
 QY 61 GGAATCGCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db 148 GlyThrAlaSerValValCysLeuLeuAenAnPheTyrProArgGluAlaLysValGln 167  
 QY 121 TGGAGGTGGATAACGCCCTCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGAC 180  
 Db 168 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 187  
 QY 181 AGCAGGACACACCTACAGCTCAGCAGCCCTGACCCCTGACGACAGCAGCTACAGAG 240  
 Db 188 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 207  
 QY 241 AAACACAAAGTCTACGCTCGGAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
 Db 208 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 227  
 QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 228 SerPheAsnArgGlyGluCys 234

## RESULT 3

Q7Z473\_HUMAN  
 ID Q7Z473\_HUMAN PRELIMINARY; PRT; 234 AA.  
 AC Q7Z473;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA	Altschul S.F., Zeeberg B., Bueto K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E., Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,00 full-length human and mouse cDNA sequences.";
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]
RN	
RP	NUCLEOTIDE SEQUENCE.
RR	NIH MGC Project;
RC	TISSUE=Lung;
RG	Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RL	EMBL; BC056256; AAHS6256.1; -; mRNA.
DR	HSSP; P01834; lHEZ.
DR	SMR; Q7Z473; 22-234.
DR	Ensembl; ENSG0000163245; Homo sapiens.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003597; IG-cl.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF07654; CI-set; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	immunoglobulin domain.
SQ	SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
Alignment Scores:	
Pred. No.:	1.35e-48 Length: 234
Score:	553.00 Matches: 107
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	98.05% Indels: 0
DB:	2 Gaps: 0
US-10-733-563-113 (1-321) x Q7Z473_HUMAN (1-234)	
Qy	1 CGTACGGTGCGTCACCATCTGTCTTCATTCTCCGCCCATCTGATGAGCAGTTGAATCT 60
Dd	128 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluInLeuIysSer 147
Qy	61 GGAACTGCCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Dd	148 GlyThrAlaSerValValCysLeuLeuAsnAnPheTyProArgGluAlaLysValGln 167
Qy	121 TGGAAAGTGGATAGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180
Dd	168 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 187
Qy	181 AGCAAGAGACACACTCACAGCCTCAGCAGCAGCCCTGAGCCCTGAGCAAGACGACTACGAG 240
Dd	188 SerLysAspSerThryrSerLysSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 207
Qy	241 AAACACAAGGTCTACGCTCGGAAGTCAACCCATCAGGCGCTGAGCTCGCCCGTCAAGAAG 300
Dd	208 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 227
Qy	301 AGCTTCAACAGGGAGAGTGT 321
Dd	228 SerPheAsnArgGlyGluCys 234

## RESULT 4

61 GGAAGCTGCGCTGTGTCGGCAGCAATAACCTTCTATCCAGAGAGGCCAAAGTACAG 120

```

Db 149 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 168
Qy 121 TGGAGGTGGATAACGCCCTCAATCGGTAACTCCAGGAGAGTGTCCACAGACAGAC 180
Db 169 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 188
Qy 181 AGCAGGACACACCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGACGACTACGAG 240
Db 189 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 208
Qy 241 AAACACAAAGTCTACGCTCGGAGCTCACCATCAGGCGCTGAGCTCCCGCTCACAAG 300
Db 209 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 228
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 229 SerPheAenArgGlyGluCys 235

RESULT 5
Q6GMW0_HUMAN
ID Q6GMW0_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RC Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -; mRNA.
DR SMR; Q6GMW0; 21-233.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPRO003599; Ig.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03597; Ig_c1.
DR InterPro; IPRO03596; Ig_MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.

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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Alignment Scores:
Pred. No.: 1.36e-48 Length: 235
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6GMW0_HUMAN (1-235)

Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCACTTCCCGCATCTGATGAGCAGTGAATCT 60
Db 129 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 148
Qy 61 GGAATCGCTCTGTGTGCTGCTGTAATACTTCTATCCAGAGAGGCCCAAGTACAG 120
Db 149 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 168
Qy 121 TGGAGGTGGATAACGCCCTCAATCGGTAACTCCAGGAGAGTGTCCACAGACAGAC 180
Db 169 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 188
Qy 181 AGCAGGACACACCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGACGACTACGAG 240
Db 189 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 208
Qy 241 AAACACAAAGTCTACGCTCGGAGCTCACCATCAGGCGCTGAGCTCCCGCTCACAAG 300
Db 209 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 228
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 229 SerPheAenArgGlyGluCys 235

RESULT 6
Q6PJF2_HUMAN
ID Q6PJF2_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

```



Db 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCACAGGGAGAGTGT 321

Db 230 SerPheAsnArgGlyGluCys 236

RESULT 8

Q6P5S8\_HUMAN

ID Q6P5S8\_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6P5S8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RA Strausberg R.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC062704; AAH62704.1; -; mRNA.

DR HSSP; P01837; 1KCU.

DR SMR; Q6P5S8; 21-236.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig c1.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig v.

DR Pfam; PF07654; CI-sec; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.

SW SEQUENCE 236 AA; 25773 MW; 953E37BB84FF5F27 CRC64;

Alignment Scores:

Pred. No.:	1,36e-48	Length:	236
Score:	553.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.05%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-113 (1-321) x Q6P5S8\_HUMAN (1-236)

QY 1 CGTAGCGTGGCTGCACCATCTGTCTTCATCTTCCCGCATCTGTAGAGCAGTTGAAATCT 60

Db 130 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 149

QY 61 GGAACTCCCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120

Db 150 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyProArgGluAlaLysValGln 169

QY 121 TGGAGGTGATGAACCGCCTCCAATCGGTAACCTCCAGAGAGAGTGTCCACAGCAGGAC 180

Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189

QY 181 AGCAAGGACAGCACCTACAGCTCAGCAGCACCTCGACCCCTGAGCAAGAGCAGATACAG 240

Db 190 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 209

QY 241 AACACAAAGTCTACGGCTGCGAAGTCACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300

Db 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCACAGGGAGAGTGT 321

Db 230 SerPheAsnArgGlyGluCys 236

RESULT 9

Q6PIH4\_HUMAN

ID Q6PIH4\_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIH4;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., Sodergren E.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC034146; AAH34146.1; -; mRNA.

DR HSSP; P01607; 1AR2.

DR SMR; Q6PIH4; 23-236.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.



DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06EBE26 CRC64;

Alignment Scores:  
 Pred. No.: 1.36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PIH4\_HUMAN (1-236)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
 Db 130 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 149

QY 61 GGAAGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 120  
 Db 150 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 169

QY 121 TGGAAAGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 180  
 Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 189

QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGAGCAGCAGCAGGAGTGTCCAGAGCAGGAC 180  
 Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 189

QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGAGCAGCAGCAGGAGTGTCCAGAGCAGGAC 240  
 Db 190 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 209

QY 241 AAACACAAAGTCTAGCGCTGCGAGTCAAGTCAAGCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
 Db 210 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 230 SerPheAsnArgGlyGluCys 236

RESULT 10  
 Q6PIL8 HUMAN  
 ID Q6PIL8\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIL8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pearce C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC032451; AAH32451.1; -; mRNA.  
 DR HSSP; P01837; 1KCU.  
 DR SMR; Q6PIL8; 21-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Alignment Scores:  
 Pred. No.: 1.36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PIL8\_HUMAN (1-236)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
 Db 130 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 149

QY 61 GGAAGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 120  
 Db 150 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 169

QY 121 TGGAAAGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 180  
 Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 189

QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGAGCAGCAGCAGGAGTGTCCAGAGCAGGAC 240  
 Db 190 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 209

QY 241 AAACACAAAGTCTAGCGCTGCGAGTCAAGTCAAGCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
 Db 210 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 230 SerPheAsnArgGlyGluCys 236

RESULT 11  
 Q6PIT5 HUMAN  
 ID Q6PIT5\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIT5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., McKernan K.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., Peters G.J., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC029444; AAH29444.1; -; mRNA.  
 DR HSSP; P01607; 1AB2.  
 DR SMR; Q6P175; 26-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; CI-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25741 MW; B050AF071FEE351 CRC64;

Alignment Scores:  
 Pred. No.: 1.36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps:

US-10-733-563-113 (1-321) x Q6PIT5\_HUMAN (1-236)

Qy 1 CGTACGGTGGTGCACCATCTGCTTCATCTTCCGCCCATCTGATGACAGTGAATCT 60  
 |||||  
 Db 130 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 149  
 |||||  
 Qy 61 GGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120  
 |||||  
 Db 150 GlyThrAlaSerValValAlaCysLeuLeuAsnAsnPheYrProArgGluAlaLysValGln 169  
 |||||  
 Qy 121 TGAAGGTGGTAAAGCCCTCCAAATCGGTGTAATCTCCAGGAGAGTGTCCACAGAGCAGGAC 180  
 |||||  
 Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189  
 |||||

Qy 181 AGCAAGGACAGCACCTACAGCCTCAGCAGACACCTGACCCCTGAGCAAGACAGACTACGAG 240  
 |||||  
 Db 190 SerLysAspSerThrTySerLysSerThrLeuThrLeuSerLysAlaAspTyRglu 209  
 |||||  
 Qy 241 AACACAAAGTCTACGGCTGCGAAGTCACCCATCAGGGCCCTGAGCTCGCCCGTCAACAAG 300  
 |||||  
 Db 210 LysHisLysValTyRAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229  
 |||||  
 Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
 |||||  
 Db 230 SerPheAsnArgGlyGluCys 236  
 |||||  
 RESULT 12  
 Q723Y4 HUMAN  
 ID Q723Y4 HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q723Y4;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal Muscle;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal Muscle;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005332; AAH05332.1; -; mRNA.  
 DR HSSP; P01834; 1HEZ.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; CI-set; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein; Immunoglobulin domain.  
 SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Alignment Scores:  
 Pred. No.: 1.36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps:

US-10-733-563-113 (1-321) x Q723V4\_HUMAN (1-236)

QY 1 CGTAGCGTGGCTGCACCATCTCTTCATCTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
 |||||  
 Db 130 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 149  
 |||||  
 QY 61 GGAACCTGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 |||||  
 Db 150 GlyThrAlaSerValValCysLeuLeuAenPheTyProArgGluAlaLysValGln 169  
 |||||  
 QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
 |||||  
 Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 189  
 |||||  
 QY 181 AGCAGGAGCAGCACTACAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGAGCAGACTACGAG 240  
 |||||  
 Db 190 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 209  
 |||||  
 QY 241 AAACACAAAGTCTAGCGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
 |||||  
 Db 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerProValThrLys 229  
 |||||  
 QY 301 AGCTTCAACAGGGGAGAGTGT 321  
 |||||  
 Db 230 SerPheAenArgGlyGluCys 236

## RESULT 13

Q6PIH7\_HUMAN  
 ID Q6PIH7\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIH7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)."  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Lung;  
 RC NIH MGC Project;  
 RG Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC034141; AAH34141.1; -; mRNA.  
 DR HSP; P01607; IAR2.  
 DR SMR; Q6PIH7; 23-236.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig.MHC.  
 DR InterPro; IPR003596; Ig.V.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN 1.  
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213P CRC64;

## Alignment Scores:

Pred. No.: 1.36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PIH7\_HUMAN (1-236)

QY 1 CGTAGCGTGGCTGCACCATCTCTTCATCTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
 |||||  
 Db 130 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 149  
 |||||  
 QY 61 GGAACCTGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 |||||  
 Db 150 GlyThrAlaSerValValCysLeuLeuAenPheTyProArgGluAlaLysValGln 169  
 |||||  
 QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
 |||||  
 Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 189  
 |||||  
 QY 181 AGCAGGAGCAGCACTACAGCAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGAGCAGACTACGAG 240  
 |||||  
 Db 190 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 209  
 |||||  
 QY 241 AAACACAAAGTCTAGCGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
 |||||  
 Db 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerProValThrLys 229  
 |||||  
 QY 301 AGCTTCAACAGGGGAGAGTGT 321  
 |||||  
 Db 230 SerPheAenArgGlyGluCys 236

## RESULT 14

Q6GKX9\_HUMAN  
 ID Q6GKX9\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6GKX9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Primary B-Cells;  
RC NIH MGC Project;  
RG Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073763; AAH73763.1; -; mRNA.  
DR SMR; Q6GMX9; 23-236.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25924 MW; FD2E093DC560CF7 CRC64;

Alignment Scores:  
Pred. No.: 1.36e-48 Length: 236  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6GMX9\_HUMAN (1-236)

Qy 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTCCGCCCATCTGATGACGAGTGAATCT 60  
|||||  
Db 130 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluInLeuLysSer 149  
|||||

Qy 61 GGAACTGCCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
|||||  
Db 150 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyProArgGluAlaLysValGln 169  
|||||

Qy 121 TGGAAAGTGGATACGCCCTCAATCGGGTAACCTCCAGGAGAGTGTCCAGAGCAGAC 180  
|||||  
Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189  
|||||

Qy 181 AGCAAGGACACACCTACAGCCTCAGCAGCAGCCCTGACCTGAGCAAGACAGATCAGAG 240  
|||||  
Db 190 SerLysAspSerThrTySerLysSerSerThrLysLeuSerLysAlaAspTyrGlu 209  
|||||

Qy 241 AAACACAAAGTCTAGCCTCGGAAGTCAACCCATCAGGCGCTGAGCTCCCGCTCACAAAG 300  
|||||  
Db 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229  
|||||

Qy 301 AGCTTCAACAGGGAGAGTGT 321  
|||||

Db 230 SerPheAsnArgGlyGluCys 236  
|||||

RESULT 15  
Q6GMX8\_HUMAN

ID AC Q6GMX8\_HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6GMX8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Primary B-Cells;  
RC NIH MGC Project;  
RG Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073764; AAH73764.1; -; mRNA.  
DR SMR; Q6GMX8; 24-235.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Alignment Scores:  
Pred. No.: 1.36e-48 Length: 236  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6GMX8\_HUMAN (1-236)

Qy 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTCCGCCCATCTGATGACGAGTGAATCT 60  
|||||  
Db 130 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluInLeuLysSer 149  
|||||

Qy 61 GGAACTGCCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
|||||

Db 150 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 169  
QY 121 TCGAAGGTGGATAACGCCCTCCAAATCGGTAACCTCCAGGAGAGTGTCAACAGAGCAGGAC 180  
Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189  
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACCCCTGAGCMAAGCAGACTACGAG 240  
Db 190 SerLysAspSerThrTyrSerSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 209  
QY 241 AAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
Db 210 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 230 SerPheAsnArgGlyGluCys 236

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Job time : 51.2425 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:22:17 ; Search time 12.6922 Seconds  
(without alignments)  
4181.924 Million cell updates/sec

Title: US-10-733-563-113

Perfect score: 564

Sequence: 1 cgtacggtggtgcaccatc.....gottcaacagggagagtgt 321

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO spool\_p/US10733563/runat\_27012006\_180006\_4815/app\_query.fasta\_1.2716  
-DB=Issued Patents\_AA -QFMT=fastcan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi  
-LIST=45 -DALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563@cgn 1 1.141@runat\_27012006\_180006\_4815 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pcp:\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pcp:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pcp:\*  
4: /cgn2\_6/ptodata/1/iaa/FCTUS COMB.pcp:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pcp:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	98.0	107	1	US-08-422-101-8
2	553	98.0	107	1	US-08-422-091-8
3	553	98.0	107	1	US-08-422-092-8
4	553	98.0	107	1	US-08-788-800-5
5	553	98.0	107	2	US-08-422-093-8
6	553	98.0	107	2	US-08-422-112-8
7	553	98.0	107	2	US-09-301-593-20
8	553	98.0	212	2	US-10-011-125A-5
9	553	98.0	213	2	US-08-630-820-6
10	553	98.0	213	2	US-08-397-411-12
11	553	98.0	213	2	US-09-273-453-6
12	553	98.0	213	2	US-09-996-288-209

13	553	98.0	213	2	US-09-996-288-211	Sequence 211, App
14	553	98.0	213	2	US-09-996-288-213	Sequence 213, App
15	553	98.0	213	2	US-09-996-288-215	Sequence 215, App
16	553	98.0	213	2	US-09-996-288-217	Sequence 217, App
17	553	98.0	213	2	US-09-996-288-219	Sequence 219, App
18	553	98.0	213	2	US-09-996-288-221	Sequence 221, App
19	553	98.0	213	2	US-09-996-288-223	Sequence 223, App
20	553	98.0	213	2	US-09-996-288-225	Sequence 225, App
21	553	98.0	213	2	US-09-996-288-227	Sequence 227, App
22	553	98.0	213	2	US-09-996-288-229	Sequence 229, App
23	553	98.0	213	2	US-09-996-288-231	Sequence 231, App
24	553	98.0	213	2	US-09-996-288-233	Sequence 233, App
25	553	98.0	213	2	US-09-996-288-235	Sequence 235, App
26	553	98.0	213	2	US-09-996-288-237	Sequence 237, App
27	553	98.0	213	2	US-09-996-288-239	Sequence 239, App
28	553	98.0	213	2	US-09-996-288-241	Sequence 241, App
29	553	98.0	213	2	US-09-996-288-243	Sequence 243, App
30	553	98.0	213	2	US-09-996-288-245	Sequence 245, App
31	553	98.0	213	2	US-09-996-288-247	Sequence 247, App
32	553	98.0	213	2	US-09-996-288-251	Sequence 251, App
33	553	98.0	213	2	US-09-996-288-253	Sequence 253, App
34	553	98.0	213	2	US-09-996-288-255	Sequence 255, App
35	553	98.0	213	2	US-09-996-288-257	Sequence 257, App
36	553	98.0	213	2	US-09-996-265-209	Sequence 209, App
37	553	98.0	213	2	US-09-996-265-211	Sequence 211, App
38	553	98.0	213	2	US-09-996-265-213	Sequence 213, App
39	553	98.0	213	2	US-09-996-265-215	Sequence 215, App
40	553	98.0	213	2	US-09-996-265-217	Sequence 217, App
41	553	98.0	213	2	US-09-996-265-219	Sequence 219, App
42	553	98.0	213	2	US-09-996-265-221	Sequence 221, App
43	553	98.0	213	2	US-09-996-265-223	Sequence 223, App
44	553	98.0	213	2	US-09-996-265-225	Sequence 225, App
45	553	98.0	213	2	US-09-996-265-227	Sequence 227, App

ALIGNMENTS

RESULT 1  
US-08-422-101-8  
; Sequence 8, Application US/08422101  
; Patent No. 5739277  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedcor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,101  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881

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; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-101-8

Alignment Scores:
Pred. No.: 2.07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-422-101-8 (1-107)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGACGAGTTGAAATCT 60
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATGCTCTGTGTGCTGCTGCTGAATACTTATCCAGAGAGGCCAAAGTACAG 120
DB 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATACGGCTCCATCGGTAACTCCAGAGAGAGTGTACAGAGCAGAC 180
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTCCATCGGTAACTCCAGAGAGTGTACAGAGCAGAC 240
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAG 300
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGGTGT 321
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 2
; Sequence 8, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,091
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
```

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;
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-091-8

Alignment Scores:
Pred. No.: 2.07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-422-091-8 (1-107)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGACGAGTTGAAATCT 60
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATGCTCTGTGTGCTGCTGCTGAATACTTATCCAGAGAGGCCAAAGTACAG 120
DB 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATACGGCTCCATCGGTAACTCCAGAGAGTGTACAGAGCAGAC 180
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTCCATCGGTAACTCCAGAGAGTGTACAGAGCAGAC 240
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAG 300
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGGTGT 321
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 3
US-08-422-092-8
; Sequence 8, Application US/08422092
; Patent No. 5869046
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,092
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08-788,800
; FILING DATE: 22-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 932-4
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/952-9881
; TELEFAX: 415/952-9881
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEFAX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-092-8

Alignment Scores:
Pred. No.: 2,07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-422-092-8 (1-107)
QY 1 CGTACGGTGGTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20
QY 61 GGAATCGCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGTAATACGCCCTCCAATCGGTAACTCCAGAGAGAGTGTACAGAGCAGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAGGAGCAGCACCCTACAGCCTCAGCAGCAGCCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 4
US-08-788-800-5
; Sequence 5, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEFAX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-5

Alignment Scores:
Pred. No.: 2,07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-788-800-5 (1-107)
QY 1 CGTACGGTGGTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20
QY 61 GGAATCGCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGTAATACGCCCTCCAATCGGTAACTCCAGAGAGAGTGTACAGAGCAGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAGGAGCAGCACCCTACAGCCTCAGCAGCAGCCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 5
US-08-422-093-8
; Sequence 8, Application US/08422093
; Patent No. 6096871
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.093
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-093-8

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Alignment Scores:
Pred. No.: 2,07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

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US-10-733-563-113 (1-321) x US-08-422-093-8 (1-107)

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Qy 1 CGTACGGTGGTGCACCATCTGTCTTCATCTTCCGGCCATCTGATGACGAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTACAGAGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTACAGAGCCAAAGTACAG 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGACAGACACCTCAGCCTCAGCAGCACCCCTGACCCCTGAGCAAGACAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGGCCCTGAGCTCGCCCGTCACAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107

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RESULT 6

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; US-08-422-112-8
; Sequence 8, Application US/08422112
; Patent No. 6121022
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco

```

```

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.112
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-112-8

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Alignment Scores:
Pred. No.: 2,07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

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US-10-733-563-113 (1-321) x US-08-422-112-8 (1-107)

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Qy 1 CGTACGGTGGTGCACCATCTGTCTTCATCTTCCGGCCATCTGATGACGAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTACAGAGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTACAGAGCCAAAGTACAG 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGACAGACACCTCAGCCTCAGCAGCACCCCTGACCCCTGAGCAAGACAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGGCCCTGAGCTCGCCCGTCACAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107

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RESULT 7

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; US-09-301-593-20
; Sequence 20, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier

```

APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.1890001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-301-593-20

Alignment Scores:  
Pred. No.: 2,076-59 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-301-593-20 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTTCCGCCCATCTGATGACAGTGTGAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGAATACTTCTATCCAGAGAGGCGCAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGAGCAGTACAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 8  
US-10-011-125A-5  
Sequence 5, Application US/10011125A  
Patent No. 6828121  
GENERAL INFORMATION:  
APPLICANT: Chen, Christina Yu-Ching  
TITLE OF INVENTION: BACTERIAL HOST STRAINS  
FILE REFERENCE: P1804R1  
CURRENT APPLICATION NUMBER: US/10/011,125A  
CURRENT FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: US 60/256,162  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 5  
LENGTH: 212  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequence is synthesized.  
Patent No. 6828121  
US-10-011-125A-5

APPLICANT: Oppen, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

Alignment Scores:  
Pred. No.: 2,626-59 Length: 212  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-10-011-125A-5 (1-212)

QY 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTTCCGCCCATCTGATGACAGTGTGAATCT 60  
DB 106 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 125  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGAATACTTCTATCCAGAGAGGCGCAAGTACAG 120  
DB 126 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 145  
QY 121 TGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180  
DB 146 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 165  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGAGCAGTACAG 240  
DB 166 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 185  
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
DB 186 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 205  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
DB 206 SerPheAsnArgGlyGluCys 212

RESULT 9  
US-08-630-820-6  
Sequence 6, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: Oppen, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-820-6

Alignment Scores:
Pred. NO.: 2.63e-59 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-08-630-820-6 (1-213)
Qy 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACGAGTTCGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPhePheProProSerAspGluGlnLeuLysSer 126
Qy 61 GGAACCTGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 146
Qy 121 TGGAGGTGGATACGCCCTCCAAATCGGGTAACCTCCAGAGAGGTTCACAGAGCAGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
Qy 181 AGCAAGGACACACCTCAGCCTCAGCAGCAGCCCTGACCCCTGACCAAGAGCAGTACGAG 240
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
Qy 241 AAACACAAAGTCTACGGCTGCGAAGTCAACCATCAGGCGCTGAGTCCGCCGTCACAAAG 300
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
Qy 301 AGCTTCAACAGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213

RESULT 10
US-08-397-411-12
; Sequence 12, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Smich, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-12

Alignment Scores:
Pred. NO.: 2.63e-59 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-08-397-411-12 (1-213)
Qy 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACGAGTTCGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPhePheProProSerAspGluGlnLeuLysSer 126
Qy 61 GGAACCTGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 146
Qy 121 TGGAGGTGGATACGCCCTCCAAATCGGGTAACCTCCAGAGAGGTTCACAGAGCAGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
Qy 181 AGCAAGGACACACCTCAGCCTCAGCAGCAGCCCTGACCCCTGACCAAGAGCAGTACGAG 240
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
Qy 241 AAACACAAAGTCTACGGCTGCGAAGTCAACCATCAGGCGCTGAGTCCGCCGTCACAAAG 300
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
Qy 301 AGCTTCAACAGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213

RESULT 11
US-09-273-453-6
; Sequence 6, Application US/09273453
; Patent No. 6602688
; GENERAL INFORMATION:
; APPLICANT: Oppen, Martin
; APPLICANT: Bosslet, Klaus
; APPLICANT: CZECH, Joerg
; TITLE OF INVENTION: CYTOLASMIC EXPRESSION OF ANTIBODIES,
; ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
; IN E. COLI
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/273,453  
FILING DATE: 22-Mar-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,820  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-273-453-6

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-273-453-6 (1-213)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACAGTTGAAATCT 60  
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaIysValGln 146  
QY 121 TGGAAAGTGGATAACGCCCTCAATCGGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAAGGACAGCACTACAGCTCAGCAGCACCTGACCCCTGAGCAAGAGCAGACTACAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 207 SerPheAsnArgGlyGluCys 213

RESULT 12  
US-09-996-288-209  
Sequence 209, Application US/09996288  
Patent No. 6818216  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 209  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-996-288-209  
Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-996-288-209 (1-213)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACAGTTGAAATCT 60  
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaIysValGln 146  
QY 121 TGGAAAGTGGATAACGCCCTCAATCGGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAAGGACAGCACTACAGCTCAGCAGCACCTGACCCCTGAGCAAGAGCAGACTACAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 207 SerPheAsnArgGlyGluCys 213

RESULT 13

US-09-996-288-211  
Sequence 211, Application US/09996288  
Patent No. 6818216  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 211  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-996-288-211

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-996-288-211 (1-213)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACAGTTGAAATCT 60  
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Db 107 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 126  
QY 61 GGAAGTGGTAAACGCTCCATCGGTAACCTCCAGGAGAGTGTACAGAGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146  
QY 121 TGGAGGTGGTAAACGCTCCATCGGTAACCTCCAGGAGAGTGTACAGAGCCAAAGTACAG 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAAAGCAGACTACAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTAGCTGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

## RESULT 14

US-09-996-288-213  
; Sequence 213, Application US/09996288  
; Patent No. 6818216

; GENERAL INFORMATION:  
; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 213

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-213

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-996-288-213 (1-213)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGTATGAGCAGTTGAAATCT 60  
Db 107 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 126  
QY 61 GGAAGTGGTAAACGCTCCATCGGTAACCTCCAGGAGAGTGTACAGAGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146  
QY 121 TGGAGGTGGTAAACGCTCCATCGGTAACCTCCAGGAGAGTGTACAGAGCCAAAGTACAG 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAAAGCAGACTACAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTAGCTGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206

QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

## RESULT 15

US-09-996-288-215  
; Sequence 215, Application US/09996288  
; Patent No. 6818216

; GENERAL INFORMATION:  
; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 215

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-215

Alignment Scores:

Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-996-288-215 (1-213)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGTATGAGCAGTTGAAATCT 60  
Db 107 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 126  
QY 61 GGAAGTGGTAAACGCTCCATCGGTAACCTCCAGGAGAGTGTACAGAGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146  
QY 121 TGGAGGTGGTAAACGCTCCATCGGTAACCTCCAGGAGAGTGTACAGAGCCAAAGTACAG 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAAAGCAGACTACAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTAGCTGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

Search completed: January 28, 2006, 08:48:59

Job time : 13.6922 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:44:22 ; Search time 39.2012 Seconds  
(without alignments)  
6842.811 Million cell updates/sec

Title: US-10-733-563-113

Perfect score: 564

Sequence: 1 cgtacggtggtgcaccatc.....gcttcaacagggagagtgt 321

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published\_Applications\_AA\_Main -QFWT=fastan -SUFFIX=n2p.rapbm  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct  
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext  
-HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 -CGEN 1 1 497 @runat\_27012006.180007.4900 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	98.0	107	3	US-09-301-593-20
2	553	98.0	107	3	US-09-811-384-5
3	553	98.0	107	3	US-09-990-586-97
4	553	98.0	107	3	US-09-990-586-99
5	553	98.0	107	4	US-10-121-464-18
6	553	98.0	107	4	US-10-269-805-67
7	553	98.0	107	4	US-10-159-006-20
8	553	98.0	107	4	US-10-310-113-166
9	553	98.0	107	4	US-10-310-113-168
10	553	98.0	107	4	US-10-230-880-97
11	553	98.0	107	4	US-10-230-880-99

12	553	98.0	107	4	US-10-366-709-54	Sequence 54, Appl
13	553	98.0	107	4	US-10-404-286-5	Sequence 5, Appl
14	553	98.0	107	4	US-10-656-769-4	Sequence 4, Appl
15	553	98.0	107	4	US-10-679-620-60	Sequence 60, Appl
16	553	98.0	107	4	US-10-733-563-112	Sequence 112, Appl
17	553	98.0	107	5	US-10-815-449-10	Sequence 10, Appl
18	553	98.0	107	5	US-10-884-957-4	Sequence 4, Appl
19	553	98.0	107	5	US-10-886-838-8	Sequence 8, Appl
20	553	98.0	107	5	US-10-822-300-9	Sequence 9, Appl
21	553	98.0	107	5	US-10-687-118-9	Sequence 9, Appl
22	553	98.0	107	5	US-10-872-932A-41	Sequence 41, Appl
23	553	98.0	107	5	US-10-891-658-8	Sequence 8, Appl
24	553	98.0	107	5	US-10-937-596-29	Sequence 29, Appl
25	553	98.0	107	5	US-10-893-576-44	Sequence 44, Appl
26	553	98.0	107	5	US-10-810-881A-40	Sequence 40, Appl
27	553	98.0	107	5	US-10-981-936-40	Sequence 40, Appl
28	553	98.0	107	6	US-11-001-980-4	Sequence 4, Appl
29	553	98.0	107	6	US-11-001-980-8	Sequence 8, Appl
30	553	98.0	107	6	US-11-132-143-60	Sequence 60, Appl
31	553	98.0	107	6	US-11-102-403-23	Sequence 23, Appl
32	553	98.0	109	4	US-10-272-899A-12	Sequence 12, Appl
33	553	98.0	109	4	US-10-733-563-116	Sequence 116, Appl
34	553	98.0	134	4	US-10-272-899A-66	Sequence 66, Appl
35	553	98.0	212	4	US-10-011-125-5	Sequence 5, Appl
36	553	98.0	212	4	US-10-320-231A-77	Sequence 77, Appl
37	553	98.0	212	5	US-10-867-506-77	Sequence 77, Appl
38	553	98.0	213	3	US-09-796-848A-38	Sequence 38, Appl
39	553	98.0	213	3	US-09-796-848A-40	Sequence 40, Appl
40	553	98.0	213	3	US-09-796-848A-42	Sequence 42, Appl
41	553	98.0	213	3	US-09-796-848A-44	Sequence 44, Appl
42	553	98.0	213	3	US-09-796-848A-46	Sequence 46, Appl
43	553	98.0	213	3	US-09-796-848A-48	Sequence 48, Appl
44	553	98.0	213	3	US-09-796-848A-50	Sequence 50, Appl
45	553	98.0	213	3	US-09-796-848A-52	Sequence 52, Appl

#### ALIGNMENTS

RESULT 1

US-09-301-593-20  
; Sequence 20, Application US/09301593A  
; Publication No. US20020052480A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John B.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Legier, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301.593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-20

Alignment Scores:  
Pred. No.: 5.01e-51  
Score: 553.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 98.05%  
DB: 3  
Length: 107  
Matches: 107  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-10-733-563-113 (1-321) x US-09-301-593-20 (1-107)

QY 1 CGTACGGTGGTGCACCATCTGTCTTCAATCTTCCCGCCATCTGATGACAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCTCTGTGTGTGCTGCTGAATACTTCTATCCAGAGAGCCCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCCAATCGGTAACTCCAGGAGAGTGTACACAGCAGGAC 180  
Db 41 TrpLysValAlaAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCACCTTGACCTGAGCAAGAGCAGACTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTAGCGCTGCGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAenArgGlyGluCys 107

## RESULT 2

US-09-811-384-5  
; Sequence 5, Application US/09811384  
; Patent No. US20020081294A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/811,384  
; FILING DATE: 20-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/251652  
; FILING DATE: 17-FEB-2000  
; APPLICATION NUMBER: 08/788800  
; FILING DATE: 22-JAN-1997  
; APPLICATION NUMBER: 60/093038  
; FILING DATE: 23-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1729C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

## Alignment Scores:

Pred. No.: 5.01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-113 (1-321) x US-09-811-384-5 (1-107)

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QY 61 GGAACCTGCTCTGTGTGTGCTGCTGAATACTTCTATCCAGAGAGCCCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCCAATCGGTAACTCCAGGAGAGTGTACACAGCAGGAC 180  
Db 41 TrpLysValAlaAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCACCTTGACCTGAGCAAGAGCAGACTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTAGCGCTGCGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAenArgGlyGluCys 107

## RESULT 3

US-09-990-586-97  
; Sequence 97, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 97  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-97

## Alignment Scores:

Pred. No.: 5.01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-113 (1-321) x US-09-990-586-97 (1-107)

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Db 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCCAATCGGTAACTCCAGGAGAGTGTACACAGCAGGAC 180  
Db 41 TrpLysValAlaAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCACCTTGACCTGAGCAAGAGCAGACTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTAGCGCTGCGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAenArgGlyGluCys 107



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Db      21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY      121 TGAAGGTGGATAACGCCCTCCAACTCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db      41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY      181 AGCAAGGACAGACCTACAGCCTCAGCAGCACCCTGACCCCTGAGCAAGAGCAGACTACGAG 240
Db      61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY      241 AAACACAAAGTCTACGCCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCTCAACAAG 300
Db      81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY      301 AGCTTCAACAGGGAGAGTGT 321
Db      101 SerPheAsnArgGlyGluCys 107

RESULT 4
US-09-990-586-99
; Sequence 99, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-99

Alignment Scores:
Pred. No.:      5,018-51      Length:      107
Score:          553.00      Matches:    107
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    98.05%      Indels:     0
DB:             3          Gaps:         0

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QY      1 CGTACGGTGGCTGCACCATCTGCTTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCT 60
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QY      61 GGAATCGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGCCCAAACTACAG 120
Db      21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY      121 TGAAGGTGGATAACGCCCTCCAACTCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db      41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY      181 AGCAAGGACAGACCTACAGCCTCAGCAGCACCCTGACCCCTGAGCAAGAGCAGACTACGAG 240
Db      61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY      241 AAACACAAAGTCTACGCCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCTCAACAAG 300
Db      81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY      301 AGCTTCAACAGGGAGAGTGT 321
Db      101 SerPheAsnArgGlyGluCys 107

RESULT 5
US-10-121-464-18
; Sequence 18, Application US/10121464
; Publication No. US20030103968A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer treatment by using FAP-alpha specific antibodies
; FILE REFERENCE: 1-1203ff
; CURRENT APPLICATION NUMBER: US/10/121,464
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/283,868
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antibody
; OTHER INFORMATION: sequence
US-10-121-464-18

Alignment Scores:
Pred. No.:      5,018-51      Length:      107
Score:          553.00      Matches:    107
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    98.05%      Indels:     0
DB:             4          Gaps:         0

US-10-733-563-113 (1-321) x US-10-121-464-18 (1-107)
QY      1 CGTACGGTGGCTGCACCATCTGCTTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db      1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
QY      61 GGAATCGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGCCCAAACTACAG 120
Db      21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY      121 TGAAGGTGGATAACGCCCTCCAACTCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db      41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY      181 AGCAAGGACAGACCTACAGCCTCAGCAGCACCCTGACCCCTGAGCAAGAGCAGACTACGAG 240
Db      61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY      241 AAACACAAAGTCTACGCCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCTCAACAAG 300
Db      81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY      301 AGCTTCAACAGGGAGAGTGT 321
Db      101 SerPheAsnArgGlyGluCys 107

RESULT 6
US-10-269-805-67
; Sequence 67, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
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! SEQ ID NO 67  
! LENGTH: 107  
! TYPE: PRT  
! ORGANISM: Homo sapiens  
US-10-269-805-67

Alignment Scores:  
Pred. No.: 5, 01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-269-805-67 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAATCGCTCTGTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGTAACTCCAGGAGAGTGCACAGAGCAGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGAGCCCTGAGCAAGAGCAGACTTACGAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAGTCTACGCTCGAAGTCAACCCATCAGGCGCTGAGCTCGCCCTCACAAG 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

## RESULT 7

US-10-159-006-20  
! Sequence 20, Application US/10159006  
! Publication No. US20030143229A1  
! GENERAL INFORMATION:  
! APPLICANT: Park, John E.  
! APPLICANT: Garin-Chesa, Pilar  
! APPLICANT: Bamberger, Uwe  
! APPLICANT: Leger, Olivier  
! APPLICANT: Saldanha, Jose W.  
! APPLICANT: Rettig, Wolfgang J.  
! TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility  
! FILE REFERENCE: 0652.1890002  
! CURRENT APPLICATION NUMBER: US/10/159,006  
! CURRENT FILING DATE: 2002-06-03  
! PRIOR APPLICATION NUMBER: US 09/301,593  
! PRIOR FILING DATE: 1999-04-29  
! PRIOR APPLICATION NUMBER: EP 98107925.4  
! PRIOR FILING DATE: 1998-04-30  
! PRIOR APPLICATION NUMBER: US 60/086,049  
! PRIOR FILING DATE: 1998-05-18  
! NUMBER OF SEQ ID NOS: 108  
! SOFTWARE: PatentIn Ver. 2.0  
! SEQ ID NO 20  
! LENGTH: 107  
! TYPE: PRT  
! ORGANISM: Homo sapiens  
US-10-159-006-20

Alignment Scores:  
Pred. No.: 5, 01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-159-006-20 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAATCGCTCTGTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGTAACTCCAGGAGAGTGCACAGAGCAGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGAGCCCTGAGCAAGAGCAGACTTACGAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAGTCTACGCTCGAAGTCAACCCATCAGGCGCTGAGCTCGCCCTCACAAG 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

## RESULT 8

US-10-310-113-166  
! Sequence 166, Application US/10310113  
! Publication No. US20030176664A1  
! GENERAL INFORMATION:  
! APPLICANT: JIAO, JIN-AN  
! APPLICANT: WONG, HING C.  
! APPLICANT: NIEVES, ESPERANZA LILIANA  
! APPLICANT: MOSQUERA, LUIS A.  
! TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING  
! FILE REFERENCE: 58122(71758)  
! CURRENT APPLICATION NUMBER: US/10/310,113  
! CURRENT FILING DATE: 2002-12-04  
! PRIOR APPLICATION NUMBER: 09/990,586  
! PRIOR FILING DATE: 2001-11-21  
! PRIOR APPLICATION NUMBER: 60/343,306  
! PRIOR FILING DATE: 2001-10-29  
! PRIOR APPLICATION NUMBER: 09/293,854  
! PRIOR FILING DATE: 1999-04-16  
! PRIOR APPLICATION NUMBER: 08/814,806  
! PRIOR FILING DATE: 1997-03-10  
! NUMBER OF SEQ ID NOS: 169  
! SOFTWARE: PatentIn Ver. 2.1  
! SEQ ID NO 166  
! LENGTH: 107  
! TYPE: PRT  
! ORGANISM: Homo sapiens  
US-10-310-113-166

Alignment Scores:  
Pred. No.: 5, 01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-310-113-166 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20

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QY 61 GGAACCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAAGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGAGAGGAC 180
Db 41 TrpLysValAlaPAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAap 60
QY 181 AGCAAGGAGCAGCACCTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAapSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAapTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenAargGlyGluCys 107
RESULT 9
US-10-310-113-168
; Sequence 168, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168
Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0
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QY 61 GGAACCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAAGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGAGAGGAC 180
Db 41 TrpLysValAlaPAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAap 60
QY 181 AGCAAGGAGCAGCACCTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAapSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAapTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAAGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGAGAGGAC 180
Db 41 TrpLysValAlaPAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAap 60
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QY 181 AGCAAGGAGCAGCACCTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAapSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAapTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenAargGlyGluCys 107
RESULT 10
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97
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Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0
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QY 61 GGAACCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAAGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGAGAGGAC 180
Db 41 TrpLysValAlaPAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAap 60
QY 181 AGCAAGGAGCAGCACCTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAapSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAapTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenAargGlyGluCys 107
RESULT 11
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US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71759/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

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Qy 61 GGAAGTGGTGTGTGCTGCTGAATTAACCTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40
Qy 121 TGAAGTGGTAAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db 41 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGCACCCTACAGCCTCAGCAGCACCCTGACCCCTGACCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 80
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGCAGCACCCTGACCAAGCAGACTACGAG 300
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 12
US-10-366-709-54
; Sequence 54, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; METHODS OF USE
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
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; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-709-54

Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

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Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAGTGGTGTGTGCTGCTGAATTAACCTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40
Qy 121 TGAAGTGGTAAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db 41 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGCACCCTACAGCCTCAGCAGCACCCTGACCCCTGACCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 80
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGCAGCACCCTGACCAAGCAGACTACGAG 300
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 13
US-10-404-286-5
; Sequence 5, Application US/10404286
; Publication No. US20040057951A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2006
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/811384
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, FILING DATE: 20-DEC-2000
, APPLICATION NUMBER: 09/251652
, FILING DATE: 17-FEB-2000
, APPLICATION NUMBER: 08/788800
, FILING DATE: 22-JAN-1997
, APPLICATION NUMBER: 60/093038
, FILING DATE: 23-JAN-1996
, ATTORNEY/AGENT INFORMATION:
, NAME: Evans, David W.
, REGISTRATION NUMBER: NONE
, REFERENCE/DOCKET NUMBER: P179C2
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 650/225-1739
, TELEFAX: 650/952-9881
, INFORMATION FOR SEQ ID NO: 5:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 107 amino acids
, TYPE: Amino Acid
, TOPOLOGY: Linear
, SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-404-286-5

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Matches:	107
Conservative:	0
Mismatches:	0
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QY	61	GGAACTCGCTCTGTTGTGTGCTGTGTAATACTTATCCACAGAGCGCCAAAGTACAG	120
Db	21	GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln	40
QY	121	TGGAGGTGGATAACGCCCTCCAACTCGGTTAACTCCACAGAGAGTGCACAGAGCAGGAC	180
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QY	181	AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTCGACCTCGACCAAGCAGACTACGAG	240
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QY	241	AAACACAAGTCTACCGCTCGGAGTACCCATCAGGGCCTGAGCTCGCCGCTCACAAG	300
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RESULT 14
US-10-656-769-4
; Sequence 4, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Allison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xuejing
; TITLE OF INVENTION: Therapeutic Hum
; FILE REFERENCE: 01,1534
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4

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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-4

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Pred. No.:	5,018-51	Length:
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Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
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QY	61	GGAACTGCTCTGTTGTGTGCTCTCTCGAATAACTTCTATCCAGAGAGGCCAAAGTACAG	120
DB	21	GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyProArgGluAlaLysValGln	40
QY	121	TGGAGTGGGATACGGCCCTCCATTCGGTTAACTCCAGGAGAGTGTACAGAGCAGGAC	180
DB	41	TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp	60
QY	181	AGCAAGGACACACCTACAGCTCAGCAGCAGCACCTCACCCTGAGCAAAAGCAGACTACGAG	240
DB	61	SerLysAspSerThrTySerSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu	80
QY	241	AAACAACAGTCTAGCGCTGGAGTCAACCATCAGGGCCTGAGCTCGCCGTCCACAAG	300
DB	81	LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys	100
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**RESULT 15**

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US-10-679-620-60
; Sequence 60, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Rejn, Stephen J
; APPLICANT: Edwards, Patricia C
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: huscFab1aI6 , see Example 15
US-10-679-620-60

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Alignment Scores:	
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Score:	553.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	98.05%
DB:	4
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	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
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US-10-733-563-113 (1-321) x US-10-679-620-60 (1-107)

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1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAC TGCTCTGTGTGTGCTGTCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCCAAGGAGGTGTACAGAGCAGGAC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGCACCTACAGCTCAGCAGCACCCCTGACCCCTGAGCAGCAGAGCTACCGAG 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
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101 SerPheAsnArgGlyGluCys 107
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Job time : 41.2012 secs

GenCore version 5.1.6  
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Run on: January 28, 2006, 08:46:13 ; Search time 4.09685 Seconds  
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Title: US-10-733-563-113

Perfect score: 564

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	553	98.0	107	US-10-866-383-8	Sequence 8, Appl
3	553	98.0	107	US-10-988-207-21	Sequence 21, Appl
4	553	98.0	107	US-11-025-712-5	Sequence 5, Appl
5	553	98.0	107	US-11-075-351-61	Sequence 61, Appl
6	553	98.0	107	US-11-061-821-40	Sequence 40, Appl
7	553	98.0	107	US-11-102-621-9	Sequence 9, Appl
8	553	98.0	110	US-11-024-251-27	Sequence 27, Appl
9	553	98.0	213	US-11-172-320-4	Sequence 4, Appl
10	553	98.0	213	US-11-172-320-8	Sequence 8, Appl

11	553	98.0	213	7	US-11-174-186-42	Sequence 42, Appl
12	553	98.0	213	7	US-11-120-338-13	Sequence 13, Appl
13	553	98.0	213	7	US-11-120-338-16	Sequence 16, Appl
14	553	98.0	213	7	US-11-173-969-4	Sequence 4, Appl
15	553	98.0	213	7	US-11-173-969-8	Sequence 8, Appl
16	553	98.0	213	7	US-11-102-621-118	Sequence 118, App
17	553	98.0	213	7	US-11-102-621-135	Sequence 135, App
18	553	98.0	213	7	US-11-107-028-31	Sequence 31, Appl
19	553	98.0	213	7	US-11-107-028-44	Sequence 44, Appl
20	553	98.0	213	7	US-11-106-820-24	Sequence 24, Appl
21	553	98.0	213	7	US-11-106-820-29	Sequence 29, Appl
22	553	98.0	213	7	US-11-106-820-44	Sequence 44, Appl
23	553	98.0	213	7	US-11-158-505-34	Sequence 34, Appl
24	553	98.0	214	7	US-11-025-712-11	Sequence 11, Appl
25	553	98.0	214	7	US-11-094-625-9	Sequence 9, Appl
26	553	98.0	214	7	US-11-102-621-129	Sequence 129, App
27	553	98.0	214	7	US-11-128-900-71	Sequence 71, Appl
28	553	98.0	214	7	US-11-154-337-14	Sequence 14, Appl
29	553	98.0	214	7	US-11-154-337-16	Sequence 16, Appl
30	553	98.0	215	7	US-11-102-621-141	Sequence 141, App
31	553	98.0	215	7	US-11-166-906-2	Sequence 2, Appl
32	553	98.0	215	6	US-10-923-327-6	Sequence 6, Appl
33	553	98.0	218	6	US-10-923-327-8	Sequence 8, Appl
34	553	98.0	218	6	US-10-923-327-10	Sequence 10, Appl
35	553	98.0	218	6	US-10-923-327-12	Sequence 12, Appl
36	553	98.0	218	6	US-10-923-327-17	Sequence 17, Appl
37	553	98.0	218	7	US-11-084-554-11	Sequence 11, Appl
38	553	98.0	218	7	US-11-158-505-4	Sequence 4, Appl
39	553	98.0	218	7	US-11-158-505-28	Sequence 28, Appl
40	553	98.0	218	7	US-11-004-590-229	Sequence 229, App
41	553	98.0	219	7	US-11-080-587-8	Sequence 8, Appl
42	553	98.0	232	7	US-11-106-820-23	Sequence 23, Appl
43	553	98.0	233	7	US-11-128-900-15	Sequence 15, Appl
44	553	98.0	233	7	US-11-128-900-67	Sequence 67, Appl
45	553	98.0	234	7	US-11-128-900-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-999-866-40

; Sequence 40, Application US/10999866

; Publication No. US20050266004A1

; GENERAL INFORMATION:

; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann

; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND

; FILE REFERENCE: CEN5042NP

; CURRENT APPLICATION NUMBER: US/10/999,866

; CURRENT FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: 60/527,794

; PRIOR FILING DATE: 2003-12-08

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 40

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(107)

; OTHER INFORMATION: Light chain kappa constant region (IgKc)

US-10-999-866-40

Alignment Scores:			
Pred. No.:	8.09e-49	Length:	107
Score:	553.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.05%	Indels:	0
DB:	6	Gaps:	0

US-10-733-563-113 (1-321) x US-10-999-866-40 (1-107)

Qy	1	CGTACGGTGGCTGCACCATCTGTCTCTTCATCTTTCCGCCCATCTGTAGAGCAGTGTGAATCT	60
Db	1	ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer	20
Qy	61	GGAATCGCTCTGTGTGTGCTGCTGTGTAATACTTCTATCCAGAGAGGCCAAAGTACAG	120
Db	21	GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln	40
Qy	121	TGGAAGTGGATAACGCCCTCCAAATCGSGTAACTCCAGGAGAGTGTACAGAGCAGGAC	180
Db	41	TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGlnSerValThrGluGlnAsp	60
Qy	181	AGCAAGAGACAGCACCTCAGAGCTCAGCAGCACCTCGACCTCAGCAAAACAGACATACGAG	240
Db	61	SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu	80
Qy	241	AAACACAAAGTCTACGCTCGGAAGTCACCCATCAGGGCTGAGCTCGCCCTGCACAAAG	300
Db	81	LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys	100
Qy	301	AGCTTCAACAGGGGAGAGTGT	321
Db	101	SerPheAsnArgGlyGluCys	107

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RESULT 2
US-10-886-383-8
; Sequence 8, Application US/10886383
; Publication No. US2006005571A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,383
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-383-8

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NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/025,712  
FILING DATE: 28-Dec-2004  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/404,286  
FILING DATE: 31-Mar-2003  
APPLICATION NUMBER: 09/811384  
FILING DATE: 20-DEC-2000  
APPLICATION NUMBER: 09/251652  
FILING DATE: 17-FEB-2000  
APPLICATION NUMBER: 08/788800  
FILING DATE: 22-JAN-1997  
APPLICATION NUMBER: 60/093038  
FILING DATE: 23-JAN-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Evans, David W.  
REGISTRATION NUMBER: NONE  
REFERENCE/DOCKET NUMBER: P1729C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1739  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-11-025-712-5

Alignment Scores:  
Pred. No.: 8,09e-49 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-025-712-5 (1-107)

Qy 1 CGTACGGTGGTGCACCATCTGCTTCATCTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAACCTGCTCTGTTGTGCTGCTGAATAACTTATCCAGAGAGCCCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAnPhePyrProArgGluAlaLysValGln 40  
Qy 121 TGGAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGAGAGAGTGTACAGAGCAGGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGCAGCTACAGCCTGAGCAGACCCCTGAGCAAGCAGTACAG 240  
Db 61 SerLysAspSerThrTyrrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
Qy 241 AACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100

Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 5  
US-11-075-351-61  
; Sequence 61, Application US/11075351  
; Publication No. US20050260716A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore, Margaret D.  
; APPLICANT: Fox, Brian A.  
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS  
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS  
; FILE REFERENCE: 02-16  
; CURRENT APPLICATION NUMBER: US/11/075,351  
; NUMBER OF SEQ ID NOS: 63  
; CURRENT FILING DATE: 2005-03-08  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-075-351-61

Alignment Scores:  
Pred. No.: 8,09e-49 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-075-351-61 (1-107)

Qy 1 CGTACGGTGGTGCACCATCTGCTTCATCTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAACCTGCTCTGTTGTGCTGCTGAATAACTTATCCAGAGAGCCCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAnPhePyrProArgGluAlaLysValGln 40  
Qy 121 TGGAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGAGAGAGTGTACAGAGCAGGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGCAGCTACAGCCTGAGCAGACCCCTGAGCAAGCAGTACAG 240  
Db 61 SerLysAspSerThrTyrrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
Qy 241 AACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 6

US-11-061-821-40  
; Sequence 40, Application US/11061821  
; Publication No. US20050266005A1  
; GENERAL INFORMATION:  
; APPLICANT: Heavner, George; Li, Li; Oneil, Karyn  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES  
; FILE REFERENCE: CEN5048 NP  
; CURRENT APPLICATION NUMBER: US/11/061,821  
; CURRENT FILING DATE: 2005-02-18  
; PRIOR APPLICATION NUMBER: 60/548,648  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver 3.3  
; SEQ ID NO 40

; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: MISC FEATURE  
 ; LOCATION: (1)..(107)  
 ; OTHER INFORMATION: Light chain kappa constant region (IgKc)  
 US-11-061-821-40

Alignment Scores:  
 Pred. No.: 8.09e-49 Length: 107  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-061-821-40 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTTCCCGCCATCTGATGACGAGTTCGAATCT 60  
 Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20  
 QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPhetyrProArgGluAlaLysValGln 40  
 QY 121 TGGAAAGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCACAGCAGGAC 180  
 Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
 QY 181 AGCAAGACACACCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGACGACTACGAG 240  
 Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80  
 QY 241 AAACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
 Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
 QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 101 SerPheAsnArgGlyGluCys 107

RESULT 7

US-11-102-621-9  
 ; Sequence 9, Application US/11102621  
 ; Publication No. US2005027679A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Protein Design Labs, Inc.  
 ; APPLICANT: Hinton, Paul R.  
 ; APPLICANT: Tsurushita, Naoya  
 ; APPLICANT: Tso, J. Yun  
 ; TITLE OF INVENTION: Vasequez, Maximiliano  
 ; TITLE OF INVENTION: ALTERATION OF FORN BINDING AFFINITIES OR SERUM HALF-LIVES OF  
 ; FILE REFERENCE: ANTIBODIES BY MUTAGENESIS  
 ; CURRENT APPLICATION NUMBER: US/11/102,621  
 ; PRIOR FILING DATE: 2005-04-08  
 ; PRIOR APPLICATION NUMBER: US 10/822,300  
 ; PRIOR FILING DATE: 2004-04-09  
 ; NUMBER OF SEQ ID NOS: 146  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 9  
 ; LENGTH: 107  
 ; TYPE: PRT  
 ; ORGANISM: artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Humanized antibody  
 US-11-102-621-9

Alignment Scores:  
 Pred. No.: 8.09e-49 Length: 107  
 Score: 553.00 Matches: 107

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-102-621-9 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTTCCCGCCATCTGATGACGAGTTCGAATCT 60  
 Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20  
 QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPhetyrProArgGluAlaLysValGln 40  
 QY 121 TGGAAAGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCACAGCAGGAC 180  
 Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
 QY 181 AGCAAGACACACCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGACGACTACGAG 240  
 Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80  
 QY 241 AAACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
 Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
 QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 101 SerPheAsnArgGlyGluCys 107

RESULT 8

US-11-024-251-27  
 ; Sequence 27, Application US/11024251  
 ; Publication No. US20050266425A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zauderer, Maurice  
 ; APPLICANT: Paris, Mark  
 ; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies  
 ; FILE REFERENCE: 1843.0230001  
 ; CURRENT APPLICATION NUMBER: US/11/024,251  
 ; CURRENT FILING DATE: 2004-12-29  
 ; PRIOR APPLICATION NUMBER: 60/533,241  
 ; PRIOR FILING DATE: 2003-12-31  
 ; NUMBER OF SEQ ID NOS: 129  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 27  
 ; LENGTH: 110  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: clambda Constant Domain  
 US-11-024-251-27

Alignment Scores:

Pred. No.: 8.1e-49 Length: 110  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-024-251-27 (1-110)

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 Db 4 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 23  
 QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db 24 GlyThrAlaSerValValCysLeuLeuAsnAsnPhetyrProArgGluAlaLysValGln 43  
 QY 121 TGGAAAGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCACAGCAGGAC 180

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Db 44 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 63
181 AGCAAGGACAGCACCTACAGCCCTCAGCAGCACCCCTGACCCTGAGCAAAAGCAGACTACGAG 240
Db 64 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 83
241 AAACACAAAGTCTAGCCTCGGAGTCAACCCATCAGGGCCTGAGTCGCCCTCAAAAG 300
Db 84 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 103
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 104 SerPheAsnArgGlyGluCys 110
RESULT 9
US-11-172-320-4
; Sequence 4, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-11-172-320-4
Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-113 (1-321) x US-11-172-320-4 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126
QY 61 GGAATCGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAsnPheTyrProArgGluAlaLysValGln 146
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
QY 181 AGCAAGGACAGCACCTACAGCCCTCAGCAGCACCCCTGAGCAAAAGCAGACTACGAG 240
Db 167 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
QY 241 AAACACAAAGTCTAGCCTCGGAGTCAACCCATCAGGGCCTGAGTCGCCCTCAAAAG 300
Db 104 SerPheAsnArgGlyGluCys 110
RESULT 11
US-11-174-186-42
; Sequence 42, Application US/11174186
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Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213
RESULT 10
US-11-172-320-8
; Sequence 8, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-11-172-320-8
Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-113 (1-321) x US-11-172-320-8 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126
QY 61 GGAATCGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAsnPheTyrProArgGluAlaLysValGln 146
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
QY 181 AGCAAGGACAGCACCTACAGCCCTCAGCAGCACCCCTGAGCAAAAGCAGACTACGAG 240
Db 167 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
QY 241 AAACACAAAGTCTAGCCTCGGAGTCAACCCATCAGGGCCTGAGTCGCCCTCAAAAG 300
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213
RESULT 11
US-11-174-186-42
; Sequence 42, Application US/11174186
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; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: light chain
US-11-174-186-42

Alignment Scores:
Pred. No.: 8.45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
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Query Match: 98.05% Indels: 0
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US-10-733-563-113 (1-321) x US-11-174-186-42 (1-213)
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Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146
QY 121 TGAAGTGGTAAACGGCTCCCAATCGGTTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 147 TrpLysValAseAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAse 166
QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
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QY 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCATCAGGAGCAGCAGCAGCAGCAGCAG 300
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QY 301 AGCTTCAACAGGGAGAGTGT 321
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RESULT 13
US-11-120-338-16
; Sequence 16, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 16
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-16

Alignment Scores:
Pred. No.: 8.45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0

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Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146
QY 121 TGAAGTGGTAAACGGCTCCCAATCGGTTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 147 TrpLysValAseAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAse 166
QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 167 SerLysAseSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAsePyrGlu 186
QY 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCATCAGGAGCAGCAGCAGCAGCAGCAG 300
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QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 207 SerPheAenArgGlyGluCys 213

RESULT 12
US-11-120-338-13
; Sequence 13, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
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Db 107 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 126
QY 61 GGAAGTGCCTGTTGTGTCCTGCTGTAATACTTCTATCCAGAGAGGCCAAAGTACAG 120
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RESULT 14
US-11-173-969-4
; Sequence 4, Application US/11173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf. G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: 4
US-11-173-969-4
Alignment Scores:
Pred. No.: 8.45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
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Db 127 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 146
QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAATCTCCAGAGAGTGTCCAGAGCAGGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166
QY 181 AGCAGGAGCAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
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QY 301 AGCTTCAACAGGGGAGAGTGT 321
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